

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 11858.6 Seconds  
(without alignments)  
10957.506 Million cell updates/sec

Title: US-10-728-051-1

Perfect score: 2032  
Sequence: 1 aataatcatatattcatc.....cggttgctgtttctcc 2032

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_env.\*

2: gb\_pat.\*

3: gb\_ph.\*

4: gb\_pl.\*

5: gb\_pr.\*

6: gb\_ro.\*

7: gb\_sts.\*

8: gb\_sy.\*

9: gb\_un.\*

10: gb\_vi.\*

11: gb\_ov.\*

12: gb\_htg.\*

13: gb\_in.\*

14: gb\_om.\*

15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2032	100.0	2032	2 AR257469	AR257469 Sequence
2	2032	100.0	2032	2 AR629098	AR629098 Sequence
3	2032	100.0	2032	2 AR716329	AR716329 Sequence
4	2032	100.0	2032	2 AX148742	AX148742 Sequence
5	2032	100.0	2032	4 ARQRAHI	L34402 Arachis hyp
6	2032	100.0	2041	2 AR257470	AR257470 Sequence
7	2019.2	99.4	2032	2 AX155331	AX155331 Sequence
8	1930	95.0	1930	2 BD107898	BD107898 Peanut al
9	1930	95.0	1930	2 BD172109	BD172109 Peanut al
10	1930	95.0	1930	2 AR257463	AX155332 Sequence
11	1805.2	88.8	1978	2 AX155332	AR257467 Sequence
12	1752.4	86.2	1949	2 AR629097	AR629097 Sequence
13	1752.4	86.2	1949	4 ARQRAH	L38853 Arachis hyp
14	1752.4	86.2	1949	4 AF432231	AF432231 Arachis h
15	1608	79.1	2674	4 AF432231	AF432231 Arachis h
16	1395.4	68.7	2332	4 AY581852	AY581852 Arachis h
17	1375.4	67.7	1418	4 AY581851	AY581851 Arachis h
18	954.4	47.0	1035	4 AY581850	AY581850 Arachis h

19	891.2	43.9	1047	4 AY581849	AY581849 Arachis h
20	750	36.9	750	2 AR257466	AR257466 Sequence
21	468.6	23.1	1257	4 LCUS51424	AJ551424 Lens culi
22	465.8	22.9	1433	4 PSVIC	Y00722 Pisum sativ
23	461	22.7	1561	4 VEVIC	Y00462 Vicia faba
24	455.4	22.4	1248	4 LCUS51425	AJ551425 Lens culi
25	449	22.1	1248	4 AJ626897	AJ626897 Pisum sat
26	449	22.1	1596	4 PSVICK	X67429 Pisum sativ
27	446	21.9	1791	4 AY500372	AY500372 Lupinus a
28	444.2	21.9	1248	4 AJ626898	AJ626898 Pisum sat
29	435.4	21.4	1548	4 VNVICLN	Z71987 V narbonens
30	408.4	20.1	1251	4 AB008679	AB008679 Glycine m
31	408.4	20.1	1350	2 AR714521	AR714521 Sequence
32	408.4	20.1	1412	4 AB197786	AB197786 Glycine m
33	408.4	20.1	3808	2 AR714525	AR714525 Sequence
34	408.4	20.1	3808	2 AR714526	AR714526 Sequence
35	406.8	20.0	1254	2 AR714452	AR714452 Sequence
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38	406.8	20.0	1320	2 AR202568	AR202568 Sequence
39	406.8	20.0	1320	2 AR486455	AR486455 Sequence
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41	406.8	20.0	1320	2 AR714443	AR714443 Sequence
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43	404	19.9	1818	2 BD175901	BD175901 Regulatio
44	404	19.9	1818	2 AR202566	AR202566 Sequence
45	404	19.9	1818	2 AR486453	AR486453 Sequence

ALIGNMENTS

RESULT 1  
AR257469  
LOCUS AR257469 2032 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 21 from patent US 6486311.  
ACCESSION AR257469  
VERSION AR257469.1 GI:27307482  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2032)  
AUTHORS Burks,A.W. Jr., Stanley,J.S., Cockrell,G., King,N.E., Sampson,H.A.,  
Helm,R.M. and Bannon,G.A.  
TITLE Peanut allergens and methods  
JOURNAL Patent: US 6486311-A, 21 26-NOV-2002;  
Mc. Sinai School of Medicine and University of Arkansas; New York,  
NY

FEATURES  
source Location/Qualifiers  
1..2032  
/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	AATAATCATATATATTCATCATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGAG	60
Qy	61	GGTTTCTCCACTGATGCTGTGTCTAGGATCCCTTGTCTGCTTTCAGTTTCTGCAACGCA	120
Db	61	GGTTTCTCCACTGATGCTGTGTCTAGGATCCCTTGTCTGCTTTCAGTTTCTGCAACGCA	120
Qy	121	TGCCAAGTCATCACCTTACAGAGAAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA	180
Db	121	TGCCAAGTCATCACCTTACAGAGAAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA	180
Qy	181	GAGTTCTCAACAGGACCGATGACTTGAAGCAAAAGGATGCGAGTCTCGCTGCACCAA	240

Db	181	GAGTTGTCAACACAGAAACCGGATGACCTTGAAGCAAAAAGGCATGCGAGTCTCGCTGCAACCA	240
Qy	241	GCTTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACACATGGCACCAACCAACCA	300
Db	241	GCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACACATGGCACCAACCAACCA	300
Qy	301	ACGTTCCCTCCAGGGGAGCGGACACGTCGCCGCCAACCCGGAGACTACGATGATGACCG	360
Db	301	ACGTTCCCTCCAGGGGAGCGGACACGTCGCCGCCAACCCGGAGACTACGATGATGACCG	360
Qy	361	CCGTCAACCCCGAAGAGAGAAAGGCGCGATGCGGACACAGCTGGACCCGAGGGAGCGTGA	420
Db	361	CCGTCAACCCCGAAGAGAGAAAGGCGCGATGCGGACACAGCTGGACCCGAGGGAGCGTGA	420
Qy	421	AAGAGAAGAGACTGGAGACAACCAAGAGAGAAGATTGGAGGCGACCAAGTCATCAGCAGCC	480
Db	421	AAGAGAAGAGACTGGAGACAACCAAGAGAGAAGATTGGAGGCGACCAAGTCATCAGCAGCC	480
Qy	481	ACGGAATAAGGCCCGAAGGAAGAGAAAGAGAAACAGAGTGGGGAACACCAGGTAGCCA	540
Db	481	ACGGAATAAGGCCCGAAGGAAGAGAAAGAGTGGGGAACACCAGGTAGCCA	540
Qy	541	TGTGAGGGAAGAAACATCTCGGAACAACCCCTTTCTACTTCCCGTCAAGGCGGTTTAGCAC	600
Db	541	TGTGAGGGAAGAAACATCTCGGAACAACCCCTTTCTACTTCCCGTCAAGGCGGTTTAGCAC	600
Qy	601	CCGCTACGGGAACCAAAACGGTAGGATCGGGTCTCGAGAGGTTTGAACAAAGGTCAAG	660
Db	601	CCGCTACGGGAACCAAAACGGTAGGATCGGGTCTCGAGAGGTTTGAACAAAGGTCAAG	660
Qy	661	CGAGTTTCAGAACTCCAGNAATCACCGTATGTGCGAGATCGAGGCCCAACCTAACACTCT	720
Db	661	CGAGTTTCAGAACTCCAGNAATCACCGTATGTGCGAGATCGAGGCCCAACCTAACACTCT	720
Qy	721	TGTTCTTCCCAAGCAGCTGATCTGATAACATCTTGTGTTATCCAGCAAGGGCAAGCCAC	780
Db	721	TGTTCTTCCCAAGCAGCTGATCTGATAACATCTTGTGTTATCCAGCAAGGGCAAGCCAC	780
Qy	781	CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTTAACTTTGACGAGGGCCATGCAT	840
Db	781	CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTTAACTTTGACGAGGGCCATGCAT	840
Qy	841	CAGAAATCCGATCCGGTTTCATTTCTTACATCTTGAACCGGCATGACAAACAGAACTCAG	900
Db	841	CAGAAATCCGATCCGGTTTCATTTCTTACATCTTGAACCGGCATGACAAACAGAACTCAG	900
Qy	901	AGTAGCTAAAATCTCCATGCCCGTTAACACACCCGGCCAGTTTGAGGATTTCTTCCCGGC	960
Db	901	AGTAGCTAAAATCTCCATGCCCGTTAACACACCCGGCCAGTTTGAGGATTTCTTCCCGGC	960
Qy	961	GAGCAGCCGAGACCAATCATCTTTCAGGGCTTCAGAGGAATACGTTGGAGGCGC	1020
Db	961	GAGCAGCCGAGACCAATCATCTTTCAGGGCTTCAGAGGAATACGTTGGAGGCGC	1020
Qy	1021	CTTCAATCCGGAATCAATCAGATACGGAGGGTCTGTTAGAGAGAAATGACGAGGTGA	1080
Db	1021	CTTCAATCCGGAATCAATCAGATACGGAGGGTCTGTTAGAGAGAAATGACGAGGTGA	1080
Qy	1081	GCAAGAGGAGAGGGCAGAGGCGATGAGTACTCGGAGTAGTGAGAAACAATGAAGAGT	1140
Db	1081	GCAAGAGGAGAGGGCAGAGGCGATGAGTACTCGGAGTAGTGAGAAACAATGAAGAGT	1140
Qy	1141	GATAGTCAAAAGTGTCAAAGAGACAAGTTGAAGAACTTACTTAAGACCGCTAAATCCGTTCT	1200
Db	1141	GATAGTCAAAAGTGTCAAAGAGACAAGTTGAAGAACTTACTTAAGACCGCTAAATCCGTTCT	1200
Qy	1201	AAGAAAGGCTCCGAGAGAGAGGAGATATCACCAACCCCAATCACTTGAGAGAGGCGA	1260
Db	1201	AAGAAAGGCTCCGAGAGAGAGGAGATATCACCAACCCCAATCACTTGAGAGAGGCGA	1260
Qy	1261	GCCCGATCTTTCTAAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAACCC	1320
Db	1261	GCCCGATCTTTCTAAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAACCC	1320

Qy	1321	CCAGCTTCAGGACCTGGACATGATGCTACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT	1380
Db	1321	CCAGCTTCAGGACCTGGACATGATGCTACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT	1380
Qy	1381	GCTCCACACTTCAACTCAAGGCCATGTTATCGTCGTCGTCACAAAGGAACCTGAAA	1440
Db	1381	GCTCCACACTTCAACTCAAGGCCATGTTATCGTCGTCGTCACAAAGGAACCTGAAA	1440
Qy	1441	CCTTGAATCTCGTGGCTTGAAGAAAAGAGCAACAAACAGAGGGGACGGCGGAAGAGGA	1500
Db	1441	CCTTGAATCTCGTGGCTTGAAGAAAAGAGCAACAAACAGAGGGGACGGCGGAAGAGGA	1500
Qy	1501	GGACGAAGACGAAGAGAGGAGGAAGTAACAGAGAGGTCGTAGTAGTACACAGCGAGGTT	1560
Db	1501	GGACGAAGACGAAGAGAGGAGGAAGTAACAGAGAGGTCGTAGTAGTACACAGCGAGGTT	1560
Qy	1561	GAGGAAGCGGATGCTTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCCTC	1620
Db	1561	GAGGAAGCGGATGCTTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCCTC	1620
Qy	1621	CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAAAACAACCCAGAAATCTTCTTGC	1680
Db	1621	CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAAAACAACCCAGAAATCTTCTTGC	1680
Qy	1681	AGGTGATAAGGACAATGTGATAGACAGATAGAGAAAGCAAGCAAGGATTTAGCATCCC	1740
Db	1681	AGGTGATAAGGACAATGTGATAGACAGATAGAGAAAGCAAGCAAGGATTTAGCATCCC	1740
Qy	1741	TGGTCCGGTGAACAAGTTGAGAAGCTCATCAAAAACCAAGAGAAATCTCACCTTTGTGAG	1800
Db	1741	TGGTCCGGTGAACAAGTTGAGAAGCTCATCAAAAACCAAGAGAAATCTCACCTTTGTGAG	1800
Qy	1801	TGCTCGTCTCAATCTCAATCTCAATCTCCGTCGTCTCTCGTGAAGAAAGTCTCCTGAGAA	1860
Db	1801	TGCTCGTCTCAATCTCAATCTCAATCTCCGTCGTCTCTCGTGAAGAAAGTCTCCTGAGAA	1860
Qy	1861	AGAGGATCAAGAGGAGGAAAAACCAAGGAGGAGGGTCCACTCTTCAATTTTGAAGGC	1920
Db	1861	AGAGGATCAAGAGGAGGAAAAACCAAGGAGGAGGGTCCACTCTTCAATTTTGAAGGC	1920
Qy	1921	TTTTAACTGAGATGAGGCAACTTGTATGATCGATAATAAGATCAAGCTTTTGTACT	1980
Db	1921	TTTTAACTGAGATGAGGCAACTTGTATGATCGATAATAAGATCAAGCTTTTGTACT	1980
Qy	1981	CTACTATCAAAAACTTATCAATAAAAAAGTTTGTGCGTTTCTCC	2032
Db	1981	CTACTATCAAAAACTTATCAATAAAAAAGTTTGTGCGTTTCTCC	2032

RESULT 2

AR629098	AR629098	2032 bp	mRNA	linear	PAT 14-FEB-2005
LOCUS	Sequence 5 from patent US 6835824.				
DEFINITION	AR629098				
ACCESSION	AR629098.1				
VERSION	GI:59756573				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2032)				
AUTHORS	Burks,A.W. Jr., Stanley,J.S., Bannon,G.A., Cockrell,G. and Helm,R.M.				
TITLE	Peanut allergens and methods				
JOURNAL	Patent: US 6835824-A 5 28-DEC-2004;				
FEATURES	University of Arkansas; Little Rock, AR				
	Location/Qualifiers				
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source		/organism="unknown"			
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ORIGIN

Query Match 100.0%; Score 2032; DB 2; Length 2032;

		Best Local Similarity 100.0%; Pred. No. 0;				Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	AAATAATCATATATATATCATCAATCATCTATATATAGTAGTACGAGGAGCAATGAGAGGAG	60						
Db	1	AAATAATCATATATATATCATCAATCATCTATATATAGTAGTACGAGGAGCAATGAGAGGAG	60						
Qy	61	GGTTTCTCCACTGATGCTGTGTGCTAGGATCCTTTGCTCCTGGCTTCAGTTTCTGCAACGCA	120						
Db	61	GGTTTCTCCACTGATGCTGTGTGCTAGGATCCTTTGCTCCTGGCTTCAGTTTCTGCAACGCA	120						
Qy	121	TGCCAGTCTACCTTACAGAGAGAAACAGAGAACCCCTGGCCGAGAGGTGCCTCCA	180						
Db	121	TGCCAGTCTACCTTACAGAGAGAAACAGAGAACCCCTGGCCGAGAGGTGCCTCCA	180						
Qy	181	GAGTTGTCAACAGGAAACCGGATGACTTGAAGCAAAAGGCGATCGAGTCTCGCTGCACCAA	240						
Db	181	GAGTTGTCAACAGGAAACCGGATGACTTGAAGCAAAAGGCGATCGAGTCTCGCTGCACCAA	240						
Qy	241	GCTCGAGTATGATCCTCGTTGTGTATGATCTCTCGAGGACACACTGGCACCAACCA	300						
Db	241	GCTCGAGTATGATCCTCGTTGTGTATGATCTCTCGAGGACACACTGGCACCAACCA	300						
Qy	301	ACGTTCCCTCCAGGAGCGGACACGTGGCGGCCAACCCGGAGACTACGATGATGCCG	360						
Db	301	ACGTTCCCTCCAGGAGCGGACACGTGGCGGCCAACCCGGAGACTACGATGATGCCG	360						
Qy	361	CCGTCAACCCCGAAGAGGAGGCGCGATGGGACACAGCTGGACCCGAGGAGCGTGA	420						
Db	361	CCGTCAACCCCGAAGAGGAGGCGCGATGGGACACAGCTGGACCCGAGGAGCGTGA	420						
Qy	421	AAGAGAGAAAGACTGGAGACAAACCAAGAGAAGATTGGAGGCGACCAAGTCAATCAGCAGCC	480						
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Qy	661	GCAGTTTCAGAACTCTCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTAACACTCT	720						
Db	661	GCAGTTTCAGAACTCTCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTAACACTCT	720						
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Db	781	CGTGACCGTAGCAATAGCAATTAACAGAAAGAGCTTTAATCTTTGACGAGGCGCATGCAC	840						
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Db	841	CAGAAATCCCATCGGTTTCAATCTTACATCTTGAACCGCCATGACCAACAGAACTCTCAG	900						
Qy	901	AGTAGCTAAATCTCCATGCGCGTTTACACACCCGCGCAGTTTGAGGATTTCTTCCCGGC	960						
Db	901	AGTAGCTAAATCTCCATGCGCGTTTACACACCCGCGCAGTTTGAGGATTTCTTCCCGGC	960						
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Db	961	GAGCAGCCGAGACCAATCTACTTTGAGGCGTTTCAGCAGGAATACGTTGGAGGCGC	1020						
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RESULT 3  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION

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Sequence 5 from patent US 6943010.  
AR716329.1 GI:77364704

2032 bp  
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linear  
PAT 07-OCT-2005

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1441	CCTTGAACCTCGTGGCTGTAAAGAAAGAGCAACCAAGAGGGGACGGCGGAAGAGAGGA	1500
1501	GGAAGAGAGCAAGAGAGAGAGAGAGTAAACAGAGAGTCCGTAGGTACACAGCGAGTT	1560
1501	GGAAGAGAGCAAGAGAGAGAGAGAGTAAACAGAGAGTCCGTAGGTACACAGCGAGTT	1560
1561	GAAGGAGGCGATGCTTCATCATGCGCAGCATCCAGTAGCCATCAACGCTTCTTCC	1620
1561	GAAGGAGGCGATGCTTCATCATGCGCAGCATCCAGTAGCCATCAACGCTTCTTCC	1620
1621	CGAATCTCAATCTCTTGGCTTCGGTATCAACCGCTGAAAAACCAACACAGAAATCTTCTTGC	1680
1621	CGAATCTCAATCTCTTGGCTTCGGTATCAACCGCTGAAAAACCAACACAGAAATCTTCTTGC	1680
1681	AGGTGATAGGACAAATGTGATAGACAGATAGAGAGCAAGCAAGCAAGATTTAGCATTTCC	1740
1681	AGGTGATAGGACAAATGTGATAGACAGATAGAGAGCAAGCAAGCAAGATTTAGCATTTCC	1740
1741	TGGGTCGGGTGACAAAGTTGAGAGCTCATCAAAACCAAGAGAAATCTCACCTTTGTAG	1800
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1801	TGCTCGCTCAATCTCAATCTCAATCTCGCTCGTCTCTCTGAGAAAGAGTCTCTGAGAA	1860
1801	TGCTCGCTCAATCTCAATCTCAATCTCGCTCGTCTCTCTGAGAAAGAGTCTCTGAGAA	1860
1861	AGAGGATCAAGAGGAGGAGAAACCAAGAGGAGAGGTCCACTCTCTTCAATTTTGAAGGC	1920
1861	AGAGGATCAAGAGGAGGAGAAACCAAGAGGAGAGGTCCACTCTCTTCAATTTTGAAGGC	1920
1921	TTTTTAATCGAATGAGGCACTTCTGATCGATATGATATGATATGATATGATATGATATG	1980
1921	TTTTTAATCGAATGAGGCACTTCTGATCGATATGATATGATATGATATGATATGATATG	1980
1981	CTACTATCAAAAACTTATCAATATAAATAAAAACTTTGTGCGTTGTTTCTCC	2032
1981	CTACTATCAAAAACTTATCAATATAAATAAAAACTTTGTGCGTTGTTTCTCC	2032





QY 1921 TTTTAACTGAGAACTGGAGGCAACTTGTATGTATCGATAATAAGATCACGCTTTGTACT 1980  
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RESULT 4  
AX148742 AX148742 2032 bp DNA linear PAT 08-JUN-2001  
LOCUS  
DEFINITION Sequence 5 from Patent WO0136621.  
ACCESSION AX148742  
VERSION AX148742.1 GI:14347296  
KEYWORDS  
SOURCE Arachis hypogaea (peanut)  
ORGANISM Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.  
1  
REFERENCE  
AUTHORS Dodo,H.W., Arntzen,C.J., Konan,K.N. and Viquez,O.M.  
TITLE Down-regulation and silencing of allergen genes in transgenic  
peanut seeds  
JOURNAL Patent: WO 0136621-A 5 25-MAY-2001;  
Alabama A & M University (US)  
FEATURES  
source Location/Qualifiers  
1. 2032  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 301 ACGTTCCTCCAGGGAGCGGACAGTGGCCGCCAACCCGGAGACTACGATGATGACCG 360  
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DEFINITION Arachis hypogaea (clone P41b) Ara h I mRNA, complete cds.

ACCESSION L34402  
VERSION L34402.1 GI:602435  
KEYWORDS allergen.  
SOURCE Arachis hypogaea (peanut)  
ORGANISM Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.

REFERENCE 1 (bases 1 to 2032)  
AUTHORS Burke,A.W., Cockrell,G., Stanley,J.S., Helm,R.M. and Bannon,G.A.  
TITLE Recombinant peanut allergen Ara h I expression and IgE binding in patients with peanut hypersensitivity  
J. Clin. Invest. 96 (4), 1715-1721 (1995)  
7560062  
COMMENT On Dec 16, 1994 this sequence version replaced gi:508640.  
Original source text: Arachis hypogaea (strain Florunner).

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ACCESSION AR257470  
VERSION AR257470.1 GI:27307483  
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REFERENCE 1 (bases 1 to 2041)  
AUTHORS Burks,A.W. Jr., Stanley,J.S., Cockrell,G., King,N.E., Sampson,H.A.,  
Heim,R.M. and Bannion,G.A.  
TITLE Peanut allergens and methods  
JOURNAL Patent: US 6486311-A 23 26-NOV-2002;  
Mt. Sinai School of Medicine and University of Arkansas; New York,  
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AUTHORS	Bannon, G.A., Burks, W.A., Caplan, M.J., Sampson, H. and Sosin, H.		
TITLE	Peptide antigens		
JOURNAL	Patent: WO 0140264-A 4 07-JUN-2001;		
	Panacea Pharmaceuticals, LLC (US); The University of Arkansas (US); MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY UNIVERSITY OF NEW YORK (US)		
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JOURNAL	
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Methods and reagents for decreasing allergic reactions.  
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Sosin H., Banon G.A., Jr. W.A.B. and Samphson, H.A.  
Methods and reagents for decreasing allergic reactions  
Patent: JP 2002501748-A 1 22-JAN-2002;  
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VERSION AX155332.1 GI:14536767
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Aeschynomeneae; Arachis.
REFERENCE 1
AUTHORS Bannon, G.A.; Burks, W.A.; Caplan, M.J.; Sampson, H. and Sosin, H.
TITLE Peptide antigens
JOURNAL Patent: WO 0140264-A 5 07-JUN-2001;
Panacea Pharmaceuticals, LLC (US); The University of Arkansas (US)
; MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY UNIVERSITY OF NEW YORK
(US)
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QY 1488 GGGAA-----GAAGAGGAGGAGCAACAGCAAGAGAGGAGGAGGAAGTAAACAGAGAGG 1538  
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QY 1539 TGGGTAGGTACACAGCGAGGTTGAAGGAAGCGGATGTGTTTCATCATGCCAGCAGCTCATC 1598  
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Db 1876 AATAAGATCACGCTTTTGTAACTTACTATCCAAAACTTATCAATAAATAAACAACGTTTG 1935  
QY 2019 TCGGTTGTTTCTCC 2032  
Db 1936 TCGGTTGTTTCTCC 1949

## RESULT 14

ARQARAH  
LOCUS Arachis hypogaea (clone p17) Ara h I mRNA linear PLN 10-JAN-1995  
DEFINITION Arachis hypogaea (clone p17) Ara h I mRNA, complete cds.  
ACCESSION L38853.1 GI:620024  
VERSION L38853.1  
KEYWORDS peanut hypersensitivity.  
SOURCE Arachis hypogaea (peanut)  
ORGANISM Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.  
REFERENCE 1 (bases 1 to 1949)  
AUTHORS Burke,A.W., Cockrell,G., Stanley,J.S., Helm,R.M. and Bannon,G.A.  
TITLE Recombinant peanut allergen Ara h I expression and IgE binding in  
patients with peanut hypersensitivity  
JOURNAL Unpublished (1994)  
COMMENT Original source text: Arachis hypogaea (strain Florunner) Seed cDNA  
to mRNA.

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## gene

## 5'UTR

## CDS







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Qy 945 ---- AGGATTTCTTCCGGCGAGCAGCGAGCAACATCATCTTTCAGGGCTTCAGC 1000
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Qy 1001 AGGAATACGTTGGAGGCGCCCTTCAAT----- 1027
Db 1362 AGGAATACGTTGGAGGCGCCCTTCAATGTAAGCAAAATGTATCATATTAGGAATTTAAAT 1421
Qy 1028 ----- GCGAATTTCAATCAGATAC 1046
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Qy 1047 GGAGGGTGCTGTTAGAAGAGAAATCAGGAGGTGAGCAAGAGGAGAGGGCGAGAGGCGAT 1106
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Qy 1107 GGAGTACTCGGAGTAGTGAGAAACAATGAAGAGGTAGTAGTCAAAGTGTCAAAGAGCACG 1166
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Qy 1167 TTGAAGAACTTACTAAGCAGCTAAATCCGTCTCAAAGAAAGGCTCCGAAGAGAGGGAG 1226
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Qy 1647 TCAACGCTGAAAAACAACAAGATCTTCTTCAGGTGATAAGGACAATGTGATAGCC 1706
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Qy 1707 AGATAGAGAGCAAGCAAGGATTTAGCATTTCCCTGGGTGGGTGAACAAGTTGAGNAGC 1766
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Job time : 11863.6 secs



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2006, 09:14:45 ; Search time 905.436 Seconds  
(without alignments)

15647.278 Million cell updates/sec

Title: US-10-728-051-1

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N Geneseq\_8:\*
- 1: Geneseqn1980s:\*
  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001as:\*
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  - 13: Geneseqn2004bs:\*
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  - 15: Geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2032	100.0	2032	4	Aaf90339 Peanut al
2	2032	100.0	2032	8	Abx70603 Peanut Ar
3	2032	100.0	2032	10	Adg27462 Peanut Ar
4	2032	100.0	2032	14	Adv97537 Peanut Ar
5	2032	100.0	2040	14	Adv97600 Peanut Ar
6	2032	100.0	2041	4	Aas08537 DNA encod
7	2025.6	99.7	2032	2	Aat76613 Peanut al
8	1930	95.0	1930	2	Aaz06382 Peanut al
9	1752.4	86.2	1949	2	Aat76612 Peanut al
10	1752.4	86.2	1949	8	Abx70604 Peanut Ar
11	1752.4	86.2	1949	14	Adv97536 Peanut Ar
12	1750.8	86.2	1949	10	Adg27463 Peanut Ar
13	1749.8	86.1	1952	4	Aas08539 Anaphylac
14	1324	65.2	1340	14	Adv97605 Peanut Ar
15	408.4	20.1	1251	6	Abx55196 Glycine m
16	406.8	20.0	1254	9	Acc49562 Mature be
17	406.8	20.0	1278	9	Acc49561 FLAG-tag9
18	406.8	20.0	1320	2	Aav17564 Coding se

19	406.8	20.0	1320	9	Acc49553	Glycine m
20	404	19.9	1632	6	Abx55198	Glycine m
21	404	19.9	1818	2	Aav17562	Coding se
22	404	19.9	2073	13	Adt17970	Plant cdn
23	402	19.8	1680	6	Abx55197	Glycine m
24	390	19.2	1656	13	Adx14996	Plant ful
25	324.2	16.0	1920	2	Aav17563	Coding se
26	293.4	14.4	1107	13	Adx13542	Plant ful
27	279.8	13.8	1088	13	Adx13070	Plant ful
28	279.4	13.7	1083	13	Adx131954	Plant ful
29	279.2	13.7	1079	13	Adx13568	Plant ful
30	267	13.1	1037	13	Adx32038	Plant ful
31	263.8	13.0	1034	13	Adx31953	Plant ful
32	260.4	12.8	1024	13	Adx13111	Plant ful
33	247.8	12.2	1011	13	Adx13980	Plant ful
34	233	11.5	951	13	Adx14004	Plant ful
35	214.8	10.6	863	13	Adx13015	Plant ful
36	214.8	10.6	880	13	Adx13092	Plant ful
37	214.8	10.6	934	13	Adx12354	Plant ful
38	199.6	9.8	720	13	Adx32347	Plant ful
39	186	9.2	673	13	Adx13078	Plant ful
40	167.2	8.2	641	13	Adx13996	Plant ful
41	160.2	7.9	2140	2	Aav42316	Macadamia
42	158.2	7.8	614	13	Adx13556	Plant ful
43	157.4	7.7	2171	2	Aav42311	Macadamia
44	152.6	7.5	2171	2	Aav42310	Macadamia
45	141.8	7.0	536	13	Adx13016	Plant ful

ALIGNMENTS

RESULT 1

AAF90339

ID AAF90339 standard; cdna; 2032 BP.

XX AAF90339;

XX 11-SEP-2003 (revised)

DT 23-JUL-2001 (first entry)

XX Peanut allergen Ara hl P41B cdna.

DE Peanut; allergen; Ara hl P41B; transgenic plant; allergy; ss.

XX Arachis hypogaea.

OS Key

FT misc\_feature

FT Location/Qualifiers

FT /tag= a

FT /note= "PCR amplified fragment"

XX WO200136621-A2.

XX 25-MAY-2001.

PD 20-NOV-2000; 2000WO-US031657.

XX 19-NOV-1999; 99US-0167255P.

XX (UYAL-) UNIV ALABAMA A & M.

PA Dodo HW, Arntzen CJ, Konan KN, Viquez OM;

XX WPI; 2001-355630/37.

XX Producing transgenic peanut plants that produce allergen-free seeds,

PT useful in non-allergenic foods, by antisense or sense co-suppression of

PT allergen-encoding genes.

XX Claim 20; Fig 5; 72pp; English.

PS The present sequence is that of peanut allergen Ara hl P41B cdna. A

XX

CC

CC portion of this gene is homologous to the corresponding region of the  
CC peanut allergen Ara hi P17 gene. This region has been PCR amplified,  
CC cloned in transformation vectors (pUC18 and pBl434) in sense and  
CC antisense orientations and used to down-regulate Ara hi P41B and Ara hi  
CC P17 allergens in peanut. This is an example of the method of the  
CC invention, which relates to the production of a peanut plant having  
CC reduced, or undetectable, allergenic protein (AP) content in its seed. A  
CC peanut plant cell is transformed with a DNA construct containing an  
CC antisense AP gene and/or sense AP gene, or their fragments, regenerated  
CC to plants, and fertile transgenic plants that produce seeds with reduced  
CC AP content are identified. The seeds are useful for preparation of  
CC allergen-free foods. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 2032 BP; 628 A; 473 C; 530 G; 401 T; 0 U; 0 Other;

Query Match 100.0%; Score 2032; DB 4; Length 2032;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GGTTCCTCCACTGATGCTGTGCTAGGGATCCTTGTCTGGCTTCAGTTTCTGCAACGCA 120  
QY 121 TGCCAAGTCATCACTTACAGAGAAACAGAGAACCCCTGCGCCAGAGGTGCTCTCA 180  
DB 121 TGCCAAGTCATCACTTACAGAGAAACAGAGAACCCCTGCGCCAGAGGTGCTCTCA 180  
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DB 181 GAGTTGTCAACAGAAACCGGATGACTTTGAAGCAAAAGGCATGCGAGTCTCGTGCACCAA 240  
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Db |||||  
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## RESULT 2

ABX70603

ID ABX70603 standard; cDNA; 2032 BP.

XX AC

XX ABX70603;

XX XX

XX 26-MAR-2003 (first entry)

XX DE

XX Peanut Ara h1 cDNA clone P41b.

XX DT

XX Peanut; ss; allergy; Ara h1; Ara h2; Ara h3; gene; IgE binding site;  
KW anaphylactic food allergen; antiallergenic; vaccine; wound healing.

XX KW

XX XX

XX Arachis hypogaea.

XX OS

XX XX

XX WO200274250-A2.

XX PN

XX XX

XX 26-SEP-2002.

XX PD

XX XX

XX 18-MAR-2002; 2002WO-US009108.

XX PF

XX XX

XX 16-MAR-2001; 2001US-0276822P.

XX PR

XX 18-MAR-2002; 2002US-00276822.

XX PR

XX XX

XX (PANA-) PANACEA PHARM.

XX PA

XX XX

XX Caplan M, Sosin H, Sampson H, Bannon GA, Burks WA, Cockrell G;  
PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;  
PI Rabinjohn PA, Shin DS, Stanley JS;

XX XX

XX WPI; 2003-018765/01.

XX DR

XX P-PSDB; ABUS2412.

XX DR

XX XX

XX New modified anaphylactic food allergen, useful for preventing or  
PT treating allergic reactions associated with e.g. anaphylactic allergens.

XX PT

XX XX

XX Example 3; Fig 10; 300pp; English.

XX PS

XX XX

XX The invention relates to a modified anaphylactic food allergen has an  
CC amino acid sequence that is substantially identical to that of natural  
CC anaphylactic food allergen, except for a cysteine residue that has been  
CC modified so that it cannot participate in the disulphide bond. The  
CC modification may also comprise mutation of the IgE binding sites to  
CC reduce allergenicity. Also included are: (1) a method of making a  
CC modified anaphylactic food allergen; (2) a nucleotide molecule encoding  
CC or for causing a site specific mutation in the modified anaphylactic food  
CC allergen; (3) a transgenic plant or animal expressing the modified  
CC anaphylactic food allergen; (4) a method of treating an individual by  
CC reducing the clinical response to a natural anaphylactic food allergen;  
CC and an isolated fragment of peanut allergen Ara h 1. The modified  
CC anaphylactic food allergen is useful for preventing or treating allergic  
CC reactions associated with any natural allergen such as food, insect,  
CC rubber or preferably anaphylactic allergens. It is also useful for  
CC treating wounds in mammals such as bovine, canine, feline, caprine,  
CC ovine, porcine, murine or equine species. The present sequence is a cDNA  
CC encoding a peanut allergen (e.g. Ara h1, h2 or h3)

XX XX

XX Sequence 2032 BP; 628 A; 473 C; 530 G; 401 T; 0 U; 0 Other;

XX SQ

XX Query Match 100.0%; Score 2032; DB 8; Length 2032;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATAATCATATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGAG 60  
Db |||||  
1 AATAATCATATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGAG 60  
Qy 61 GGTTCCTCCTCACTGATGCTGTGTAGGATCCTTGTCTGCTTTCAGTTTCTGCAACGCA 120  
Db |||||  
61 GGTTCCTCCTCACTGATGCTGTGTAGGATCCTTGTCTGCTTTCAGTTTCTGCAACGCA 120  
Qy 121 TGCAAGTCATCATCACTTTACCCAGAGAGAAACAGAGAGACCCCTGCGCCAGAGGTGCTCCA 180  
Db |||||  
121 TGCAAGTCATCATCACTTTACCCAGAGAGAAACAGAGAGACCCCTGCGCCAGAGGTGCTCCA 180  
Qy 181 GAGTTGTCAAACAGAGAACCCGATGACCTTGAAGAAAAGGATGCGAGTCTCGCTGCACCAA 240  
Db |||||  
181 GAGTTGTCAAACAGAGAACCCGATGACCTTGAAGAAAAGGATGCGAGTCTCGCTGCACCAA 240  
Qy 241 GCTCGAGTATGATCCTCGTTGTCTATGATCTCGAGGACACACTGGCACCAACCA 300  
Db |||||  
241 GCTCGAGTATGATCCTCGTTGTCTATGATCTCGAGGACACACTGGCACCAACCA 300  
Qy 301 ACCTTCCCTCCAGGGGAGCGGACACGTGGCCGCCAACCCGGAGACTACGATGATGACCG 360  
Db |||||  
301 ACCTTCCCTCCAGGGGAGCGGACACGTGGCCGCCAACCCGGAGACTACGATGATGACCG 360  
Qy 361 CCCTCAACCCCGAAGAGAGAGGAGCCCGATGGGACACAGCTGGACCCGAGGGAGCGTGA 420  
Db |||||  
361 CCCTCAACCCCGAAGAGAGAGGAGCCCGATGGGACACAGCTGGACCCGAGGGAGCGTGA 420  
Qy 421 AAGAGAGAGAGACTGGAGACCAACAGAGAGAGATTGGAGGCGACCAAGTCTATCAGCAGCC 480  
Db |||||  
421 AAGAGAGAGAGACTGGAGACCAACAGAGAGAGATTGGAGGCGACCAAGTCTATCAGCAGCC 480  
Qy 481 ACGGAAAAATAAGGCCCGAAG 540  
Db |||||  
481 ACGGAAAAATAAGGCCCGAAG 540  
Qy 541 TGTGAGGAGAGAAACATCTCGGAAACACCCCTTTCTACTTCCCGTCAAGGCGGTTAGCAC 600  
Db |||||  
541 TGTGAGGAGAGAAACATCTCGGAAACACCCCTTTCTACTTCCCGTCAAGGCGGTTAGCAC 600  
Qy 601 CCGCTACGGGAGCAAAACCGGTAGGATCCGGGTCTCGAGAGGTTTGACCAAGGTCAAG 660  
Db |||||  
601 CCGCTACGGGAGCAAAACCGGTAGGATCCGGGTCTCGAGAGGTTTGACCAAGGTCAAG 660  
Qy 661 GCAGTTTTCAGAAATCTCCAGAAATCACCGTATTGTGAGAGTCCAGGCCCAACCTAACCTCT 720  
Db |||||  
661 GCAGTTTTCAGAAATCTCCAGAAATCACCGTATTGTGAGAGTCCAGGCCCAACCTAACCTCT 720  
Qy 721 TGTTCCTCCCAAGCAGCTGATGCTGATAACATCTTGTATCCAGCAAGGCAAGCCAC 780  
Db |||||  
721 TGTTCCTCCCAAGCAGCTGATGCTGATAACATCTTGTATCCAGCAAGGCAAGCCAC 780  
Qy 781 CGTGACCGTAGCAAAATGGCAATTAACAGAGAGCTTTAATCTTGACGAGGGCCATGCAC 840  
Db |||||  
781 CGTGACCGTAGCAAAATGGCAATTAACAGAGAGCTTTAATCTTGACGAGGGCCATGCAC 840  
Qy 841 CAGAATCCCATCCGGTTTCATTTCCTACATCTTGAACCGCATGACCAACAGAACCTCAG 900  
Db |||||  
841 CAGAATCCCATCCGGTTTCATTTCCTACATCTTGAACCGCATGACCAACAGAACCTCAG 900  
Qy 901 AGTAGCTAAATTCCTCATCCCGGTTTAAACACACCCCGCCAGTTTGTAGAGATTTCTCCCGG 960  
Db |||||  
901 AGTAGCTAAATTCCTCATCCCGGTTTAAACACACCCCGCCAGTTTGTAGAGATTTCTCCCGG 960  
Qy 961 GAGCAGCCGAGACCAATCATCTTCTACTTTCAGGGCTTCAGCAGGAATACGTTGGAGGCGC 1020  
Db |||||  
961 GAGCAGCCGAGACCAATCATCTTCTACTTTCAGGGCTTCAGCAGGAATACGTTGGAGGCGC 1020  
Qy 1021 CTTCAATGCGGAATTCATGAGATACCGAGGGTGTCTGTAGAGAGAGATCAGAGAGTGA 1080  
Db |||||  
1021 CTTCAATGCGGAATTCATGAGATACCGAGGGTGTCTGTAGAGAGAGATCAGAGAGTGA 1080  
Qy 1081 GCAAGAGGAGAGAGGCGAGAGCGGATGGAGTACTCGGAGTAGTGAGAGAAATGAAGAGT 1140

||||| 1081 GCAAGAGGAGAGAGGAGAGGCGATGCGAGTATCGGAGTAGTGAGAACAAATGAAGAGT 1140  
||||| 1141 GATAGTCAAAGTGTCAAAGAGACACGTTGAAGAACTTACTTAAGCAGCGCTAAATCCGCTCTC 1200  
||||| 1141 GATAGTCAAAGTGTCAAAGAGACACGTTGAAGAACTTACTTAAGCAGCGCTAAATCCGCTCTC 1200  
||||| 1201 AAAGAAGGCTCCGAAGAAGAGGAGATATCAACAACCCCAATCAACTTTGAGAGAAGCGGA 1260  
||||| 1201 AAAGAAGGCTCCGAAGAAGAGGAGATATCAACAACCCCAATCAACTTTGAGAGAAGCGGA 1260  
||||| 1261 GCCCGATCTTTCTAAACAACCTTTGGGAGGTTATTTGAGGTGAAGCCAGACAAGAGAACC 1320  
||||| 1261 GCCCGATCTTTCTAAACAACCTTTGGGAGGTTATTTGAGGTGAAGCCAGACAAGAGAACC 1320  
||||| 1321 CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAGAAGAGGAGCTTTGAT 1380  
||||| 1321 CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAGAAGAGGAGCTTTGAT 1380  
||||| 1381 GCTCCACACTTCAACTCAAGGCCATGGTTATCGTCTGCTCAACAAGGAACTCGAAA 1440  
||||| 1381 GCTCCACACTTCAACTCAAGGCCATGGTTATCGTCTGCTCAACAAGGAACTCGAAA 1440  
||||| 1441 CCTTGAACCTGGCTGTAGAAAGAGCAACACAGAGGGGACGGCGGAAGAAGGGA 1500  
||||| 1441 CCTTGAACCTGGCTGTAGAAAGAGCAACACAGAGGGGACGGCGGAAGAAGGGA 1500  
||||| 1501 GGACGAAGACGAAGAAGAGAGGAGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTT 1560  
||||| 1501 GGACGAAGACGAAGAAGAGAGGAGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTT 1560  
||||| 1561 GAAGGAAGGCGATGTTTCATCATGCCAGCAGCTCATCCGATAGCCATCAACGCTTCTC 1620  
||||| 1561 GAAGGAAGGCGATGTTTCATCATGCCAGCAGCTCATCCGATAGCCATCAACGCTTCTC 1620  
||||| 1621 CGAATCTCATCTCGCTTGGCTTCCGTTATCAACGCTGAAACCAACAGAACTTCTCTTGC 1680  
||||| 1621 CGAATCTCATCTCGCTTGGCTTCCGTTATCAACGCTGAAACCAACAGAACTTCTCTTGC 1680  
||||| 1681 AGGTGATAAGGACAATGTGTATAGACAGATAGAGAAGCAAGCAAGGATTTAGCAATCCC 1740  
||||| 1681 AGGTGATAAGGACAATGTGTATAGACAGATAGAGAAGCAAGCAAGGATTTAGCAATCCC 1740  
||||| 1741 TGGTCTGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAAGCAAGTCTCAGTTCTGAG 1800  
||||| 1741 TGGTCTGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAAGCAAGTCTCAGTTCTGAG 1800  
||||| 1801 TGCTCGTCTCAATCTCAATCTCAATCTCCGTCGTCTCCTGAGAAAGAGTCTCCTGAGAA 1860  
||||| 1801 TGCTCGTCTCAATCTCAATCTCAATCTCCGTCGTCTCCTGAGAAAGAGTCTCCTGAGAA 1860  
||||| 1861 AGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGTCACCTCTTCAATTTTGAAGGC 1920  
||||| 1861 AGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGTCACCTCTTCAATTTTGAAGGC 1920  
||||| 1921 TTTTAAGTGAAGTGAAGGCACTTGTATGTATCGATATAGATCAAGCTTTTCTACT 1980  
||||| 1921 TTTTAAGTGAAGTGAAGGCACTTGTATGTATCGATATAGATCAAGCTTTTCTACT 1980  
||||| 1981 CTACTATCCAAAACCTTATCAATAAATAAAGGTTTGTGCGTTGTTCTCC 2032  
||||| 1981 CTACTATCCAAAACCTTATCAATAAATAAAGGTTTGTGCGTTGTTCTCC 2032

RESULT 3  
ADG27462  
ID ADG27462 standard; cDNA; 2032 BP.

XX AC ADG27462;

XX DT 26-FEB-2004 (first entry)

XX DE Peanut Ara h1 cDNA clone P41b.

XX KW Peanut; plant; ss; gene; allergen; Ara h1; Ara h2; Ara h3;  
KW glycinin A2B1a; Jug n1; antiallergic; vulnerary;  
KW anaphylactic food allergen; IgE; allergy; wound.  
XX OS Arachis hypogaea.  
XX PN US2003202980-A1.  
XX PD 30-OCT-2003.  
XX PF 18-MAR-2002; 2002US-00100303.  
XX PR 29-DEC-1995; 95US-0009455P.  
PR 23-SEP-1996; 96US-00717933.  
PR 31-JAN-1998; 98US-0073283P.  
PR 13-FEB-1998; 98US-0074590P.  
PR 13-FEB-1998; 98US-0074624P.  
PR 13-FEB-1998; 98US-0074633P.  
PR 29-JUN-1998; 98US-00106872.  
PR 27-AUG-1998; 98US-00141220.  
PR 13-NOV-1998; 98US-00191593.  
PR 29-JAN-1999; 99US-00240557.  
PR 29-JAN-1999; 99US-00241101.  
PR 11-FEB-1999; 99US-00248673.  
PR 11-FEB-1999; 99US-00248674.  
PR 02-MAR-1999; 99US-0122450P.  
PR 02-MAR-1999; 99US-0122452P.  
PR 02-MAR-1999; 99US-0122560P.  
PR 02-MAR-1999; 99US-0122565P.  
PR 02-MAR-1999; 99US-0122566P.  
PR 11-MAR-1999; 99US-00267719.  
PR 28-JAN-2000; 2000US-00494096.  
PR 16-MAR-2001; 2001US-0276822P.  
XX (CAPL/) CAPLAN M J.  
PA (SOSI/) SOSIN H B.  
PA (SAMP/) SAMPSON H.  
PA (BANN/) BANNON G A.  
PA (BURK/) BURKS A W.  
PA (COCK/) COCKRELL G.  
PA (COMP/) COMPADRE C M.  
PA (CONN/) CONNAUGHTON C.  
PA (HELM/) HELM R M.  
PA (KING/) KING N E.  
PA (KOPP/) KOPPER R A.  
PA (MALE/) MALEKI S J.  
PA (RABJ/) RABJOHN P A.  
PA (SHIN/) SHIN D S.  
PA (STAN/) STANLEY J S.  
XX Caplan MJ, Sosin HB, Sampson H, Bannan GA, Burks AW, Cockrell G;  
PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;  
PI Rabinjohn PA, Shin DS, Stanley JS;  
XX WPI: 2003-875632/81.  
DR P-PSDB; ADG27464.  
XX New modified anaphylactic food allergen comprising a cysteine residue  
PT which has been modified so that it cannot participate in the disulfide  
PT bond, useful for treating allergic reactions or wounds.  
XX Example 4; SEQ ID NO 5; 194pp; English.  
XX The invention relates to a modified anaphylactic food allergen whose  
CC amino acid sequence is substantially identical to that of a natural  
CC anaphylactic food allergen. The natural anaphylactic food allergen  
CC includes at least one cysteine residue that participates in a disulphide  
CC bond when the natural anaphylactic food allergen is in its native  
CC conformation, except that the cysteine residue has been modified so that  
CC it cannot participate in the disulphide bond. Also included are a method  
CC of making a modified anaphylactic food allergen, a nucleotide molecule  
CC encoding a modified anaphylactic food allergen defined above, a

CC nucleotide molecule for causing a site specific mutation in a gene  
CC encoding a natural anaphylactic food allergen, a transgenic plant or  
CC animal expressing a modified anaphylactic food allergen defined above, a  
CC method of treating an individual by reducing the clinical response to a  
CC natural anaphylactic food allergen by administering a modified  
CC anaphylactic food allergen and an isolated fragment of peanut allergen  
CC Ara h 1, comprising at least 10 consecutive amino acids of ADG27464 or  
CC ADG27465. About 10-17% of the amino acids have been modified in at least  
CC one IGE epitope or all the IGE epitopes recognised when the natural  
CC anaphylactic food allergen is contacted with serum IGE from individual(s)  
CC allergic to the natural anaphylactic food allergen. The invention  
CC discloses Peanut allergens Ara h1, Ara h2, Ara h3 (and their encoding  
CC cDNAs), Soybean Glycinin A2B4 and IGE-binding epitopes of the English  
CC walnut allergen Jug n1. The modified anaphylactic food allergen can be  
CC used for treating allergic reactions or wounds. The present sequence  
CC encodes a Peanut allergen of the invention.  
XX  
SQ

Sequence 2032 BP; 628 A; 473 C; 530 G; 401 T; 0 U; 0 Other;

Query Match 100.0%; Score 2032; DB 10; Length 2032;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AATAATCATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGGGAG	60
Db	1	AATAATCATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGGGAG	60
Qy	61	GGTTTCTCCACTGATGCTGTGTGAGGGATCCTTGTCTCGCTTCAGTTCTGCAACGCA	120
Db	61	GGTTTCTCCACTGATGCTGTGTGAGGGATCCTTGTCTCGCTTCAGTTCTGCAACGCA	120
Qy	121	TGCCAAGTCATCACTTTACAGAGAGAAACAGAGAACCCCTCGGCCAGAGGTCCTTCCA	180
Db	121	TGCCAAGTCATCACTTTACAGAGAGAAACAGAGAACCCCTCGGCCAGAGGTCCTTCCA	180
Qy	181	GAGTTGTCAACAGAAACCGATGACTTGAAGCAAAAGCGATGCGAGTCTCGCTGCACCA	240
Db	181	GAGTTGTCAACAGAAACCGATGACTTGAAGCAAAAGCGATGCGAGTCTCGCTGCACCA	240
Qy	241	GCTCGAGTATGATCCTCGTTGTGTCTATGATCTCTCGAGGACACACTGGCACCAACCA	300
Db	241	GCTCGAGTATGATCCTCGTTGTGTCTATGATCTCTCGAGGACACACTGGCACCAACCA	300
Qy	301	ACGTTCCCTCCAGGGAGCGGACACGTCGCGCCAAACCCGGAGACTACGATGATGACCG	360
Db	301	ACGTTCCCTCCAGGGAGCGGACACGTCGCGCCAAACCCGGAGACTACGATGATGACCG	360
Qy	361	CCGTCAACCCCGAAGAGAGAGAGGCGCCGATGGGGACACGCTGGACCCGAGGAGCGTGA	420
Db	361	CCGTCAACCCCGAAGAGAGAGAGGCGCCGATGGGGACACGCTGGACCCGAGGAGCGTGA	420
Qy	421	AAGAGAGAGAGACTGGAGACAAACCAAGAGAGATTGGAGGCGCAAGTCTCAGCAGCC	480
Db	421	AAGAGAGAGAGACTGGAGACAAACCAAGAGAGATTGGAGGCGCAAGTCTCAGCAGCC	480
Qy	481	ACGGAATAAAGCCCGAAGAGAGAGAGAGAGAAACAGAGTGGGGAAACACAGGTAGCCA	540
Db	481	ACGGAATAAAGCCCGAAGAGAGAGAGAGAGAAACAGAGTGGGGAAACACAGGTAGCCA	540
Qy	541	TGTGAGGAGAGAAACATCTCGGAACACCCCTTCTACTTCCCGTCAAGGCGGTTTAGCAC	600
Db	541	TGTGAGGAGAGAAACATCTCGGAACACCCCTTCTACTTCCCGTCAAGGCGGTTTAGCAC	600
Qy	601	CCGCTACGGGAACCAAAACCGTAGGATCCGGGTCTCGAGAGGTTTGAACCAAGGTCAG	660
Db	601	CCGCTACGGGAACCAAAACCGTAGGATCCGGGTCTCGAGAGGTTTGAACCAAGGTCAG	660
Qy	661	GCAGTTTCAGAACTCCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTAACACTCT	720
Db	661	GCAGTTTCAGAACTCCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTAACACTCT	720
Qy	721	TGTTCTTCCCAAGCAGCTGATGCTGATACATCTCTTGTATCCAGCAAGGGCAAGCCAC	780

Db	721	TGTTCTTCCCAAGCAGCTGATGCTGATAAACATCTTGTATTCCAGCAAGGGCAAGCCAC	780
Qy	781	CGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAAATCTTCCAGGAGGCCATGCACT	840
Db	781	CGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAAATCTTCCAGGAGGCCATGCACT	840
Qy	841	CAGAATCCCATCCGGTTTCATTTCTTACATCTTTGAACCGCCATGACAAACCAAGACCTCAG	900
Db	841	CAGAATCCCATCCGGTTTCATTTCTTACATCTTTGAACCGCCATGACAAACCAAGACCTCAG	900
Qy	901	AGTAGCTAAAATCTCCATGCGCCGTTAAACACACCCCGGCGAGTTTGAGGATTTCTTCCCGGC	960
Db	901	AGTAGCTAAAATCTCCATGCGCCGTTAAACACACCCCGGCGAGTTTGAGGATTTCTTCCCGGC	960
Qy	961	GAGCAGCCGAGAGCAATCATCTACTTTGAGGGCTTCAGCAGGAAATACGTTGGAGGGCGC	1020
Db	961	GAGCAGCCGAGAGCAATCATCTACTTTGAGGGCTTCAGCAGGAAATACGTTGGAGGGCGC	1020
Qy	1021	CTTCAATGCGGAATTTCAATGAGATACGAGGGTCTCTTTAGAGAGAAATGAGAGGTGA	1080
Db	1021	CTTCAATGCGGAATTTCAATGAGATACGAGGGTCTCTTTAGAGAGAAATGAGAGGTGA	1080
Qy	1081	GCAAGGAGAGAGGGCGAGGCGATGCGAGTACTCGGAGTAGTGAGAACATGAGAGGT	1140
Db	1081	GCAAGGAGAGAGGGCGAGGCGATGCGAGTACTCGGAGTAGTGAGAACATGAGAGGT	1140
Qy	1141	GATAGTCAAAAGTGTCAAAGGAGGACGTTGAAGAACTTACTTAAGCAGCTAAATCCGTCTC	1200
Db	1141	GATAGTCAAAAGTGTCAAAGGAGGACGTTGAAGAACTTACTTAAGCAGCTAAATCCGTCTC	1200
Qy	1201	AAAGAAAGGCTCCGAAGAGAGAGGAGATATCAACCAACCCCAATCAACTTTGAGAGAGGCGA	1260
Db	1201	AAAGAAAGGCTCCGAAGAGAGAGGAGATATCAACCAACCCCAATCAACTTTGAGAGAGGCGA	1260
Qy	1261	GCCGATCTTTCTTAAACAACTTTGCGGAGTTATTTGAGGTGAAGGCGAGCAAGAGAACCC	1320
Db	1261	GCCGATCTTTCTTAAACAACTTTGCGGAGTTATTTGAGGTGAAGGCGAGCAAGAGAACCC	1320
Qy	1321	CCAGCTTCAGGACCTGGACATGATGCTCAGCTGTGTAGAGATCAAGAGAGGAGCTTTGAT	1380
Db	1321	CCAGCTTCAGGACCTGGACATGATGCTCAGCTGTGTAGAGATCAAGAGAGGAGCTTTGAT	1380
Qy	1381	GCTCCCAACCTTCAAGGCGCATGGTTATCTGCTGCTGCTCAACAAAGGAACTGGA	1440
Db	1381	GCTCCCAACCTTCAAGGCGCATGGTTATCTGCTGCTGCTCAACAAAGGAACTGGA	1440
Qy	1441	CTTTGAACCTCGTGGCTGTAAAGAAAGAGCAACACAGAGGGGACGGCGGAAGAGAGGA	1500
Db	1441	CTTTGAACCTCGTGGCTGTAAAGAAAGAGCAACACAGAGGGGACGGCGGAAGAGAGGA	1500
Qy	1501	GGACGAAGACGAAGAGAGAGGAAAGTAAACAGAGAGGTCGTAGGTACACAGCGAGGTT	1560
Db	1501	GGACGAAGACGAAGAGAGAGGAAAGTAAACAGAGAGGTCGTAGGTACACAGCGAGGTT	1560
Qy	1561	GAAGGAGGCGATGTTTCAATGTCAGCAGCTCATCTCAGTAGGCTCAACCGCTTCTCTC	1620
Db	1561	GAAGGAGGCGATGTTTCAATGTCAGCAGCTCATCTCAGTAGGCTCAACCGCTTCTCTC	1620
Qy	1621	CGAATCTCATCTCTTGGCTTCGATCAACGCTGAAACCAACACAGAGATCTTCTCTTC	1680
Db	1621	CGAATCTCATCTCTTGGCTTCGATCAACGCTGAAACCAACACAGAGATCTTCTCTTC	1680
Qy	1681	AGGTGATAGGGAACAATGTGATAGCAGATAGAGAAAGCAAGCGAAGGATTTAGCATTTCC	1740
Db	1681	AGGTGATAGGGAACAATGTGATAGCAGATAGAGAAAGCAAGCGAAGGATTTAGCATTTCC	1740
Qy	1741	TGGGTGGGTGAACAAGTTGAGAGGCTCATCAAAAAACCAAGAGGAAATCTCCTTTGTGAG	1800
Db	1741	TGGGTGGGTGAACAAGTTGAGAGGCTCATCAAAAAACCAAGAGGAAATCTCCTTTGTGAG	1800
Qy	1801	TGCTCGTCTCAATCTCAATCTCCGTCGTCTCTCTGAGAAAGAGTCTCTCTGAGAA	1860
Db	1801	TGCTCGTCTCAATCTCAATCTCCGTCGTCTCTCTGAGAAAGAGTCTCTCTGAGAA	1860



QY 1861 AGAGGATCAAGAGGAGGAAACCAAGGAGGAGGAGGTCCTCTTCAATTTGAAGGC 1920  
Db |||||  
1861 AGAGGATCAAGAGGAGGAAACCAAGGAGGAGGAGGTCCTCTTCAATTTGAAGGC 1920  
QY 1921 TTTTAACTGAGATGAGGCAACTTGTATGATCGATATAGATCAGCGTTTGTACT 1980  
Db |||||  
1921 TTTTAACTGAGATGAGGCAACTTGTATGATCGATATAGATCAGCGTTTGTACT 1980  
QY 1981 CTACTATCCAAAACTTATCAATAAATAAAAGCTTGTGCGTGTGTTCTCC 2032  
Db |||||  
1981 CTACTATCCAAAACTTATCAATAAATAAAAGCTTGTGCGTGTGTTCTCC 2032

## RESULT 4

ADV97537

ID ADV97537 standard; cDNA; 2032 BP.

XX ADV97537;

XX 10-MAR-2005 (first entry)

XX Peanut Ara h I allergen beta P41b cDNA encoding a seed storage protein.

XX allergen; atopic dermatitis; diagnostic; immunotherapy;

KW immediate type hypersensitivity; Ara h I; dermatological; antiallergic;

KW immunosuppressive; antibody engineering; ss.

XX

OS Arachis hypogaea.

XX

FH Key Location/Qualifiers

FT CDS 50..1930

FT /\*tag= a

FT /product= "Ara h I allergen protein (P17 clone)"

XX

PN US6835824-B1.

XX

PD 28-DEC-2004.

XX

PF 13-NOV-1998; 98US-00191593.

XX

PR 29-DEC-1995; 95US-0009455P.

XX

PR 23-SEP-1996; 96US-00717933.

XX

PA (UYAR-) UNIV ARKANSAS.

XX

XX Burks AW, Stanley JS, Bannion GA, Cockrell G, Helm RM;

XX

XX WPI; 2005-045982/05.

XX

XX New isolated nucleic acid encoding peanut allergen Ara h 1, useful for

PT obtaining diagnostics with optimal concentrations of each allergen, for

PT developing panels of mixtures of recombinant allergens, and in

PT immunotherapy.

XX

PS Claim 2; SEQ ID NO 5; 141pp; English.

XX

XX This invention relates to a novel isolated nucleic acid molecule encoding

CC the peanut allergen Ara h I that has been identified in patients with

CC atopic dermatitis. Specifically, it refers to a monoclonal antibody

CC enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the

CC peanut allergens, where the monoclonal antibodies have specificity for a

CC selected peanut allergen antigen. The present invention also describes

CC hybridomas that produce two-site monoclonal antibodies specific for a

CC peanut allergen that can be used in an ELISA to detect and determine the

CC concentration of a specific peanut allergen in a food product or in food

CC processing. Furthermore, it provides an expression vector and the

CC isolated nucleic acid or its fraction can include a diagnostic label.

CC Accordingly, these nucleic acids are useful for obtaining diagnostics

CC with optimal concentrations of each allergen or for developing panels of

CC mixtures of large numbers of recombinant allergens such that it can be

CC used in immunotherapy for the treatment of food hypersensitivity

CC reactions. This polynucleotide sequence is the peanut Ara h I allergen

CC cDNA (P41b clone) of the invention.

XX

SQ Sequence 2032 BP; 628 A; 473 C; 530 G; 401 T; 0 U; 0 Other;

Query Match 100.0%; Score 2032; DB 14; Length 2032;

Best Local Similarity 100.0%; Pred No. 0;

Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATAATCATATATATTTTCATCAATCATCTATATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60

Db |||||

1 AATAATCATATATATTTTCATCAATCATCTATATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60

QY 61 GGTTCCTCCACTGATGCTGCTAGGATCCTTGTCTAGGATCCTTGTCTGGCTTCAGTTCTGCAACGCA 120

Db |||||

61 GGTTCCTCCACTGATGCTGCTAGGATCCTTGTCTAGGATCCTTGTCTGGCTTCAGTTCTGCAACGCA 120

QY 121 TGCCAAGTCATCACTTTACGAGAAGAAAAACAGAGAAACCCCTGCGCCACAGAGTGCTCTCA 180

Db |||||

121 TGCCAAGTCATCACTTTACGAGAAGAAAAACAGAGAAACCCCTGCGCCACAGAGTGCTCTCA 180

QY 181 GAGTTCTCAACAGGAAACCGGATGACTTGAAGCAAAAAGGATGCGAGTCTGCTGCACCAA 240

Db |||||

181 GAGTTCTCAACAGGAAACCGGATGACTTGAAGCAAAAAGGATGCGAGTCTGCTGCACCAA 240

QY 241 GCTCGAGTATGATCCTCGTGTGTCTATGATCCTCGAGGACACACTGGCAACCAACCA 300

Db |||||

241 GCTCGAGTATGATCCTCGTGTGTCTATGATCCTCGAGGACACACTGGCAACCAACCA 300

QY 301 ACCTTCCCTCCAGGGAGCGGACACGTCGCGCCCAACCCGGAGACTACGATGATGACCG 360

Db |||||

301 ACCTTCCCTCCAGGGAGCGGACACGTCGCGCCCAACCCGGAGACTACGATGATGACCG 360

QY 361 CGCTCAACCCGAAAGAGAGGAGCGGATGCGGACACGTCGCGCCCAACCCGGAGACTG 420

Db |||||

361 CGCTCAACCCGAAAGAGAGGAGCGGATGCGGACACGTCGCGCCCAACCCGGAGACTG 420

QY 421 AAGAGAAGAGACTGAGAGCAACCAAGAGAAGATTGGAGCGCACCAAGTCTCATCAGCAGCC 480

Db |||||

421 AAGAGAAGAGACTGAGAGCAACCAAGAGAAGATTGGAGCGCACCAAGTCTCATCAGCAGCC 480

QY 481 ACGGAAAAATAAGGCCCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

Db |||||

481 ACGGAAAAATAAGGCCCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 541 TGTGAGGAG 600

Db |||||

541 TGTGAGGAG 600

QY 601 CCGCTACGGGAAACAAAACGGTAGGATCCGGGTCCTGCGAGAGGTTTGACCAAAAGGTCAG 660

Db |||||

601 CCGCTACGGGAAACAAAACGGTAGGATCCGGGTCCTGCGAGAGGTTTGACCAAAAGGTCAG 660

QY 661 GCAGTTTCAGAAATCTCCAGAAATCACCGTATTTGTCAGATCGAGGCGGCAAACTAACACTCT 720

Db |||||

661 GCAGTTTCAGAAATCTCCAGAAATCACCGTATTTGTCAGATCGAGGCGGCAAACTAACACTCT 720

QY 721 TGTTCCTCCCAAGCAGCGTGTATCAATCAATCTTGTATCCAGCAAGGCGCAAGCCAC 780

Db |||||

721 TGTTCCTCCCAAGCAGCGTGTATCAATCAATCTTGTATCCAGCAAGGCGCAAGCCAC 780

QY 781 CGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTTCAGCAGGCGCCATGCAC 840

Db |||||

781 CGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTTCAGCAGGCGCCATGCAC 840

QY 841 CAGAAATCCCATCCGGTTTCAATTTCTTACATCTTGAACCGGCATGACACCAAGACCTCAG 900

Db |||||

841 CAGAAATCCCATCCGGTTTCAATTTCTTACATCTTGAACCGGCATGACACCAAGACCTCAG 900

QY 901 AGTAGCTAAATCTCCATGCCCGTCTTAACACACCCCGCAGTTTGAGGATTTCTTCCCGGC 960

Db |||||

901 AGTAGCTAAATCTCCATGCCCGTCTTAACACACCCCGCAGTTTGAGGATTTCTTCCCGGC 960

QY 961 GAGCAGCCGAGACCAATCATCTTACTTTCAGAGGCTTTCAGCAGGAATACGTTGGAGGCCGC 1020

Db 961 GAGCAGCGGACCAATCATCTACTTTCAGGGCTTCAGCAGGAATACGTTGGAGCGC 1020  
Qy 1021 CTTCAATGCGGAATTCATAGATACGAGGCTCTGTATAGAGAGATCAGGAGTGA 1080  
Db 1021 CTTCAATGCGGAATTCATAGATACGAGGCTCTGTATAGAGAGATCAGGAGTGA 1080  
Qy 1081 GCAAGAGGAGAGGGCAGAGGCGATGGAGTACTCGGAGTAGTGAGAACAAATGAAGAGT 1140  
Db 1081 GCAAGAGGAGAGGGCAGAGGCGATGGAGTACTCGGAGTAGTGAGAACAAATGAAGAGT 1140  
Qy 1141 GATAGTCAAAAGTCAAGAGAGCAGTGTGAAGAACTTACTAAGCAGCCTAAATCGTCTC 1200  
Db 1141 GATAGTCAAAAGTCAAGAGAGCAGTGTGAAGAACTTACTAAGCAGCCTAAATCGTCTC 1200  
Qy 1201 AAAGAAAGGCTCCGAAGAGGAGAGATATACCAACCCCAATCAACTTTGAGAGAAGCGGA 1260  
Db 1201 AAAGAAAGGCTCCGAAGAGGAGAGATATACCAACCCCAATCAACTTTGAGAGAAGCGGA 1260  
Qy 1261 GCCGATCTTTTCTAACAACTTTGGGAAAGTTATTGGAGTGAAGCCAGACAAAGAAACCC 1320  
Db 1261 GCCGATCTTTTCTAACAACTTTGGGAAAGTTATTGGAGTGAAGCCAGACAAAGAAACCC 1320  
Qy 1321 CCAGCTTCAGGACTGACATGATGCTCACCTGTGTAGAGATCAAGAGAGGCTTTGAT 1380  
Db 1321 CCAGCTTCAGGACTGACATGATGCTCACCTGTGTAGAGATCAAGAGAGGCTTTGAT 1380  
Qy 1381 GCTCCCACTTCAACTCAAGGCCATGTTATCGTCGTCAACAAAGGAACTCGGAA 1440  
Db 1381 GCTCCCACTTCAACTCAAGGCCATGTTATCGTCGTCAACAAAGGAACTCGGAA 1440  
Qy 1441 CTTGAACTCGTGGCTGTAAGAAAAGAGCAACACAGAGGGGACGGCGGAAGAAGGA 1500  
Db 1441 CTTGAACTCGTGGCTGTAAGAAAAGAGCAACACAGAGGGGACGGCGGAAGAAGGA 1500  
Qy 1501 GGAAGAGAGCAAGAGAGAGGGAAGTAAACAGAGAGTCCGTAGGTACACAGCGAGTT 1560  
Db 1501 GGAAGAGAGCAAGAGAGAGGGAAGTAAACAGAGAGTCCGTAGGTACACAGCGAGTT 1560  
Qy 1561 GAAGGAGGCGATGTTTCATCATCGCAGCAGTCCATCAGTAGCCATCAACCTTCCTC 1620  
Db 1561 GAAGGAGGCGATGTTTCATCATCGCAGCAGTCCATCAGTAGCCATCAACCTTCCTC 1620  
Qy 1621 CGAACTCCATCTCGTGGCTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCCTTC 1680  
Db 1621 CGAACTCCATCTCGTGGCTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCCTTC 1680  
Qy 1681 AGGTGATAAGGACAATGTGTAGACACAGATAGAGAGCAAGCAAGGATTTAGCATCC 1740  
Db 1681 AGGTGATAAGGACAATGTGTAGACACAGATAGAGAGCAAGCAAGGATTTAGCATCC 1740  
Qy 1741 TGGGTCGGGTGAACAAGTTGAGAGCTCATCAAAACCAAGGAATCTCACTTTCTGAG 1800  
Db 1741 TGGGTCGGGTGAACAAGTTGAGAGCTCATCAAAACCAAGGAATCTCACTTTCTGAG 1800  
Qy 1801 TGCTCGCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAGAGTCTCTCAGAA 1860  
Db 1801 TGCTCGCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAGAGTCTCTCAGAA 1860  
Qy 1861 AGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGTCCTCTCTCAATTTGAAGGC 1920  
Db 1861 AGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGTCCTCTCTCAATTTGAAGGC 1920  
Qy 1921 TTTTAAGTGAATGGAGCAACTGTATGTATCGATATAGATACAGCTTTTGTACT 1980  
Db 1921 TTTTAAGTGAATGGAGCAACTGTATGTATCGATATAGATACAGCTTTTGTACT 1980  
Qy 1981 CTACTATCCAAAACTTATCAATAAATAAAGCGTTTGTGCGTGTGTTCTCC 2032  
Db 1981 CTACTATCCAAAACTTATCAATAAATAAAGCGTTTGTGCGTGTGTTCTCC 2032

ADV97600  
ID ADV97600 standard; cDNA; 2040 BP.  
XX AC ADV97600;  
XX DT 10-MAR-2005 (first entry)  
XX Peanut Ara h I allergen alpha P17 cDNA encoding a seed storage protein.  
DE allergen; atopic dermatitis; diagnostic; immunotherapy;  
KW immediate type hypersensitivity; Ara h I; dermatological; antiallergic;  
KW immunosuppressive; antibody engineering; gene; ss.  
XX Arachis hypogaea.  
XX Key Location/Qualifiers  
FT CDS 50..1930  
FT /\*tag= a  
FT /product= "Ara h I allergen protein (P17 clone)"  
XX US6835824-B1.  
XX 28-DEC-2004.  
XX 13-NOV-1998; 98US-00191593.  
XX 29-DEC-1995; 95US-0009455P.  
XX 23-SEP-1996; 96US-00717933.  
XX (UYAR-) UNIV ARKANSAS.  
XX Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;  
WPI; 2005-045982/05.  
DR P-PSDB; ADV97601.  
XX New isolated nucleic acid encoding peanut allergen Ara h 1, useful for  
PT obtaining diagnostics with optimal concentrations of each allergen, for  
PT developing panels of mixtures of recombinant allergens, and in  
PT immunotherapy.  
XX Disclosure; Fig 16; 14pp; English.  
XX This invention relates to a novel isolated nucleic acid molecule encoding  
CC the peanut allergen Ara h I that has been identified in patients with  
CC atopic dermatitis. Specifically, it refers to a monoclonal antibody  
CC enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the  
CC peanut allergens, where the monoclonal antibodies have specificity for a  
CC selected peanut allergen antigen. The present invention also describes  
CC hybridomas that produce two-site monoclonal antibodies specific for a  
CC peanut allergen that can be used in an ELISA to detect and determine the  
CC concentration of a specific peanut allergen in a food product or in food  
CC processing. Furthermore, it provides an expression vector and the  
CC isolated nucleic acid or its fraction can include a diagnostic label.  
CC Accordingly, these nucleic acids are useful for obtaining diagnostics  
CC with optimal concentrations of each allergen or for developing panels of  
CC mixtures of large numbers of recombinant allergens such that it can be  
CC used in immunotherapy for the treatment of food hypersensitivity  
CC reactions. This polynucleotide sequence is the peanut Ara h I allergen  
CC cDNA (P17 clone) of the invention.  
XX Sequence 2040 BP; 636 A; 473 C; 530 G; 401 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 2032; DB 14; Length 2040;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGGGAG 60  
Db 1 AATAATCATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGGGAG 60  
Qy 61 GGTTCCTCACTGATGCTGTTGCTAGGATCCTGTGCTGGCTTCAAGTTCCTCAACGCA 120  
|||||















QY 1068 ATGCAGAGGTGAGCAAGAGGAGAGAGGCGAGAGGCGATGGAGTACTCGAGTAGTGAGA 1127  
DB |||||||  
QY 1003 ATGCAGAGGAGAGCAAGAGGAGAGAGGCGAGAGGCGACGGAGTACTCGGAGTAGTG- 1059  
DB |||||||  
QY 1128 ACAATCAAGAGAGTAGTCAAAGTGTCAAAGGAGCAGCGTTGGAAGAACTTACTAAGCAGC 1187  
DB |||||||  
QY 1060 ATATATGAGAGTAGTCAAAGTGTCAAAGGAGCAGCGTTCAAGAACTTACTAAGCAGC 1119  
DB |||||||  
QY 1188 CTAATCCGTCTCAAAGAAGGCTCCGAAGAAGAGGAGATATCAACAACCCCAATCAACT 1247  
DB |||||||  
QY 1120 CTAATCCGTCTCAAAGAAGGCTCC- --GAAGAGGAAGATATCAACAACCCCAATCAACT 1176  
DB |||||||  
QY 1248 TGAGAGAGGCGAGCCGATCTTTCTAAACAATTTGGGAAGTTATTTGAGGTGAAGCCAG 1307  
DB |||||||  
QY 1177 TGAGAGATGGCAGCCGATCTTTCTAAACAATTTGGGAAGTTATTTGAGGTGAAGCCAG 1236  
DB |||||||  
QY 1308 ACAAGAAGAACCCCAAGCTTCAGGACCTGGACATGATGCTCACTGTGTAGAGATCAAAG 1367  
DB |||||||  
QY 1237 ACAGAAGAACCCCAAGCTTCAGGACCTGGACATGATGCTCACTGTGTAGAGATCAAAG 1296  
DB |||||||  
QY 1368 AAGGAGCTTTGATGTCTCCACACTTCAACTCAAAGGCCATGGTTATGTCGTCGTCACAA 1427  
DB |||||||  
QY 1297 AAGGAGCTTTGATGTCTCCACACTTCAACTCAAAGGCCATGGTCACTGTCGTCGTCACAA 1356  
DB |||||||  
QY 1428 AAGGAATCGAAACCTTGAACCTGCTGGCTGTAGAAAGAGCAACAACAGAGGGGACGCG 1487  
DB |||||||  
QY 1357 AAGGAATCGAAACCTTGAACCTGCTAGCTGTAGAAAGAGCAACAACAGAGGGGACGCG 1416  
DB |||||||  
QY 1488 GGGAA-----GAAGAGGAGGAGCAAGACCAAGAGGAGGGAAGTAACAGAGAGG 1538  
DB |||||||  
QY 1417 GGGAAACAGNGTGGGAAGAGAGGAGGAGAGATGAAGAGAGGAGGAGTAACAGAGAGG 1476  
DB |||||||  
QY 1539 TGCCTAGGTACACAGCAGAGGTTGAAGAGGCGCATGTGTTATCATATGCCAGAGCTCATC 1598  
DB |||||||  
QY 1477 TGCCTAGGTACACAGCAGGTTGAAGAGGCGCATGTGTTATCATATGCCAGAGCTCATC 1536  
DB |||||||  
QY 1599 CAGTAGCCATCAACGCTTCTCCGAACCTCATCTGCTTGGCTTCGCTCAACGCTGAA 1658  
DB |||||||  
QY 1537 CAGTAGCCATCAACGCTTCTCCGAACCTCATCTGCTTGGCTTCGCTCAACGCTGAA 1596  
DB |||||||  
QY 1659 ACAACACAGAACTTCTTGCAGGTGATAAGGACAAATGTATAGACCAGATAGAAGC 1718  
DB |||||||  
QY 1597 ACAACACAGAACTTCTTGCAGGTGATAAGGACAAATGTATAGACCAGATAGAAGC 1656  
DB |||||||  
QY 1719 AAGCGAAGATTTAGCAATTCCTGGGTGCGGTGAACAAGTTGAGAAGCTCATCAAAAACC 1778  
DB |||||||  
QY 1657 AAGCGAAGATTTAGCAATTCCTGGGTGCGGTGAACAAGTTGAGAAGCTCATCAAAAACC 1716  
DB |||||||  
QY 1779 AAGGAATCTCACTTTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCCGTCGTC 1838  
DB |||||||  
QY 1717 AAGAGGAGTCTCACTTTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCCGTC- 1765  
DB |||||||  
QY 1839 CTGAGAAAGAGTCTCTCGAAGAGAGGATCAAGAGGAGGAAAAACCAAGGAGGGAAGGTC 1898  
DB |||||||  
QY 1766 -----GTCTCTGAAAGAGAGATCAAGAGGAGGAAACCAAGGAGGGAAGGTC 1815  
DB |||||||  
QY 1899 CACTCCTTCAATTTGAAGCTTTTAACTGAGAAATGGAGGCAACTTTGTTATGTATCGAT 1958  
DB |||||||  
QY 1816 CACTCCTTCAATTTGAAGCTTTTAACTGAGAAATGGAGGAACTTTGTTATGTATCCAT 1875  
DB |||||||  
QY 1959 AATAAGATCAAGCTTTGTGACTCTACTATATCAAAAACCTTATCAATAAATAAAAACGTTG 2018  
DB |||||||  
QY 1876 AATAAGATCAAGCTTTGTGAACTTACTATCTCAAAAACCTTATCAATAAATAAAAACGTTG 1935  
DB |||||||  
QY 2019 TGGGTTGTTTCTCC 2032  
DB |||||||  
QY 1936 TGGGTTGTTTCTCC 1949  
DB |||||||

RESULT 10  
ABX70604  
ID ABX70604 standard; cDNA; 1949 BP.  
XX

AC ABX70604;  
XX 26-MAR-2003 (first entry)  
XX Peanut Ara h1 cDNA clone P17.  
XX DE Peanut; ss; allergy; Ara h1; Ara h2; Ara h3; gene; IgE binding site;  
XX KW anaphylactic food allergen; antiallergenic; vaccine; wound healing.  
XX OS Arachis hypogaea.  
XX PN WO200274250-A2.  
XX PD 26-SEP-2002.  
XX PF 18-MAR-2002; 2002WO-US009108.  
XX PR 16-MAR-2001; 2001US-0276822P.  
XX PR 18-MAR-2002; 2002US-00276822.  
XX PA (PANA-) PANACEA PHARM.  
XX PI Caplan M, Sosin H, Sampson H, Bannon GA, Burks WA, Cockrell G;  
PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Mailek SJ;  
PI Rabjohn PA, Shin DS, Stanley JS;  
XX WPI; 2003-018765/01.  
DR P-PSDB; ABU52413.  
XX New modified anaphylactic food allergen, useful for preventing or  
XX treating allergic reactions associated with e.g. anaphylactic allergens.  
XX Example 3; Fig 11; 300pp; English.  
XX The invention relates to a modified anaphylactic food allergen has an  
XX amino acid sequence that is substantially identical to that of natural  
XX anaphylactic food allergen, except for a cysteine residue that has been  
XX modified so that it cannot participate in the disulphide bond. The  
XX modification may also comprise mutation of the IgE binding sites to  
XX reduce allergenicity. Also included are: (1) a method of making a  
XX modified anaphylactic food allergen; (2) a nucleotide molecule encoding  
XX or for causing a site specific mutation in the modified anaphylactic food  
XX allergen; (3) a transgenic plant or animal expressing the modified  
XX anaphylactic food allergen; (4) a method of treating an individual by  
XX reducing the clinical response to a natural anaphylactic food allergen;  
XX and an isolated fragment of peanut allergen Ara h 1. The modified  
XX anaphylactic food allergen is useful for preventing or treating allergic  
XX reactions associated with any natural allergen such as food, insect,  
XX rubber or preferably anaphylactic allergens. It is also useful for  
XX treating wounds in mammals such as bovine, canine, feline, caprine,  
XX ovine, porcine, murine or equine species. The present sequence is a cDNA  
XX encoding a peanut allergen (e.g. Ara h1, h2 or h3)  
SQ Sequence 1949 BP; 599 A; 455 C; 517 G; 378 T; 0 U; 0 Other;  
Query Match 86.2%; Score 1752.4; DB 8; Length 1949;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;  
QY 48 CAATGAGAGGAGGGTTTCTCCACTGATGCTGTGTAGGATCCTTGTCTGCTTCAG 107  
DB 1 CAATGAGAGGAGGGTTTCTCCACTGATGCTGTGTGTGGATCCTTGTCTGCTTCAG 60  
QY 108 TTTCTGCAACGATGCCAGTGCATCACCCTTACAGAGAAACAGAGAACCCCTGCCGCC 167  
DB 61 TTTCTGCAACGAGGCGCAAGTCAC-----TTACCGGAAACAGAGAACCCCTGCCGCC 114  
QY 168 AGAGGTGCCTCCAGAGTTGTCAACAGGAAACCGGATGACTTTGAAGCAAAAGGCATGCGAGT 227  
DB 115 AGAGGTGCCTCCAGAGTTGTCAACAGGAAACCGGACGACTTTGAAGCAAAAGGCATGCGAGT 174  
QY 228 CTCGCTGCACCAAGCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACACTG 287  
DB |||||||



XX PD 28-DEC-2004 .  
XX PF 13-NOV-1998; 98US-00191593 .  
XX PR 29-DEC-1995; 95US-0009455P.  
XX PR 23-SEP-1996; 96US-00717933 .  
XX PA (UYAR-) UNIV ARKANSAS.  
XX PI Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;  
XX WPI; 2005-045982/05.  
XX DR P-PSDB; ADV97606.  
XX PT New isolated nucleic acid encoding peanut allergen Ara h 1, useful for  
XX PT obtaining diagnostics with optimal concentrations of each allergen, for  
XX PT developing panels of mixtures of recombinant allergens, and in  
XX PT immunotherapy.  
XX PS Claim 2; SEQ ID NO 4; 141pp; English.  
XX CC This invention relates to a novel isolated nucleic acid molecule encoding  
XX CC the peanut allergen Ara h 1 that has been identified in patients with  
XX CC atopic dermatitis. Specifically, it refers to a monoclonal antibody  
XX CC enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the  
XX CC peanut allergens, where the monoclonal antibodies have specificity for a  
XX CC selected peanut allergen antigen. The present invention also describes  
XX CC hybridomas that produce two-site monoclonal antibodies specific for a  
XX CC peanut allergen that can be used in an ELISA to detect and determine the  
XX CC concentration of a specific peanut allergen in a food product or in food  
XX CC processing. Furthermore, it provides an expression vector and the  
XX CC isolated nucleic acid or its fraction can include a diagnostic label.  
XX CC Accordingly, these nucleic acids are useful for obtaining diagnostics  
XX CC with optimal concentrations of each allergen or for developing panels of  
XX CC mixtures of large numbers of recombinant allergens such that it can be  
XX CC used in immunotherapy for the treatment of food hypersensitivity  
XX CC reactions. This polynucleotide sequence is the peanut Ara h 1 allergen  
XX CC cDNA (P17 clone) of the invention.  
XX SQ Sequence 1949 BP; 599 A; 455 C; 517 G; 378 T; 0 U; 0 Other;  
Query Match 86.2%; Score 1752.4; DB 14; Length 1949;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;  
QY 48 CAATGAGAGGGAGGGTTCTCCACTGATGCTGTGTCTAGGGATCCTTGTCTGGCTTCAG 107  
DB 1 CAATGAGAGGGAGGGTTCTCCACTGATGCTGTGTGTCTGGGATCCTTGTCTGGCTTCAG 60  
QY 108 TTTCTGCAAGCGATGCCAGTGTGTCACAGGAACCGGATGACTTGAAGCAAAAGGCGATGCGAGT 167  
DB 61 TTTCTGCAAGCGAGGCGCAAGTCACC-----TTACCGGAAACAGAGAACCCTCGCGCC 114  
QY 168 AGAGGTGCTTCCAGAGTGTGTCACAGGAACCGGATGACTTGAAGCAAAAGGCGATGCGAGT 227  
DB 115 AGAGGTGCTTCCAGAGTGTGTCACAGGAACCGGATGACTTGAAGCAAAAGGCGATGCGAGT 174  
QY 228 CTCGCTGCACCAAGCTCGAGTATGATCCTCTGTGTGTCTATGATCCTCGAGGACACACTG 287  
DB 175 CTCGCTGCACCAAGCTCGAGTATGATCCTCTGTGTGTCTATG-----ACACTG 222  
QY 288 GCACCAACCAACCGTTTCCCTTCAGGGAGCGGACAGCTGCGCGCCCAACCCGGAGACT 347  
DB 223 GCGCCACCAACCAACCGTTCACCTTCAGGGAGCGGACAGCTGCGCGCCCAACCCGGAGACT 282  
QY 348 ACCATGATGACCGCGTCAACCCCGAGAGGAAGGAGCGCGATGGGGACCACTGGAC 407  
DB 283 ACCATGATGACCGCGTCAACCCCGAGAGGAAGGAGCGCGATGGGNACCACTGAC 342  
QY 408 CGAGGGAGCGTGAAGAGGAAGAAGACTGGAGACAAACAAGAGAAATTTGAGGCGCAACAA 467  
DB 343 CGAGGGAGCGTGAAGAGGAAGAAGACTGGAGACAAACAAGAGAAATTTGAGGCGCAACAA 402

QY 468 GTCATCAGCAGCCACCGAATAAAGCCCGAAGAGAGAGAAAGAGTGGGAA 527  
DB |||||  
DB 403 GTCATCAGCAGCCACCGAATAAAGCCCGAAGAGAGAGAAAGAGTGGGAA 462  
QY 528 CACCAGGTAGCATGTGAGGGAAGAAACATCTCGGAACAACCCCTTTCTACTTCCCGTCAA 587  
DB |||||  
DB 463 CACCAGGTAGCAGGTGAGGGAAGAAACATCAGGGAACAACCCCTTTCTACTTCCCGTCAA 522  
QY 588 GCGGTTTATGACCCCGCTACGGGAACCAAAACGGTAGGATCCGGGTCTTCGAGAGGTTTG 647  
DB |||||  
DB 523 GCGGTTTATGACCCCGCTACGGGAACCAAAACGGTAGGATCCGGGTCTTCGAGAGGTTTG 582  
QY 648 ACCAAGGTACAGGCAAGTTTTCAGATCTCCAGATCAACCGTATTTGCGAGATCGAGGCA 707  
DB |||||  
DB 583 ACCAAGGTCAAAAGCAGTTTTCAGATCTCCAGATCAACCGTATTTGCGAGATCGAGGCA 642  
QY 708 AACCTAACACTCTTTGTTCTTCCCAAGCAGCTGATCTGATACATCTTTGTTATCCAGC 767  
DB |||||  
DB 643 GACCTAACACTCTTTGTTCTTCCCAAGCAGCTGATCTGATACATCTTTGTTATCCAGC 702  
QY 768 AAGGCAAGCCACCGTAGCAGTAAATGCGAATAACAGAAAGAGCTTTAATCTTGACG 827  
DB |||||  
DB 703 AAGGCAAGCCACCGTAGCAGTAAATGCGAATAACAGAAAGAGCTTTAATCTTGACG 762  
QY 828 AGGCGCATGCACCTCAGAAATCCCATCCGTTTCAATTTCTTACATCTTTGAACCGCATGACA 887  
DB |||||  
DB 763 AGGCGCATGCACCTCAGAAATCCCATCCGTTTCAATTTCTTACATCTTTGAATCGACATGACA 822  
QY 888 ACCAGAACCTCAGAGTAGCTAAATCTCCATGCCCTTAAACACACCCGGCAGTTTGAGG 947  
DB |||||  
DB 823 ACCAGAACCTCAGAGTAGCTAAATCTCCATGCCCTTAAACACCGCCGCGCAGTTTGAGG 882  
QY 948 ATTTCTTCCGGCAGCAGCCGAGACCAATCATCTTCTTACAGGCTTCAGCAGGAATA 1007  
DB |||||  
DB 883 ATTTCTTCCGGCAGCAGCCGAGACCAATCATCTTCTTACAGGATTCAGCAGGAATA 942  
QY 1008 CGTTGAGGCCCTTCAATGCGGATTTCAATGAGATACGAGGCTGTGTTAGAAGAGA 1067  
DB |||||  
DB 943 CTTTGAGGCCCTTCAATGCGGATTTCAATGAGATACGAGGCTGTGTTAGAAGAGA 1002  
QY 1068 ATGCAAGGAGTGAGCAAGAGGAGAGGCGCAGAGCTGGAGTACTCGGAGTAGTGAGA 1127  
DB |||||  
DB 1003 ATGCAAGGAGTGAGCAAGAGGAGAGGAGAGGCGCAGAGTACTCGGAGTAGTG-- 1059  
QY 1128 ACATGAAGAGTAGTAGTCAAAGTGTCAAAGGACACGTTGAGAACTTACTTAAGCAGC 1187  
DB |||||  
DB 1060 ATAATGAAGAGTAGTAGTCAAAGTGTCAAAGGAGCACGTTCAAGAACTTTACTAAGCAGC 1119  
QY 1188 CTAAATCCGTCTCAAAGAAAGGCTCCGAAGAGAGGAGATATCAACCAACCCCAATCAACT 1247  
DB |||||  
DB 1120 CTAAATCCGTCTCAAAGAAAGGCTCC--GAAGAGGAAGATATCAACCAACCCCAATCAACT 1176  
QY 1248 TGAGAGAGGCGAGCCCGATCTTTCTAAACACTTTTGGGAAGTTATTTGAGGTGAAGCCAG 1307  
DB |||||  
DB 1177 TGAGAGATGGGAGCCCGATCTTTCTAAACACTTTGGGAGGTTATTTGAGGTGAAGCCAG 1236  
QY 1308 ACAGAAAGACCCCGAGCTTCAGGACCTGGACATGATGCTCAGCTGTGTAGAGATCAAG 1367  
DB |||||  
DB 1237 ACAAGAAAGACCCCGAGCTTCAGGACCTGGACATGATGCTCAGCTGTGTAGAGATCAAG 1296  
QY 1368 AAGGAGCTTTGATGCTCCACACTTCAACTCAAAGGCCATGGTTATCTGCTCGTCAACA 1427  
DB |||||  
DB 1297 AAGGAGCTTTGATGCTCCACACTTCAACTCAAAGGCCATGGTTCATGCTCGTCAACA 1356  
QY 1428 AAGGAACTGGAAACCTTGAACTCGTGGCTGTGAAGAAAGAGCAACCAACAGAGGGGCGGC 1487  
DB |||||  
DB 1357 AAGGAACTGGAAACCTTGAACTCGTGGCTGTGAAGAAAGAGCAACCAACAGAGGGGCGGC 1416  
QY 1488 GGGAA-----GAAGAGGAGGAGCAACCAAGAGGAGGGAAGTAAACAGAGAGG 1538  
DB |||||  
DB 1417 GGGAAACAGAGTGGGAAGAGAGGAGGAAGATGAAGAGAGGAGGAAGTAAACAGAGAGG 1476

QY 1539 TGGTAGGTACACAGCGAGGTGAAGGAAGCGATGTGTTTCATCATGCGACGACTCATC 1598  
 Db 1477 TGGTAGGTACACAGCGAGGTGAAGGAAGCGATGTGTTTCATCATGCGACGACTCATC 1536  
 QY 1599 CAGTAGGCATCAAGCGTTCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAA 1658  
 Db 1537 CAGTAGGCATCAAGCGTTCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAA 1596  
 QY 1659 ACAACACACAGAACTTCTCTTGCAGGTGATAGGACAAATGTAGACCAATAGAGAAGC 1718  
 Db 1597 ACAACACACAGAACTTCTCTTGCAGGTGATAGGACAAATGTAGACCAATAGAGAAGC 1656  
 QY 1719 AAGCGAAGGATTTAGCATTCCTCGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACC 1778  
 Db 1657 AAGCGAAGGATTTAGCATTCCTCGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACC 1716  
 QY 1779 AGAAGGAATCTCACTTTGTGAGTGTCTGCTCTCAATCTCAATCTCAATCTCCGTC 1838  
 Db 1717 AGAGGGAGTCTCACTTTGTGAGTGTCTGCTCTCAATCTCAATCTCAATCTCCGTC 1765  
 QY 1839 CTGAGAAAGAGTCTCTGAGAAAGAGGATCAAGAGGAGGAAACCAAGAGGGAAGGTC 1898  
 Db 1766 -----GTCTCTGAAAAGAGGATCAAGAGGAGGAAACCAAGAGGGAAGGTC 1815  
 QY 1899 CACTCTCTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTGTATGATCGAT 1958  
 Db 1816 CACTCTCTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTGTATGATCGAT 1875  
 QY 1959 AATAAGATCAAGCTTTTGTACTCTACTATCCAAAACCTTATCAATAAATAAAGCTTTG 2018  
 Db 1876 AATAAGATCAAGCTTTTGTAACTACTATCTCAATCAATCAATCAATCAATCAATCAAT 1935  
 QY 2019 TGGGTTGTTTCTCC 2032  
 Db 1936 TGGGTTGTTTCTCC 1949

RESULT 12  
 ADG27463  
 ID ADG27463 standard; cDNA; 1949 BP.  
 XX AC ADG27463;  
 DT 26-FEB-2004 (first entry)  
 XX DE Peanut Ara h1 cDNA clone P17.  
 XX KW Peanut; plant; ss; gene; allergen; Ara h1; Ara h2; Ara h3;  
 KW glycinin A2B1a; Jug n1; anti-allergic; vulnerary;  
 KW anaphylactic food allergen; IgE; allergy; wound.  
 XX OS Arachis hypogaea.  
 XX PN US2003202980-A1.  
 XX PD 30-OCT-2003.  
 XX PF 18-MAR-2002; 2002US-00100303.  
 XX PR 29-DEC-1995; 95US-0009455P.  
 PR 23-SEP-1996; 96US-00717933.  
 PR 31-JAN-1998; 98US-0073283P.  
 PR 13-FEB-1998; 98US-0074590P.  
 PR 13-FEB-1998; 98US-0074624P.  
 PR 13-FEB-1998; 98US-0074633P.  
 PR 29-JUN-1998; 98US-00106872.  
 PR 27-AUG-1998; 98US-00141220.  
 PR 13-NOV-1998; 98US-00191593.  
 PR 29-JAN-1999; 99US-00240557.  
 PR 29-JAN-1999; 99US-00241101.  
 PR 11-FEB-1999; 99US-00248673.  
 PR 11-FEB-1999; 99US-00248674.  
 PR 02-MAR-1999; 99US-0122450P.

PR 02-MAR-1999; 99US-0122452P.  
 PR 02-MAR-1999; 99US-0122560P.  
 PR 02-MAR-1999; 99US-0122565P.  
 PR 02-MAR-1999; 99US-0122566P.  
 PR 11-MAR-1999; 99US-00267719.  
 PR 28-JAN-2000; 2000US-00494096.  
 PR 16-MAR-2001; 2001US-0276822P.  
 XX (CAPL/) CAPLAN M J.  
 PA (SOSI/) SOSIN H B.  
 PA (SAMP/) SAMPSON H.  
 PA (BANN/) BANNON G A.  
 PA (BURK/) BURKS A W.  
 PA (COCK/) COCKRELL G.  
 PA (COMP/) COMPADRE C M.  
 PA (CONV/) CONNAUGHTON C.  
 PA (HELM/) HELM R M.  
 PA (KING/) KING N E.  
 PA (KOPP/) KOPPER R A.  
 PA (MALE/) MALEKI S J.  
 PA (RABJ/) RABJOHN P A.  
 PA (SHIN/) SHIN D S.  
 PA (STAN/) STANLEY J S.  
 XX Caplan MJ, Sosin HB, Sampson H, Bannon GA, Burks AW, Cockrell G;  
 PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;  
 PI Rabjohn PA, Shin DS, Stanley JS;  
 XX WPI; 2003-875632/81.  
 DR P-PSDB; ADG27465.  
 DR PI  
 XX New modified anaphylactic food allergen comprising a cysteine residue  
 PT which has been modified so that it cannot participate in the disulfide  
 PT bond, useful for treating allergic reactions or wounds.  
 XX  
 PS Example 4; SEQ ID NO 6; 194pp; English.  
 XX  
 CC The invention relates to a modified anaphylactic food allergen whose  
 CC amino acid sequence is substantially identical to that of a natural  
 CC anaphylactic food allergen. The natural anaphylactic food allergen  
 CC includes at least one cysteine residue that participates in a disulfide  
 CC bond when the natural anaphylactic food allergen is in its native  
 CC conformation, except that the cysteine residue has been modified so that  
 CC it cannot participate in the disulfide bond. Also included are a method  
 CC of making a modified anaphylactic food allergen, a nucleotide molecule  
 CC encoding a modified anaphylactic food allergen defined above, a  
 CC nucleotide molecule for causing a site specific mutation in a gene  
 CC encoding a natural anaphylactic food allergen, a transgenic plant or  
 CC animal expressing a modified anaphylactic food allergen defined above, a  
 CC method of treating an individual by reducing the clinical response to a  
 CC natural anaphylactic food allergen by administering a modified  
 CC anaphylactic food allergen and an isolated fragment of peanut allergen  
 CC Ara h 1, comprising at least 10 consecutive amino acids of ADG27464 or  
 CC ADG27465. About 10-17% of the amino acids have been modified in at least  
 CC one IgE epitope or all the IgE epitopes recognised when the natural  
 CC anaphylactic food allergen is contacted with serum IgE from individual(s)  
 CC allergic to the natural anaphylactic food allergen. The invention  
 CC discloses peanut allergens Ara h1, Ara h2, Ara h3 (and their encoding  
 CC cDNAs), Soybean Glycinin A2B1a and IgE-binding epitopes of the English  
 CC walnut allergen Jug n1. The modified anaphylactic food allergen can be  
 CC used for treating allergic reactions or wounds. The present sequence  
 CC encodes a Peanut allergen of the invention.  
 XX  
 SQ Sequence 1949 BP; 599 A; 456 C; 516 G; 378 T; 0 U; 0 Other;

Query Match 86.2%; Score 1750.8; DB 10; Length 1949;  
 Best Local Similarity 94.9%; Pred. No. 0;  
 Matches 1893; Conservative 0; Mismatches 47; Indels 54; Gaps 6;  
 QY 48 CAATGAGAGGAGGTTTCTCCACTGATGCTGTGTAGGATCCTTGTCTGGCTTCAG 107  
 Db 1 CAATGAGAGGAGGTTTCTCCACTGATGCTGTGTAGGATCCTTGTCTGGCTTCAG 60







1358	1358	AAGAACTCGTGAACCTTGTAACCTCGTCTGTAGAAAAAGACAAACAGAGGGGACGGC	1411
1488	1488	GGGAA-----GAAGAGGAGGACGAAGACGAAGAAAGAGGAGGAAAGTAACAGAGAGGT	1539
1418	1418	GGGAAACAAGAGTCGAACAGAGAAGGACGAAGACTAAGAAAGAGGAGGAAAGTAACAGAGAGGT	1477
1540	1540	CGCTAGGTACACAGCGAGGTTTGAAGGAAGGGGATGTGTTTCATCATGCCAGAGCTCATCC	1599
1478	1478	CGCTAGGTACACAGCGAGGTTTGAAGGAAGGGGATGTGTTTCATCATGCCAGAGCTCATCC	1537
1600	1600	AGTAGCCATCAACCGCTTCCCTCCGAACCTCCATCTCGTCTGGGCTTCGGTATCAACGCTGAAAA	1659
1538	1538	AGTAGCCATCAACCGCTTCCCTCCGAACCTCCATCTCGTCTGGGCTTCGGTATCAACGCTGAAAA	1597
1660	1660	CAACCAAGAAATCTTCTTCGAGGTGATAGGACAATGTGATAGACCAGATAGAGAAAGCA	1719
1598	1598	CAACCAAGAAATCTTCTTCGAGGTGATAGGACAATGTGATAGACCAGATAGAGAAAGCA	1657
1720	1720	AGCGAAGGATTTAGCATTTCCCTGGTTCGGGTGAACAAGTTGAGAAAGCTCATCAAAAACCA	1779
1658	1658	AGCGAAGGATTTAGCATTTCCCTGGTTCGGGTGAACAAGTTGAGAAAGCTCATCAAAAACCA	1717
1780	1780	GAAGGAATCTCACTTTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCCGTCGTCCTCC	1839
1718	1718	GAGGAGTCTCACTTTGTGAGTGTCTGCTCAATCTCAATCTCCGTCCTCCGTC-----	1759
1840	1840	TGAAAGAGTCTCTGAGAAAGGATCAAGAGGAGGAAAAACCAAGGAGGAGGAGGTCC	1899
1760	1760	-----GTCTCTCAAAAAGAGGATCAAGAGGAGGAAAAACCAAGGAGGAGGAGGTCC	1810
1900	1900	ACTCTTTCAATTTTGAAGGCTTTTAACTGAGAAATGGAGGCAACTTCTTATGATCGATA	1959
1811	1811	ACTCTTTCAATTTTGAAGGCTTTTAACTGAGAAATGGAGGCAACTTCTTATGATCGATA	1870
1960	1960	ATAAGATCAGCGTTTGTACTCTACTATCCAAAACTTATCAATAATAATAAACGTTTGT	2019
1871	1871	ATAAGATCAGCGTTTGTGTACTTACTATCCAAAACTTATCAATAATAATAAACGTTTGT	1930
2020	2020	CGGTTGTTTCTCC 2032	
1931	1931	CGGTGTTTCTCC 1943	
RESULT 14			
ADV97605			
ID	ADV97605	standard; cDNA; 1340 BP.	
XX	ADV97605;		
XX			
DT	10-MAR-2005	(first entry)	
XX			
DE	Peanut Ara h I allergen alpha (clone 5 Ala) cDNA.		
XX			
KW	allergen; atopic dermatitis; diagnostic; immunotherapy;		
KW	immediate type hypersensitivity; Ara h I; dermatological; anti-allergic;		
KW	immunosuppressive; antibody engineering; gene; ss.		
XX			
OS	Arachis hypogaea.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	231..1238	
FT		/*tag= a	
FT		/product= "Ara h I (clone 5 Ala) protein"	
XX			
PN	US6835824-B1.		
XX			
PD	28-DEC-2004.		
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PF	13-NOV-1998;	98US-00191593.	
XX			
PR	29-DEC-1995;	95US-0009455P.	
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PR	23-SEP-1996;	96US-00717933.	
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(UYAR-) UNIV ARKANSAS-

Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;

WPI; 2005-045982/05.

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new isolated molecules and emerging panel allergens. Obtaining diagnostics with optimal concentrations of each allergen, for developing panels of mixtures of recombinant allergens, and in immunotherapy.

Disclosure; Col 75-78; 141pp; English.

CC This invention relates to a novel isolated nucleic acid molecule encoding  
CC the peanut allergen Ara h I that has been identified in patients with  
CC atopic dermatitis. Specifically, it refers to a monoclonal antibody  
CC enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the  
CC peanut allergens, where the monoclonal antibodies have specificity for a  
CC selected peanut allergen antigen. The present invention also describes  
CC hybridomas that produce two-site monoclonal antibodies specific for a  
CC peanut allergen that can be used in an ELISA to detect and determine the  
CC concentration of a specific peanut allergen in a food product or in food  
CC processing. Furthermore, it provides an expression vector and the  
CC isolated nucleic acid or its fraction can include a diagnostic label.  
CC Accordingly, these nucleic acids are useful for obtaining diagnostics  
CC with optimal concentrations of each allergen or for developing panels of  
CC mixtures of large numbers of recombinant allergens such that it can be  
CC used in immunotherapy for the treatment of food hypersensitivity  
CC reactions. This polynucleotide sequence is the peanut Ara h I allergen  
CC cDNA (clone 5 Ala) of the invention.

Sequence 1340 BP: 422 A; 296 C; 340 G; 282 T; 0 U; 0 Other;

Query Match 65.2%; Score 1324; DB 14; Length 1340;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1340: Conservative 0; Mismatches 0; Indels 6;

687 GTATTGTCAGATCGAGGCCAAACCTAACACTCTTGTTCTTCCCACGACGCTGATGCTG 746

Db 1 GTATTGTGCAGATCGAGGCCAAACCTAACACTCTTGTTCTTCCCAAGCACGCTGATGCTG 60

QY 747 ATAACATCCTTGTTATCCAGCAAGGCCAGCCCGTAGCAAATGGCAATAACA 806

Db  
61 ATAACATCCTTGTATTCCAGCAAGGCAAGCCACCGTAGCAATGGCAATAACA 120

QY 807 GAAAGAGCTTTAATCTTGACGAGGGCCATGCCACTCAGAAATCCCATCCGGTTTCATTTCTCT 866

Db 121 GAAAGAGCTTTAA TCTTGACGAGGGCCATGCAC TCAGAA TCCCATCCGGTTTCATTTCT 180

QY 867 ACATCTTGAACCGCCATGACAACCAAGACCTCAGAGTAGCTAAATCTCCATGCCCGTTA 926

Db 181 ACATCTTGAACCGCCATGACAAACCAGAACCTCAGAGTAGCTAAATCTCCATGCCCGTTA 240

QY 927 ACACACCCGGCCAGTTTGAGGATTTCTTCCCGGAGCAGCCGAGACCAATCATCCTACT 986

Db 241 ACACACCCGGCCAGTTTGAGGATTTCTTCCCGGAGCAGCCGAGACCAATCATCCTACT 300

QY 987 TGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGCTTCAATGCGGAATTC AATGAGATAC 104

Db 301 TGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGCTTCAATGCGGAATTCAATGAGATAC 360

QY 1047 GGAGGGTCTGTTAGAAAGAAATGCAGGAGGTGAGCAAGAGGAGAGGGCAGAGCGGAT 110

Db 361 GGAGGGTCTGTTAGCAAGAGAAATGCAGGAGGTGAGCAAGAGAGAGGGCAGAGCGCAT 4200

QY  
1107 GGAGTACTCGAGTAGTGAGAACAAATGAAGGAGTGATAGTCAAAGTGTCAAAGGAGCAG 116

Db 421 GGAGTACTCGGAGTAGTGAGAACAAATGAAGGAGTGATAGTCAAAGTGTCAAAGGAGCACG 480

QY 1167 TTGAAGAACTTACTAAGCACGCTAAATCCGCTCTCAAAGAAAGGCTCCGAAGAGAGGGAG 122

Db 481 TTGAAGAACTTACTAAGCACGCTAAATCCGCTCTCAAAGAAAGGCTCCGAAGAGAGGGAG 540

Qy	1227	ATATCAACAACCCCAATCAACTGTGAGAGAGCGAGCCCGATCTTTTCTAAACAACCTTTGGGA	1286
Db	541	ATATCAACAACCCCAATCAACTGTGAGAGAGCGAGCCCGATCTTTTCTAAACAACCTTTGGGA	600
Qy	1287	AGTTATTGTAGGTGAAGCCAGACAAGAAGAAACCCCAAGCTTTCAGGACCTCGACATGATGC	1346
Db	601	AGTTATTGTAGGTGAGCCAGACAAGAAGAAACCCCAAGCTTTCAGGACCTCGACATGATGC	660
Qy	1347	TCACCTGTGTAGAGATCAAGAAGAGAGCTTTGATGCTCCACACTTCAACTCAAAAGGCCA	1406
Db	661	TCACCTGTGTAGAGATCAAGAAGAGAGCTTTGATGCTCCACACTTCAACTCAAAAGGCCA	720
Qy	1407	TGGTTATTCGTCGTCGTCACAAACAAGAACTGGAACCTTTGAACTCGTCGCTGTAAGAAAG	1466
Db	721	TGGTTATTCGTCGTCGTCACAAAGAAGAACTGGAACCTTTGAACTCGTCGCTGTAAGAAAG	780
Qy	1467	AGCAACAACAGAGGGGACGGCGGAAGAAGAGGAGGACGAAGACGAAGAAGAGAGGGAA	1526
Db	781	AGCAACAACAGAGGGGACGGCGGAAGAAGAGGAGGACGAAGACGAAGAAGAGAGGGAA	840
Qy	1527	GTAACAGAGAGGTGCGTAGGTACACAGCGAGTTGAAGGAGGCGATGCTTCATCATGC	1586
Db	841	GTAACAGAGAGGTGCGTAGGTACACAGCGAGTTGAAGGAGGCGATGCTTCATCATGC	900
Qy	1587	CAGCAGCTCATCCAGTAGGCCATCAACGCTTCTCCGAACTCCATCTGCTTTGGCTTCGGTA	1646
Db	901	CAGCAGCTCATCCAGTAGGCCATCAACGCTTCTCCGAACTCCATCTGCTTTGGCTTCGGTA	960
Qy	1647	TCAACGCTGAAMACAACCAACAGATCTTCCTTGCAAGTGATAGGACAATGTGATAGCC	1706
Db	961	TCAACGCTGAAMACAACCAACAGATCTTCCTTGCAAGTGATAGGACAATGTGATAGCC	1020
Qy	1707	AGATAGAGAAGCAAGCGAAGGATTTAGCATTCCTCGGTCGGGTGAAACAAGTTGAGAAGC	1766
Db	1021	AGATAGAGAAGCAAGCGAAGGATTTAGCATTCCTCGGTCGGGTGAAACAAGTTGAGAAGC	1080
Qy	1767	TCATCAAAAACCAAGAGGATCTCAGCTTTGTGAGTGTCTGCTCCTCAATCTCAATCTCAAT	1826
Db	1081	TCATCAAAAACCAAGAGGATCTCAGCTTTGTGAGTGTCTGCTCCTCAATCTCAATCTCAAT	1134
Qy	1827	CTCCGTCGTCCTCGAGAAAGAGTCTCCTCGAGAAAGAGGATCAAGAGGAGGAAAAACAAG	1886
Db	1135	CTCCGTCGTCCTCGAGAAAGAGTCTCCTCGAGAAAGAGGATCAAGAGGAGGAAAAACAAG	1194
Qy	1887	GAGGGAAGGGTCCACTCCTTTCAATTTTGAAGGCTTTTAACTGAGAAATGAGGCAACTTG	1946
Db	1195	GAGGGAAGGGTCCACTCCTTTCAATTTTGAAGGCTTTTAACTGAGAAATGAGGCAACTTG	1254
Qy	1947	TTATGTATCGATATAAGATCACGCTTTTGTACTCTACTATCCAAAAAATTTATCAATAAA	2006
Db	1255	TTATGTATCGATATAAGATCACGCTTTTGTACTCTACTATCCAAAAAATTTATCAATAAA	1314
Qy	2007	TAAAAACGTTGTGCGTTGTTCTTCC	2032
Db	1315	TAAAAACGTTGTGCGTTGTTCTTCC	1340

Key	Location/Qualifiers
CDS	1. .1251
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FT	/product= "Glycine max (Soybean) var. Wasesuzunari
FT	protein #2"
FT	/note= "This sequence lacks a stop codon"
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XX	10-JUL-2002.
PD	
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XX	21-DEC-2000; 2000JP-00405097.
PF	
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XX	21-DEC-2000; 2000JP-00405097.
PR	
XX	
XX	(KYOU ) UNIV KYOTO.
PA	
XX	
XX	WPI; 2002-685438/74.
DR	
XX	P-PSDB; ABG71269.
PT	
PT	Glycinin, beta-conglycinin and proglycinin, their crystal structures,
PT	three dimensional coordinates, three dimensional structured and models
PT	and their uses.
XX	
PS	Disclosure; Page 1282-1283; 1298pp; Japanese.
XX	
XX	The present invention relates to a new Glycinin characterised by the
CC	atomic coordinate data fully defined in the specification. The structure
CC	can be used for improving processability of soya protein. The present
CC	nucleic acid sequence encodes the Glycine max (Soybean) var. Wasesuzunari
CC	protein #2, as described in the specification
XX	
XX	Sequence 1251 BP; 385 A; 304 C; 265 G; 297 T; 0 U; 0 Other;

Query Match	20.1%	Score 408.4	DB 6	Length 1251
Best Local Similarity	62.2%	Pred. No. 1.3e-109		
Matches 780	Conservative 0	Mismatches 381	Indels 93	Gaps 5
Qy	562	GAACAAACCCCTTTCTACTT---CCCGTCAAGCGCGTTT	TAGCACCCGCTACGGGAACCAAAA	618
Db				
Db	24	GAATAACCCCTTTCTACTTTAGAACTCTAACAGCTT	CCAAACTCTCTTTGAGAACCAAAA	83
Qy	619	CGGTAGGATCCGGGTCTCTGCAGAGTTTGTACCAAAGGT	CAAGGAGGTTTTCAGAAATCTCCA	678
Db				
Db	84	CGGTGCGATTTCGTCTCTCCAGAGATTCAACAAACGCT	CCCCCAACTTGGAGAACCTTCG	143
Qy	679	GAATCACCGGTATTGTGCAGATCGAGGCCAAACCTTA	CACACTTCTTCTTCCCAAGCAGCG	738
Db				
Db	144	AGACTACCGGATTGTCTCAGTTTCACTCAAAACCCCA	CAACAACTCTTCTCCCAACCATGC	203
Qy	739	TGATGCTGATAACATCTCTTGTTATCCAGCAAGGCCA	AGCCACCGTACCGTAGCAAAATGG	798
Db				
Db	204	TGACGCCGATTTCTCTCTCTTTGTCTTTAGCGGAG	AGCCATACTTACCTTTGGTGAACAA	263
Qy	799	CAATAACAGAAAGAGCTTTTAATCTTGACGAGGGCC	ATGCACCTAGAATCCCATCCGTTT	858
Db				
Db	264	CGACGACAGAGATCTCTTACAACCTTACCCTGGCG	ATGCCAGAGAATCCCACTGGGAAC	323
Qy	859	CAATTCTCTACATCTTGAACCGCCATGACAAACCAGA	ACCTCAGAGTAGCTAAAAATCTCCAT	918
Db				
Db	324	CACTTACTATTGGTTAAACCTTCAGCACACAGAACT	CTCAAATAATCAAACCTTGCCAT	383
Qy	919	GCCCGTTAACACACCCGGCCAGTTTGAGGATTTCTT	CCCGGCGAGCAGCCGAGACCAATC	978
Db				
Db	384	ACCCGTCAACAAACCTGGCAGATATGATGATTTCTT	CTTATCTAGCACTCAAGGCCAACCA	443
Qy	979	ATCCTACTCTCGAGGCTTCAGCAGGAATACGTTGG	AGCGCCCTTCAATGCGGAATTCAA	1038
Db				
Db	444	GTCTCTCTTCGAAGCTTTCAGGCCAATAATTTCTA	GAGACCTCTTCTCATTACCGAATTCGA	503
Qy	1039	TGAGATACGGAGGGTGCTGTTTAGAAGAGAATGCA	GAGGAGTGTAGCAAGGAGAGAGGCA	1098

RESULT 15

REGD. I.  
ABS55196

ID ABS55196 standard; DNA; 1251 BP.

2 XX  
3  
4  
5  
6  
7  
8  
9  
10

AC ABS55196;

XX  
XX  
XX

DT 17-DEC-2002 (first entry)

XX

DE Glycine m

XX

KW Soybean;

Db 504 GGAGATAAACAGGGTTTTGTTGGAGAGGAGAGGAGCAGCAGCAAGAG----- 555  
Qy 1099 GAGGCCATGAGTACTCGGAGTAGTGAGAACAAATGAAGGAGTGATAGTCAAAGTGTCAAA 1158  
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Qy 1159 GGAGCAGGTGAAGAACTTACTAAGCACGCTAAATCCGTCCTCAAGAAAGGCTCCGAGA 1218  
Db 579 GGAACAAATTCGGCAATTCAGCAGAGCGTGCCAAATCTAGTTCAGGAAACCAATTCCTC 638  
Qy 1219 AGAGGGAGATATCACCAACCCCAATCAACTTGAGAGAGGCGGCCGATCTTTCTAACAA 1278  
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Qy 1279 CTTTGGGAAGTTATTTGAGGTGAAGCGAGACAAGAGAACCCCCAGCTTCAGGACCTGGA 1338  
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Qy 1459 AAGAAAGAGCAACAACAGAGGGGACGGCGGGAAGAGAGGAGGACGAAGACGAAGA 1518  
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Qy 1519 GGAGGGNAGTTAACAGAGAGGTGCGTAGGTACACAGCGAGGTTGAAGGAGGCGATGT 1578  
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Db 954 TGTAAATCCAGCAGCTTATCCATTGTGCTCAACGCTACCTCAAACTCAATTTCTTGC 1013  
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Qy 1699 GATAGACCAGATAGAGAGCAAGCGAGGATTTAGCATTCCTGGGTCGGGTGAACAAGT 1758  
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Search completed: June 22, 2006, 11:35:24  
Job time : 914.436 secs

November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 10443.4 Seconds  
(without alignments)  
10880.347 Million cell updates/sec

Title: US-10-728-051-1  
Perfect score: 2032  
Sequence: 1 aataatcatatattcatc.....cgttgtgcgtgtttcttc 2032

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues  
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_est7:\*
- 7: gb\_est8:\*
- 8: gb\_est9:\*
- 9: gb\_est10:\*
- 10: gb\_est11:\*
- 11: gb\_est12:\*
- 12: gb\_est13:\*
- 13: gb\_est14:\*
- 14: gb\_est15:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	719	35.4	721	4	CD038628
2	713	35.1	714	4	CD038277
3	711.4	35.0	723	4	CD038527
4	681	33.5	717	4	CD038837
5	657.2	32.3	724	4	CD038648
6	629.2	31.0	719	4	CD038172
7	626	30.8	676	4	CD038790
8	602	29.6	685	4	CD038555
9	576	28.3	588	4	CD038119
10	527.6	26.0	684	4	CD038540
11	473	23.3	474	4	CD038694
12	471	23.2	582	4	CD038620
13	458.8	22.6	509	4	CD038253
14	436	21.5	484	4	CD038101
15	428.6	21.1	443	8	CO897502
16	425	20.9	425	4	CD038284
17	419.6	20.6	536	4	CD038075
18	392	19.3	411	8	CO897503
19	358.6	17.6	406	4	CD038765

20	307.6	15.1	823	4	CA858229	EST635484
21	306.2	15.1	851	4	CA858769	EST636024
22	296.8	14.6	894	4	CA858664	EST635919
23	296.6	14.6	806	2	BI310422	EST531217
24	292.2	14.4	864	3	BI312471	EST609047
25	290.8	14.3	780	2	BI311149	EST531289
26	290.6	14.3	823	3	BI312251	EST608090
27	290	14.3	862	3	BI312313	EST608807
28	285.8	14.1	854	3	BI312341	EST608987
29	285.4	14.0	830	4	CA858151	EST635406
30	283	13.9	805	2	BI312339	EST531408
31	281.4	13.8	760	4	CA858137	EST635392
32	281.4	13.8	769	2	BI311022	EST531277
33	280.2	13.8	847	4	CA858293	EST635548
34	278.4	13.7	781	2	BI311613	EST531336
35	274.6	13.5	765	3	BI312251	EST608086
36	273.2	13.4	804	4	CA858167	EST635422
37	272.4	13.4	843	2	BI311012	EST531276
38	271.8	13.4	805	4	CA858433	EST635688
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42	271	13.3	860	3	BI312453	EST608029
43	270.4	13.3	701	3	BI312484	EST610416
44	270.4	13.3	727	2	BI309850	EST531160
45	270.4	13.3	837	2	BI310945	EST531269

ALIGNMENTS

RESULT 1  
LOCUS CD038628 721 bp mRNA linear EST 07-MAY-2003  
DEFINITION UTPPI010.A05 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
Arachis hypogaea cDNA clone UTPPI010\_A05 5', mRNA sequence.  
ACCESSION CD038628  
VERSION CD038628.1 GI:30420466  
KEYWORDS EST.  
SOURCE Arachis hypogaea (peanut)  
ORGANISM Arachis hypogaea  
REFERENCE 1 (bases 1 to 721)  
AUTHORS Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.  
TITLE Generation and Analyses of ESTs for Arachis hypogaea  
JOURNAL Unpublished (2003)  
COMMENT Contact: Baozhu Guo  
Molecular Genetics  
USDA/ARS, Crop Protection and Management Research Unit  
2747 Davis Rd., Tifton, GA 31794, USA  
Tel: 229-387-2334  
Fax: 229-387-2321  
Email: bguo@tifton.usda.gov  
Seq primer: T3

FEATURES  
source

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/notes="Vector: Uni-ZAP XR; Site\_1: EcoRI; Site\_2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection"

and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match		35.4%;	Score 719;	DB 4;	Length 721;
Best Local Similarity		99.7%;	Pred. No. 6.3e-191;		
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				Gaps	0;
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DB	61	ATTGTAGGTGAAGCCGACAGAAAGAACCCCGAGCTTCAGGACCTGGACATGATGCTCAC	120		
QY	1351	CTGTGTAGAGATCAAGAAGGAGCTTTGATGCTCCACACTTCAACTCAAGGCCATGTT	1410		
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QY	1411	TATCGTCGTCGTCAACAAAGGAACCTGGAACCTTGAACCTCGTGGCTGTAAAGAAAAGACA	1470		
DB	181	TATCGTCGTCGTCAACAAAGGAACCTGGAACCTTGAACCTCGTGGCTGTAAAGAAAAGACA	240		
QY	1471	ACAACAGAGGGGACGGCGGAAAGAAGAGGAGGACGAAGACGAAGAAGAGGAGGGAAGTAA	1530		
DB	241	ACAACAGAGGGGACGGCGGAAAGAAGAGGAGGACGAAGACGAAGAAGAGGAGGGAAGTAA	300		
QY	1531	CAGAGAGTGCCTAGGTACACAGCGAGTTTGAAGGAAGGCGATGTTTCATCATGCCAGC	1590		
DB	301	CAGAGAGTGCCTAGGTACACAGCGAGTTTGAAGGAAGGCGATGTTTCATCATGCCAGC	360		
QY	1591	AGTCTATCCAGTAGCCATCAACGCTTCTCCGAACCTCCATCTGCTGGCTTCGGTATCAA	1650		
DB	361	AGTCTATCCAGTAGCCATCAACGCTTCTCCGAACCTCCATCTGCTGGCTTCGGTATCAA	420		
QY	1651	CGCTGAAAAACAACAGAAATCTTCTTGAGAGGTGATAAGGACAATGTGTATAGACCAGAT	1710		
DB	421	CGCTGAAAAACAACAGAAATCTTCTTGAGAGGTGATAAGGACAATGTGTATAGACCAGAT	480		
QY	1711	AGAGAGCAAGCGAAGGATTTAGCATTCCTCGGTCGGGTGAACAAGTTGAGAAGCTCAT	1770		
DB	481	AGAGAGCAAGCGAAGGATTTAGCATTCCTCGGTCGGGTGAACAAGTTGAGAAGCTCAT	540		
QY	1771	CAAAAACCAAGGAATCTCACATTTGTGAGTGTCTGTCCTCAATCTCAATCTCAATCTCC	1830		
DB	541	CAAAAACCAAGGAATCTCACATTTGTGAGTGTCTGTCCTCAATCTCAATCTCAATCTCC	600		
QY	1831	GTCTCTCTCTGAGAAAGAGTCTCTGAGAAAGAGGATCAAGAGGAGGAAAAACCAAGAGG	1890		
DB	601	GTCTCTCTCTGAGAAAGAGTCTCTGAGAAAGAGGATCAAGAGGAGGAAAAACCAAGAGG	660		
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DB	661	GAGGGTCCACTCCTTTCAATTTTGAAGGCTTTTAACTGAGATGAGGCAACTTGTAT	720		
QY	1951	G 1951			
DB	721	G 721			

RESULT 2

CD038277

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CD038277 714 bp mRNA linear EST 07-MAY-2003  
UTPPI005 A03 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
Arachis hypogaea cDNA clone UTPPI005\_A03 5', mRNA sequence.  
CD038277  
CD038277.1 GI:30420115  
EST.  
Arachis hypogaea (peanut)  
Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.  
1 (bases 1 to 714)  
Luo M., Dang P., Guo B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.  
and Lynch, R.E.  
Generation and Analyses of ESTs for Arachis hypogaea  
Unpublished (2003)  
Contact: Baozhu Guo  
Molecular Genetics  
USDA/ARS, Crop Protection and Management Research Unit  
2747 Davis Rd., Tifton, GA 31794, USA  
Tel: 229-387-2334  
Fax: 229-387-2321  
Email: bguo@tifton.usda.gov  
Seq primer: T3.  
Location/Qualifiers  
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cDNA library was constructed from peanut cultivar A13  
(NCV11XAR4). A13 has resistance to Aspergillus infection  
and drought tolerance. The immature pods that developed to  
R6 stage were collected from different plants, and placed  
into liquid N2 immediately and stored in -80oC freezer.  
Total RNA was isolated with TRIzol-Reagent  
ultrapure (GIBCOBRL). mRNA was extracted and purified from  
total RNA (Promega). cDNA synthesis and library  
construction followed the protocol of by ZAP-cDNA Gigapack  
III Gold cloning kit (Stratagene). The cDNA above 500bp  
were collected after size-fraction. The inserts were  
directionally cloned into Uni-ZAP XR vector using XhoI  
EcoRI sites adapters. The lambda library was packed into  
phages using Gigapack III Gold (Stratagene). The  
un-amplified library was used to excise pBluescript  
phagemids from the Uni-ZAP XR vector, and the phagemids  
was used to transform the host bacteria SOLR. The library  
was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match		35.1%;	Score 713;	DB 4;	Length 714;
Best Local Similarity		99.9%;	Pred. No. 3.1e-189;		
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				Gaps	0;
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Db	1	AAACAGAGAAACCCCTGGCCAGAGGTGCTCCAGAGTTGTCAACAGGAAACCGATGAC	60		
Qy	206	TTGAAGCAAAAGGCATCGAGTCTCGTCGACCAAGCTCGAGTATGATCTCGTTGTGTC	265		
Db	61	TTGAAGCAAAAGGCATCGAGTCTCGTCGACCAAGCTCGAGTATGATCTCGTTGTGTC	120		



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Qy 266 TATGATCTTCGAGGACACACTGGCACCACCAACCAACGTTTCCCTCCAGGGGACGCGACA 325
Db 121 TATGATCTTCGAGGACACACTGGCACCACCAACCAACGTTTCCCTCCAGGGGACGCGACA 180
Qy 326 CGTGGCCGCCAACCCGAGAGACTAGCATGATGACCGCGTCAACCCCGGAAGAGGAAGGA 385
Db 181 CGTGGCCGCCAACCCGAGAGACTAGCATGATGACCGCGTCAACCCCGGAAGAGGAAGGA 240
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RESULT 3
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  Arachis hypogaea cDNA clone UTPI008_E12 5', mRNA sequence.
ACCESSION
  CD038527
VERSION
  EST.
KEYWORDS
  CD038527.1 GI:30420365
SOURCE
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  Arachis hypogaea
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
  Aeschynomeneae; Arachis.
  1 (bases 1 to 723)
REFERENCE
  Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.
  and Lynch, R. E.
  Generation and Analyses of ESTs for Arachis hypogaea
  Unpublished (2003)
  Contact: Baozhu Guo
  Molecular Genetics
  USDA/ARS, Crop Protection and Management Research Unit
  2747 Davis Rd., Tifton, GA 31794, USA
  Tel: 229-387-2334
  Fax: 229-387-2321
  Email: bguo@tifton.usda.gov
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cDNA library was constructed from peanut cultivar A13
(NCV11XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise phagescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
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## ORIGIN

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Query Match 35.0%; Score 711.4; DB 4; Length 723;
Best Local Similarity 99.4%; Pred. No. 8.9e-189;
Matches 712; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1210 CTCGGAAGAGGAGGAGATATCACCAACCAATCACTTCAGAGAAGCGCAGCCGATCT 1269
Db 1 CTCGGAAGAGGAGGAGATATCACCAACCAATCACTTCAGAGAAGCGCAGCCGATCT 60

Qy 1270 TTCTAACAACTTTGGGAAGTTATTGAGGTGAAGCCAGCAAGAAAGAACCCCAAGTTCA 1329
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Qy 1330 GGACCTGGACATGATGCTCACCTGTGTAGAGATCAAGAAGGAGCTTTGATGCTCCACA 1389
Db 121 GGACCTGGACATGATGCTCACCTGTGTAGAGATCAAGAAGGAGCTTTGATGCTCCACA 180

Qy 1390 CTTCAACTCAAGGCGCATGTTATCGTCGTCGCAACAAAGGAACCTGGAACCTTGAAC 1449
Db 181 CTTCAACTCAAGGCGCATGTTATCGTCGTCGTCACAAAGGAACCTTGAACCTTGAAC 240

Qy 1450 CGTGGCTGTAAAGAAAAGAGCAACACAGAGGGGACGCGGGAAGAGAGGAGGACGAAGA 1509
Db 241 CGTGGCTGTAAAGAAAAGAGCAACACAGAGGGGACGCGGGAAGAGAGGAGGACGAAGA 300

Qy 1510 CGAAGAGAGGAGGGAAGTAACAGAGAGTGTCGTAGTACACAGCGAGGTTGAAGGAAG 1569
Db 301 CGAAGAGAGGAGGGAAGTAACAGAGAGTGTCGTAGTACACAGCGAGGTTGAAGGAAG 360

Qy 1570 CGATGTTTCATCATGCCAGCCTCATCCAGTAGCCATCAACGCTTCCTCCGAACCTCCA 1629
Db 361 CGATGTTTCATCATGCCAGCCTCATCCAGTAGCCATCAACGCTTCCTCCGAACCTCCA 420

Qy 1630 TCTGCTTGGCTTCGGTATCAACGCTGAAACCAACACAGAGATCTTCTTCAGGTGATAA 1689
Db 421 TCTGCTTGGCTTCGGTATCAACGCTGAAACCAACACAGAGATCTTCTTCAGGTGATAA 480

Qy 1690 GGCATATGTATAGACAGATAGAGAGCAGGAGGATTTAGCATTTCCCTGGTCCGG 1749
Db 481 GGCATATGTATAGACAGATAGAGAGCAGGAGGATTTAGCATTTCCCTGGTCCGG 540

Qy 1750 TGAACAGTTGAGAAGCTCATCAAAACCAAGAGGAATCTCCTTTGTAGTGTCTCTCC 1809
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QY 1810 TCAATCTCAATCTCAATCTCCGTCGTCCTGAGAAAGAGTCTCCCTGAGAAAGAGGATCA 1869  
 Db 601 TCAATCTCAATCTCAATCTCCGTCGTCCTGAGAAAGAGTCTCCCTGAGAAAGAGGATCN 660  
 QY 1870 AGAGGAGGAAACCAAGGAGGAGGAGGTCACCTCTTCAATTTTGAAGGCTTTTGA 1925  
 Db 661 AGAGGAGGAAACCAAGGAGGAGGAGGTCACCTCTTCAATTTTGAAGGCTTTTGA 716

RESULT 4  
 CD038837  
 LOCUS  
 DEFINITION  
 Arachis hypogaea cDNA clone UTPI012\_H04 5', mRNA sequence.  
 CD038837  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Arachis hypogaea (peanut)  
 Arachis hypogaea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
 Aeschynomeneae; Arachis.  
 1 (bases 1 to 717)

REFERENCE  
 AUTHORS

Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.

and Lynch, R. E.

Generation and Analyses of ESTs for Arachis hypogaea

Unpublished (2003)

Contact: Baozhu Guo

Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd., Tifton, GA 31794, USA

Tel: 229-387-2334

Fax: 229-387-2321

Email: bguo@tifton.usda.gov

Seq primer: T3.

FEATURES

source

1..717

/organism="Arachis hypogaea"

/mol\_type="mRNA"

/cultivar="A13"

/db\_xref="taxon:3818"

/clone="UTPI012\_H04"

/tissue\_type="Immature pods"

/dev\_stage="R6"

/lab\_host="Xli-blue"

/clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library

(UTPP)"

/notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;

cDNA library was constructed from peanut cultivar A13

(NCV11XAR4). A13 has resistance to Aspergillus infection

and drought tolerance. The immature pods that developed to

R6 stage were collected from different plants, and placed

into liquid N2 immediately and stored in -80oC freezer.

Total RNA was isolated with TRIzol-Reagent

ultrapure (GIBCOBRL). mRNA was extracted and purified from

total RNA (Promega). cDNA synthesis and library

construction followed the protocol of by ZAP-cDNA Gigapack

III Gold cloning kit (Stratagene). The cDNA above 500bp

were collected after size-fraction. The inserts were

directionally cloned into Uni-ZAP XR vector using XhoI

EcoRI sites adapters. The lambda library was packed into

phages using Gigapack III Gold (Stratagene). The

un-amplified library was used to excise pBluescript

phagemids from the Uni-ZAP XR vector, and the phagemids

was used to transform the host bacteria SOLR. The library

was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match

Best Local Similarity 33.5%; Score 681; DB 4; Length 717;

Matches 714; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 967 CCGAGACCACATCTCTAGTTCAGGGCTTCAGCAGGAATACGTTGAGGCGCCCTTCAA 1026  
 Db 1 CCGAGACCACATCTCTAGTTCAGGGCTTCAGCAGGAATACGTTGAGGCGCCCTTCAA 60  
 QY 1027 TCGCGAATTCATAGATACCGAGGGTGTGTTAGAAAGAAATGCGAGGAGGTGAGCAAGA 1086  
 Db 61 TCGCGAATTCATAGATACCGAGGGTGTGTTAGAAAGAAATGCGAGGAGGTGAGCAAGA 120  
 QY 1087 GGAGAGGGCAGAGCGGATGAGTACTCGGAGTAGTGAGAACATTAAGGAGTGTAGT 1146  
 Db 121 GGAGAGGGCAGAGCGGATGAGTACTCGGAGTAGTGAGAACATTAAGGAGTGTAGT 180  
 QY 1147 CAAAGTGTCAAAGGAGCAGCTTGAAGAACTTACTTAAGCAGCGTAAATTCGTTCTCAAAGAA 1206  
 Db 181 CAAAGTGTCAAAGGAGCAGCTTGAAGAACTTACTTAAGCAGCGTAAATTCGTTCTCAAAGAA 240  
 QY 1207 AGGCTCCGAAGAGAGGGAGATATACCAACCCCAATCAACTTGAGAGAAGCGAGCCGA 1266  
 Db 241 AGGCTCCGAAGAGAGGGAGATATACCAACCCCAATCAACTTGAGAGAAGCGAGCCGA 300  
 QY 1267 TCTTTCTAACAACTTTGGGAAGTTATTGAGGTGAAGCCAGACAAGAACCCCGAGCT 1326  
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 QY 1327 TCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAGAGGAGCTTTGATGCTCCC 1386  
 Db 361 TCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAGAGGAGCTTTGATGCTCCC 420  
 QY 1387 ACACCTTCAACTCAAAGGCCATGGTTATCGTCGTCAACAAAGGAACCTGGAACCTTGA 1446  
 Db 421 ACACCTTCAACTCAAAGGCCATGGTTATCGTCGTCAACAAAGGAACCTGGAACCTTGA 480  
 QY 1447 ACTCTGGCTGTGAAGAAAGAGCAACACAGAGGGGACCGCGGGAAGAGAGGAGACGA 1506  
 Db 481 ACTCTGGCTGTGAAGAAAGAGCAACACAGAGGGGACCGCGGGAAGAGAGGAGACGA 540  
 QY 1507 AGACGAAGAAG-AGGAGGAAGTTAAACAGA-GAGGTGCGTAGGTACACACGAGGTTGAAG 1564  
 Db 541 AGACGAAGAAGAGGAGGAAGTTAAACAGAGGAGGTGCGTAGGTACACACGAGGTTGAAG 600  
 QY 1565 GAAGCGAGTGTTCATCATGCCAGAGCTCATCCAGTATCCAGTATCAACGCTTCTCCGAA 1624  
 Db 601 GAAGCGAGTGTTCATCATGCCAGAGCTCATCCAGTATCAACGCTTCTCCGAA 660  
 QY 1625 CTCATCTCTGGCTTCGGTATCAACGCTGAAACAAACACAGATCTCTCTTGA 1681  
 Db 661 CTCATCTCTGGCTTCGGTATCAACGCTG-AAACAAACACAGATCTCTCTTGA 716

RESULT 5

CD038648

LOCUS

DEFINITION

Arachis hypogaea cDNA clone UTPI010\_C11 5', mRNA sequence.

CD038648

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arachis hypogaea (peanut)

Arachis hypogaea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;

Aeschynomeneae; Arachis.

1 (bases 1 to 724)

REFERENCE

AUTHORS

Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.

and Lynch, R. E.

Generation and Analyses of ESTs for Arachis hypogaea

Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Baozhu Guo

Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd., Tifton, GA 31794, USA

Tel: 229-387-2334

Fax: 229-387-2321  
Email: bguo@tifon.usda.gov  
Seq primer: T3.

FEATURES  
source

Location/Qualifiers  
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/organism="Arachis hypogaea"  
/mol\_type="mRNA"  
/cultivar="A13"  
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/lab\_host="XLI-blue"  
/clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"  
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat bang."

## ORIGIN

Query Match 32.3%; Score 657.2; DB 4; Length 724;  
Best Local Similarity 95.9%; Pred. No. 1.8e-173;  
Matches 697; Conservative 0; Mismatches 24; Indels 6; Gaps 2;  
QY 799 CAATAACAGAAAGAGCTTTAATCTTGACGAGGGCCATGCACCTCAGATCCCATCCGCTTT 858  
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QY 859 CATTTCCTACATCTTGAAACCGCCATGACCAACAGAACTCAGAGTACTAAATCTCCAT 918  
DB 61 CATTTCCTACATCTTGAAACCGCCATGACCAACAGAACTCAGAGTACTAAATCTCCAT 120  
QY 919 GCCCGTTAACACACCCCGCCAGTTTGAGGATTTCTCCCGCGAGCCGAGACCAATC 978  
DB 121 GCCCGTTAACACACCCCGCCAGTTTGAGGATTTCTCCCGCGAGCCGAGACCAATC 180  
QY 979 ATCTTACTTCGAGGCTTCACGAGGATACGTTGGAGCCGCTTCATCGGNAATCAA 1038  
DB 181 ATCTTACTTCGAGGATTCACGAGGATACGTTGGAGCCGCTTCATCGGNAATCAA 240  
QY 1039 TGAGATACGAGGGTGCTGTGTAGAAAGAAATGACAGGAGGTGAGCAAGAGGAGAGGGCA 1098  
DB 241 TGAGATACGAGGGTGCTGTGTAGAAAGAAATGACAGGAGGAGCAAGAGGAGAGGGCA 300  
QY 1099 GAGCGATGGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGTGTAGTCAAGTGTCAA 1158  
DB 301 GAGCGAGCGGAGTACTCGGAGTAGTG--ATAATGAAGGAGTGTAGTCAAGTGTCAA 357  
QY 1159 GGACACGTTGAACAATCTTACTAGCAGCGTAAATCGTCTCAAGAAAGGCTCCGAGA 1218  
DB 358 GGACACGTTGAACAATCTTACTAGCAGCGTAAATCGTCTCAAGAAAGGCTCC--GA 414  
QY 1219 AGAGGAGATATACCAACCAATCAACTTGAGAGAGGCGAGCCGATCTTTCTAACAA 1278  
DB 415 AGAGGAGATATACCAACCAATCAACTTGAGAGATGGGAGGCCCGATCTTTCTAACAA 474  
QY 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAAGACCCCGAGCTTCAGGACCTGGA 1338

DB 475 CTTTGGGAGGTATTTGAGGTGAAGCCAGACAAGAAACCCCGAGCTTCAGGACCTGGA 534  
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DB 535 CATGATGCTCACCTGCTAGAGATCAAGAGGAGCTTTGATGCTCCACACTTCAACTC 594  
QY 1399 AAAGGCCATGTTATCGTCTGTCGTCACAAAGGAACCTTGAACCTTCGTTGGTGT 1458  
DB 595 AAAGGCCATGTTATCGTCTGTCGTCACAAAGGAACCTTGAACCTTCGTTGGTGT 654  
QY 1459 AAGAAAAGACCAACACAGAGGGGACGCGCGGGAAGAGAGGAGCAAGACGAAGAAGA 1518  
DB 655 AAGAAAAGACCAACACAGAGGGGACGCGCGGGAACAGAGTGGGAAGAAGAGGAGGA 714  
QY 1519 GGAGGGA 1525  
DB 715 TGAAGAA 721  
RESULT 6  
CD038172  
LOCUS  
DEFINITION  
CD038172  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arachis hypogaea (peanut)  
Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.  
1 (bases 1 to 719)  
Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.  
and Lynch, R. E.  
Generation and Analyses of ESTs for Arachis hypogaea  
Unpublished (2003)  
Contact: Baozhu Guo  
Molecular Genetics  
USDA/ARS, Crop Protection and Management Research Unit  
2747 Davis Rd., Tifton, GA 31794, USA  
Tel: 229-387-2334  
Fax: 229-387-2321  
Email: bguo@tifon.usda.gov  
Seq primer: T3.  
Location/Qualifiers  
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/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into

phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."									
ORIGIN									
Query Match		31.0%;		Score 629.2;		DB 4;		Length 719;	
Best Local Similarity		95.6%;		Pred. No. 1.4e-165;					
Matches 693;		Conservative 0;		Mismatches 16;		Indels 16;		Gaps 4;	
QY	1040	GAGATACGGAGGTCGTGTTAGAGAGAAATGCAGGAGTGCAGCAAGAGGAGAGGGCAG	1099						
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QY	1100	AGCGGATGGAGTACTCGGAGTAGTGAGAACAAATGAAGGAGTGATAGTCAAAGTGTCAAAG	1159						
DB	61	AGCGGAGGAGTACTCGGAGTAGTG---ATAATGAAGGAGTGATAGTCAAAGTGTCAAAG	117						
QY	1160	GAGCAGCTTGAAGAACTTACTAGCAGCGCTAAATCGTCTCAAGAAAGGCTCCGAGAA	1219						
DB	118	GAGCAGCTTCAAGAACTTACTAGCAGCGCTAAATCGTCTCAAGAAAGGCTCC--GAA	174						
QY	1220	GAGGAGATATCAACCAACCAATCACTTGAGAGAGGCGGAGCCGATCTTTCTTAACAAC	1279						
DB	175	GAGGAAGATATCAACCAACCAATCACTTGAGAGATGGCGAGCCGATCTTTCTTAACAAC	234						
QY	1280	TTTGGGAGTTATTGAGGTGAAGCCACAGCAAGAAACCCAGCTTCAGGACCTGGAC	1339						
DB	235	TTTGGGAGGTTATTGAGGTGAAGCCACAGCAAGAAACCCAGCTTCAGGACCTGGAC	294						
QY	1340	ATGATGCTCACTGTGTAGAGATCAAGAAAGGAGCTTTGATGCTCCACACTTCAACTCA	1399						
DB	295	ATGATGCTCACTGTGTAGAGATCAAGAAAGGAGCTTTGATGCTCCACACTTCAACTCA	354						
QY	1400	AAGCCATGTTATCGTCGTCGTCACAAAGGAACTGGAACCTTGAACTCGTGGCTGTA	1459						
DB	355	AAGCCATGTCATCGTCGTCGTCACAAAGGAACTGGAACCTTGAACTCGTAGCTGTA	414						
QY	1460	AGAAAGAGCAACACAGAGGGGACGCGGGAA-----GAAGAGGAGGACGAAGAC	1510						
DB	415	AGAAAGAGCAACACAGAGGGGACGCGGGAA-----GAAGAGGAGGAGGAAGAT	474						
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QY	1571	GATGTGTTTCATCGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCAT	1630						
DB	535	GATGTGTTTCATCGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCAT	594						
QY	1631	CTGCTTGGCTTCGGTATCAACGGTGAAACCAACACAGAAATCTTCC--TTGCAGGTGATAA	1689						
DB	595	CTGCTTGGCTTCGGTATCAACGGTGAAACCAACACAGAAATCTTCTTTTCAGGTGATAA	654						
QY	1690	GGCAATGTCATAGACAGATAGAGAGCAAGCGAAGGATTTAGCATTTCCCTGGTCCGG	1749						
DB	655	GGACNATGTGATAGACAGATAGAGAGCAAGCGAAGGATTTAGCATTTCCCTGGTCCGG	714						
QY	1750	TGAAC	1754						
DB	715	TGAAC	719						
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CD038790									
LOCUS									
DEFINITION									
CD038790									
Arachis hypogaea cDNA clone UTPI012_C06 5', mRNA sequence.									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
Arachis hypogaea (peanut)									

ORGANISM	Arachis hypogaea Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.									
REFERENCE	1 (bases 1 to 676)									
AUTHORS	Luo M., Dang P., Guo B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G. and Lynch, R.E.									
TITLE	Generation and Analyses of ESTs for Arachis hypogaea									
JOURNAL	Unpublished (2003)									
COMMENT	Contact: Baozhu Guo Molecular Genetics USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd, Tifton, GA 31794, USA Tel: 229-387-2334 Fax: 229-387-2321 Email: bguo@tifton.usda.gov Seq primer: T3.									
FEATURES	Location/Qualifiers									
source	1..676 /organism="Arachis hypogaea" /mol_type="mRNA" /cultivar="A13" /db_xref="taxon:3818" /clone="UTPP1012_C06" /tissue_type="Immature pods" /dev_stage="R6" /lab_host="XL1-blue" /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)" /note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."									
ORIGIN	Query Match 30.8%; Score 626; DB 4; Length 676; Best Local Similarity 99.0%; Pred. No. 1.1e-164; Matches 670; Conservative 0; Mismatches 3; Indels 4; Gaps 4;									
QY	834	ATGCATTCAGAAATCCCATCCGGTTTCATTTCTTCATCTTGAACCGCCATGACAAACGAGA								893
DB	1	ATGCATTCAGAAATCCCATCCGGTTTCATTTCTTCATCTTGAACCGCCATGACAAACGAGA								60
QY	894	ACCTCAGAGTAGTAAATCTCCATGCCGTTAAACACACCCCGCCAGTTTGAGGATTTCT								953
DB	61	ACCTCAGAGTAGTAAATCTCCATGCCGTTAAACACACCCCGCCAGTTTGAGGATTTCT								120
QY	954	TCCCGGCGAGCGAGCCGAGCAATCATCTTTCAGGGCTTCAGAGGAATACGTTGG								1013
DB	121	TCCCGGCGAGCGAGCCGAGCAATCATCTTTCAGGGCTTCAGAGGAATACGTTGG								180
QY	1014	AGGCCGCTTCATTCGCGAATTCGAATCAGATACGAGGGTCTGTTAGAGAGAAATCGAG								1073
DB	181	AGGCCGCTTCATTCGCGAATTCGAATCAGATACGAGGGTCTGTTAGAGAGAAATCGAG								240
QY	1074	GAGGTGAGCAAGAGGAGAGGCGCATGGAGTACTCGGAGTAGTCGAGACAAATG								1133











Molecular Genetics  
 USDA/ARS, Crop Protection and Management Research Unit  
 2747 Davis Rd., Tifton, GA 31794, USA  
 Tel: 229-387-2334  
 Fax: 229-387-2321  
 Email: bguo@tifton.usda.gov  
 Seq primer: T3.

## FEATURES

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 /organism="Arachis hypogaea"  
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 /note="Vector: Uni-ZAP XR; Site\_1: EcoRI; Site\_2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80°C freezer. Total RNA was isolated with TRIzol-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

## ORIGIN

Query Match 22.6%; Score 458.8; DB 4; Length 509;  
 Best Local Similarity 93.8%; Pred. No. 1.6e-117;  
 Matches 497; Conservative 0; Mismatches 12; Indels 21; Gaps 1;  
 1494 AAGAGGAGGACGAAGACGAAGAGGAGGAGGAGTAAACAGAGAGGTGCGTAGGTACACAG 1553  
 Db 1 AAGAGGAGGAGGAGATGAAGAGAGAGGAGGAGGAGTAAACAGAGAGGTGCGTAGGTACACAG 60  
 1554 CGAGGTTGAAGGAGGCGATGTGTTTCATATGCCAGCAGTCTATCCAGTAGCCATCAACG 1613  
 Db 61 CGAGGTTGAAGGAGGCGATGTGTTTCATATGCCAGCAGTCTATCCAGTAGCCATCAACG 120  
 1614 CTTCTCCGAACCTCCATCTCTGGCTTCGGTATCAACGCTGAACCAACACAGATCT 1673  
 Db 121 CTTCTCCGAACCTCCATCTCTGGCTTCGGTATCAACGCTGAACCAACACAGATCT 180  
 1674 TCCTTGCGGTGTAAGCAATGTGTATAGACAGATAGAGAGCAAGCAAGGATTAG 1733  
 Db 181 TCCTTGCGGTGTAAGCAATGTGTATAGACAGATAGAGAGCAAGCAAGGATTAG 240  
 1734 CATTCCCTGGGTGGGTGAACAAAGTTGAGAGGTCATCAAAAAACCAAGAGGAATCTCACT 1793  
 Db 241 CATTCCCTGGGTGGGTGAACAAAGTTGAGAGGTCATCAAAAAACCAAGAGGAGTCTCACT 300  
 1794 TTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCGTTCGTCTCCTGAGAAAGAGTCTC 1853  
 Db 301 TTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCGTTCGTCTCCTGAGAAAGAGTCTC 339  
 1854 CTGAGAAAGAGGATCAAGAGGAGGAGAAACCAAGGAGGAGGTCCTCACTCTTTCAATTT 1913  
 Db 340 CTGAGAAAGAGGATCAAGAGGAGGAGAAACCAAGGAGGAGGTCCTCACTCTTTCAATTT 399  
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 LOCUS  
 DEFINITION  
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 ACCESSION  
 CD038101  
 VERSION  
 CD038101.1  
 GI:30419939  
 KEYWORDS  
 EST.  
 SOURCE  
 Arachis hypogaea (peanut)  
 ORGANISM  
 Arachis hypogaea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eutosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.  
 REFERENCE  
 1 (bases 1 to 484)  
 Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.  
 Generation and Analyses of ESTs for Arachis hypogaea  
 Unpublished (2003)  
 CONTACT: Baozhu Guo  
 Molecular Genetics  
 USDA/ARS, Crop Protection and Management Research Unit  
 2747 Davis Rd., Tifton, GA 31794, USA  
 Tel: 229-387-2334  
 Fax: 229-387-2321  
 Email: bguo@tifton.usda.gov  
 Seq primer: T3.  
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 Location/Qualifiers  
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 /lab\_host="XLI-blue"  
 /clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"  
 /note="Vector: Uni-ZAP XR; Site\_1: EcoRI; Site\_2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80°C freezer. Total RNA was isolated with TRIzol-Reagent ultrapure(GIBCOBRL). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

## ORIGIN

Query Match 21.5%; Score 436; DB 4; Length 484;  
 Best Local Similarity 93.8%; Pred. No. 4.2e-111;  
 Matches 473; Conservative 0; Mismatches 10; Indels 21; Gaps 1;  
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Qy	1565	GAAGGCGATGTGTTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCTCGAA	1624
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Qy	1625	CTCCATCTGTTGGCTTCGCGTATCAACGCTGAAAAACAACACAGAAATCTTCTCTGACGGT	1684
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Db	182	GATAAGACAAATGTGATAGACCATAGAGAGCAACGCGAAGGATTTAGCATTCCTCGGGT	241
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 DEFINITION  
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 LOCUS EST00007 Peanut Lambda Express library Arachis hypogaea cDNA 5',  
 mRNA sequence.

ACCESSION	C0897502
VERSION	C0897502.1
KEYWORDS	GI:51237292
SOURCE	EST.
ORGANISM	Arachis hypogaea (peanut)
	Arachis hypogaea
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.
REFERENCE	1 (bases 1 to 443)
AUTHORS	Yan, Y.S., Wang, L., Zhong, Y.J. and Huang, S.Z.
TITLE	Expressed sequence tags of mid-matured cotyledons of peanut
JOURNAL	Unpublished (2004)
COMMENT	Contact: Shangzhi Huang

## FEATURES

## ORIGIN

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:43:18 ; Search time 316.712 Seconds  
(without alignments)  
12004.877 Million cell updates/sec

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Perfect score: 2032  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2032	100.0	2032	3	US-09-191-593-5
3	2032	100.0	2032	3	US-09-715-036-5
4	2032	100.0	2041	3	US-09-106-872A-23
5	1930	95.0	1930	3	US-09-106-872A-3
6	1752.4	86.2	1949	3	US-09-106-872A-19
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8	750	36.9	750	3	US-09-106-872A-18
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13	406.8	20.0	1278	3	US-10-245-227D-13
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15	406.8	20.0	1320	3	US-09-758-652-3
16	406.8	20.0	1320	3	US-10-684-651-3
17	406.8	20.0	1320	3	US-10-245-227D-3
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22	403.6	19.9	3808	3	US-10-245-227D-92
23	402	19.8	1350	3	US-10-245-227D-86

ALIGNMENTS

RESULT 1  
US-09-106-872A-21

; Sequence 21, Application US/09106872A  
; Patent No. 6486311  
; GENERAL INFORMATION:  
; APPLICANT: Burks Jr., A. Wesley  
; APPLICANT: Stanley, J. Steven  
; APPLICANT: Cockrell, Gael  
; APPLICANT: King, Nina E.  
; APPLICANT: Sampson, Hugh A.  
; APPLICANT: Helm, Ricki M.  
; APPLICANT: Bannan, Gary A.  
; TITLE OF INVENTION: Peanut Allergens and Methods  
; FILE REFERENCE: HS 103 CIP  
; CURRENT APPLICATION NUMBER: US/09/106, 872A  
; CURRENT FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: PCT/US96/15222  
; PRIOR FILING DATE: 1996-09-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 2032  
; TYPE: DNA  
; ORGANISM: Atachis hypogaea  
US-09-106-872A-21

Query Match 100.0%; Score 2032; DB 3; Length 2032;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 13632, A  
Sequence 15, Appl  
Sequence 13308, A  
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Sequence 1, Appl  
Sequence 11, Appl



APPLICATION NUMBER: US/09/191,593  
FILING DATE: 13 NOVEMBER 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/717,933  
FILING DATE: 23 SEPTEMBER 1996  
APPLICATION NUMBER: US 07/998,377  
FILING DATE: 30 DECEMBER 1992  
APPLICATION NUMBER: US 08/158,704  
FILING DATE: 29 NOVEMBER 1993  
APPLICATION NUMBER: US 60/009,455  
FILING DATE: 29 DECEMBER 1995  
APPLICATION NUMBER: US 08/610,424  
FILING DATE: 04 MARCH 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: ALEXANDER, DANIEL R  
REGISTRATION NUMBER: 32,604  
REFERENCE/DOCKET NUMBER: ARK00895601B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (501) 582-9111  
TELEFAX: (501) 521-4931  
TELEX: NO. 6835824 applicable  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2032 bases  
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STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
DESCRIPTION: Identified as Ara h I Beta P41b  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE: No. 6835824 applicable  
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ORGANISM: Arachis hypogaea  
STRAIN: Florunner  
INDIVIDUAL ISOLATE: Clone P41b  
DEVELOPMENTAL STAGE: Seed  
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IMMEDIATE SOURCE:  
LIBRARY: Florunner seed cDNA expression  
LIBRARY: library in Uni-ZAP XR vector  
CLONE: P41b  
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CHROMOSOME/SEGMENT: No. 6835824 applicable  
MAP POSITION: No. 6835824 applicable  
UNITS: No. 6835824 applicable  
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LOCATION: 50..1930  
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IDENTIFICATION METHOD: protein information and established  
IDENTIFICATION METHOD: consensus sequence  
OTHER INFORMATION: Seed storage protein and  
OTHER INFORMATION: allergen  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-09-191-593-5

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; Sequence 5, Application US/09715036  
; Patent No. 6943010  
; GENERAL INFORMATION:

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; APPLICANT: DODO, HORTENSE W.  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: KONAN, KOFFI N'DA  
; APPLICANT: VIQUEZ, OLGA  
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN  
; FILE REFERENCE: 072121/0104  
; CURRENT APPLICATION NUMBER: US/09/715,036  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/167,255  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
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; ORGANISM: Arachis hypogaea  
; US-09-715-036-5
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Best Local Similarity 100.0%; Pred. No. 0;  
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QY 481 ACGGAAAATAAGGCCCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Db 481 ACGGAAAATAAGGCCCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
  
QY 541 TGTGAGGAGAGAAACAATCTCGGAACAACCTTTCTACTTCCCTCAAGGCGGTTTAGCAC 600  
Db 541 TGTGAGGAGAGAAACAATCTCGGAACAACCTTTCTACTTCCCTCAAGGCGGTTTAGCAC 600  
  
QY 601 CCGCTACGGGAACCAAAAACGGTAGGATCGGGTCTCGAGAGGTTTGACCAAGAGGTCAG 660  
Db 601 CCGCTACGGGAACCAAAAACGGTAGGATCGGGTCTCGAGAGGTTTGACCAAGAGGTCAG 660  
  
QY 661 GCAGTTTCAGAAATCTCCAGAAATCACCGTATTGTGAGAGTCGAGGCCCAAACTAACCTCT 720  
Db 661 GCAGTTTCAGAAATCTCCAGAAATCACCGTATTGTGAGAGTCGAGGCCCAAACTAACCTCT 720  
  
QY 721 TGTTCCTCCAAAGCAGCGTGATCTGATTAACATCTCTTGTATTCCAGAGGGAAGCCAC 780  
Db 721 TGTTCCTCCAAAGCAGCGTGATCTGATTAACATCTCTTGTATTCCAGAGGGAAGCCAC 780
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Db 721 TGTCTTTCCCAAGCAGCGCTGATGCTGATAATCATCTTTGTTATCCAGAGGGCAAGCCAC 780  
Qy 781 CGTGACCGTAGCAATGGCAATTAACAGAAAGAGCTTTAATCTTGACGAGGCGCATGCACT 840  
Db 781 CGTGACCGTAGCAATGGCAATTAACAGAAAGAGCTTTAATCTTGACGAGGCGCATGCACT 840  
Qy 841 CAGAAATCCCAATCCGGTTTCAATTTCTTCTATCTTGAACCGGCATGACAAACCAAGAACTCTCAG 900  
Db 841 CAGAAATCCCAATCCGGTTTCAATTTCTTCTATCTTGAACCGGCATGACAAACCAAGAACTCTCAG 900  
Qy 901 AGTAGCTTAAATCTCCATGCCGTTTAAACACACCCGGCCAGTTTGAAGATTTCTTCCCGGC 960  
Db 901 AGTAGCTTAAATCTCCATGCCGTTTAAACACACCCGGCCAGTTTGAAGATTTCTTCCCGGC 960  
Qy 961 GAGCAGCGGAGACCAATCATCTTACTTTGACGGGCTTCAGCAGGAATACGTTGGAGGCGC 1020  
Db 961 GAGCAGCGGAGACCAATCATCTTACTTTGACGGGCTTCAGCAGGAATACGTTGGAGGCGC 1020  
Qy 1021 CTTCAATGCCGAATTCATGAGATACGAGGGTCTCTTTAGAGAGAAATCGAGAGGTGA 1080  
Db 1021 CTTCAATGCCGAATTCATGAGATACGAGGGTCTCTTTAGAGAGAAATCGAGAGGTGA 1080  
Qy 1081 GCAGAGGAGAGGGCAGAGGCGATGAGTACTCGGAGTAGTCAGAACCAATGAGGAGT 1140  
Db 1081 GCAGAGGAGAGGGCAGAGGCGATGAGTACTCGGAGTAGTCAGAACCAATGAGGAGT 1140  
Qy 1141 GATAGTCAAAAGTGTCAAAGAGCAGCTTTGAAGAACTTACTAAGCAGCGCTAAATCCGTC 1200  
Db 1141 GATAGTCAAAAGTGTCAAAGAGCAGCTTTGAAGAACTTACTAAGCAGCGCTAAATCCGTC 1200  
Qy 1201 AAGAAAGGCTCCGAAGAAGAGGAGATATCAACAAACCCCAATCAACTTTGAGAGAGCGGA 1260  
Db 1201 AAGAAAGGCTCCGAAGAAGAGGAGATATCAACAAACCCCAATCAACTTTGAGAGAGCGGA 1260  
Qy 1261 GCCCGATCTTTCTAAACAACTTTGGGAGTTATTGAGGTGAAGCCAGACAAAGAAACCC 1320  
Db 1261 GCCCGATCTTTCTAAACAACTTTGGGAGTTATTGAGGTGAAGCCAGACAAAGAAACCC 1320  
Qy 1321 CCAGCTTCAGGACTCGACATGATGCTCAGCTGTGAGAGATCAAGAAGAGCTTTGAT 1380  
Db 1321 CCAGCTTCAGGACTCGACATGATGCTCAGCTGTGAGAGATCAAGAAGAGCTTTGAT 1380  
Qy 1381 GTTCCACACTTCAACTCAAGGCCATGTTGTTATCGTGTGCTCAACAAAGGAACTGGAA 1440  
Db 1381 GCTCCACACTTCAACTCAAGGCCATGTTGTTATCGTGTGCTCAACAAAGGAACTGGAA 1440  
Qy 1441 CTTTGAACCTGTGCTTAAGAAAGCAACACAGAGGGGCGCGGGAAGAGGA 1500  
Db 1441 CTTTGAACCTGTGCTTAAGAAAGCAACACAGAGGGGCGCGGGAAGAGGA 1500  
Qy 1501 GGACGAAGACGAAGAGAGGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTT 1560  
Db 1501 GGACGAAGACGAAGAGAGGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTT 1560  
Qy 1561 GAAGGAAGGCGATGTTTCATATGCGCAGAGCTCATCCAGTAGCCATCAACGCTTCC 1620  
Db 1561 GAAGGAAGGCGATGTTTCATATGCGCAGAGCTCATCCAGTAGCCATCAACGCTTCC 1620  
Qy 1621 CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAACCAACAGAAATCTTCC 1680  
Db 1621 CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAACCAACAGAAATCTTCC 1680  
Qy 1681 AGGTGATAGGACAAATGTGTAGACACAGATAGAGAGCAAGCGAAGATTTAGCATTTCC 1740  
Db 1681 AGGTGATAGGACAAATGTGTAGACACAGATAGAGAGCAAGCGAAGATTTAGCATTTCC 1740  
Qy 1741 TGGGTCCGGTGAAACAAAGTTGAGAGGCTCATCAAAAAACGAAGAAATCTCACTTTGAG 1800  
Db 1741 TGGGTCCGGTGAAACAAAGTTGAGAGGCTCATCAAAAAACGAAGAAATCTCACTTTGAG 1800  
Qy 1801 TGCTCGTCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAAAGAGTCTCTCTGAGAA 1860  
Db 1801 TGCTCGTCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAAAGAGTCTCTCTGAGAA 1860

Qy 1861 AGAGGATCAAGAGAGGAAAAACAAGGAGGAAAGGTCCACTCTCTTCAATTTTGAAGGC 1920  
Db 1861 AGAGGATCAAGAGAGGAAAAACAAGGAGGAAAGGTCCACTCTCTTCAATTTTGAAGGC 1920  
Qy 1921 TTTTAACTGAGAATGAGGCAACTTGTATGATATCGATAAAGATCACGCTTTTGTACT 1980  
Db 1921 TTTTAACTGAGAATGAGGCAACTTGTATGATATCGATAAAGATCACGCTTTTGTACT 1980  
Qy 1981 CTACTATCCAAAACCTTATCAATAAATAAAAAAGTTTGTGCGTTGTTTCTCC 2032  
Db 1981 CTACTATCCAAAACCTTATCAATAAATAAAAAAGTTTGTGCGTTGTTTCTCC 2032

## RESULT 4

US-09-106-872A-23  
; Sequence 23, Application US/09106872A  
; Patent No. 6486311  
; GENERAL INFORMATION:  
; APPLICANT: Burks Jr., A. Wesley  
; APPLICANT: Stanley, J. Steven  
; APPLICANT: Cockrell, Gael  
; APPLICANT: King, Nina E.  
; APPLICANT: Sampson, Hugh A.  
; APPLICANT: Helm, Ricki M.  
; APPLICANT: Bannon, Gary A.  
; TITLE OF INVENTION: Peanut Allergens and Methods  
; FILE REFERENCE: HS 103 CIP  
; CURRENT APPLICATION NUMBER: US/09/106, 872A  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: PCT/US96/15222  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 2041  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea  
US-09-106-872A-23

Query Match 100.0%; Score 2032; DB 3; Length 2041;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60  
Db 1 AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60  
Qy 61 GGTTCCTCACATGATGCTGTTGCTAGGGATCTTGTCTCTGGCTTCAGTTTCTGCAACGCA 120  
Db 61 GGTTCCTCACATGATGCTGTTGCTAGGGATCTTGTCTCTGGCTTCAGTTTCTGCAACGCA 120  
Qy 121 TGCCAAGTATCATCTTACAGAGAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180  
Db 121 TGCCAAGTATCATCTTACAGAGAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180  
Qy 181 GAGTTGCTCAACAGGAACCGGATGACTTGAAGCAAAAGGATGCGAGTCTCGCTGCACAA 240  
Db 181 GAGTTGCTCAACAGGAACCGGATGACTTGAAGCAAAAGGATGCGAGTCTCGCTGCACAA 240  
Qy 241 GCTCGAGTATGATCTCTGTTGTGTCTATGATCTCTCGAGGACACATGCGGACCAACCA 300  
Db 241 GCTCGAGTATGATCTCTGTTGTGTCTATGATCTCTCGAGGACACATGCGGACCAACCA 300  
Qy 301 AGTTTCCCTCCAGGGGAGGAGCAGCTGCGCCCAACCCGGAGACTACGATGATGACCG 360  
Db 301 AGTTTCCCTCCAGGGGAGGAGCAGCTGCGCCCAACCCGGAGACTACGATGATGACCG 360  
Qy 361 CGGTCAACCCCAAGAGAGAGGAGGCGGATGCGGACCAAGCTGGACCCAGAGGAGGCTGA 420  
Db 361 CGGTCAACCCCAAGAGAGAGGAGGCGGATGCGGACCAAGCTGGACCCAGAGGAGGCTGA 420  
Qy 421 AAGAGAAGAAGACTGGAGACAAACCAAGAGAAGATTGGAGCGGACCAAGTATCAGCAGCC 480

421	Db	 AAGAGAAAGAACTTGGAGACAACCAAGAGAGATTGGAGGCGACCAAGTTCATCAGCAGCC	480
481	Qy	 ACGAAATTAAGGCCGCAAGAGAGAGAGAAACAAGATGGGGAAACACCAAGTAGCCA	540
481	Db	 ACGAAATTAAGGCCGCAAGAGAGAGAGAAACAAGATGGGGAAACACCAAGTAGCCA	540
541	Qy	 TGTGAGGGAAGAAACATCTCGGAACAACCCCTTTCTACTTCCCGTCAAGCGGTTTAGCAC	600
541	Db	 TGTGAGGGAAGAAACATCTCGGAACAACCCCTTTCTACTTCCCGTCAAGCGGTTTAGCAC	600
601	Qy	 CCGCTACGGGAAACAAACCGTAGTACCGGGTCTCGAGAGGTTTGACCAAGGTCAAG	660
601	Db	 CCGCTACGGGAAACAAACCGTAGTACCGGGTCTCGAGAGGTTTGACCAAGGTCAAG	660
661	Qy	 GCAGTTTCAGAACTCCAGAAATCACCGTATTGTGCAGATCAGGCGCAAACTAACACTCT	720
661	Db	 GCAGTTTCAGAACTCCAGAAATCACCGTATTGTGCAGATCAGGCGCAAACTAACACTCT	720
721	Qy	 TGTTCTTTCCCAAGCAGCGTGATGCTGATAACATCCTTTGTTTATCCAGCAAGGCGCAAGCCAC	780
721	Db	 TGTTCTTTCCCAAGCAGCGTGATGCTGATAACATCCTTTGTTTATCCAGCAAGGCGCAAGCCAC	780
781	Qy	 CGTGACCGTAGCAAAATGCGCAATAACAGAAAGAGCTTTAACTTTGACGAGGGCCATGCAC	840
781	Db	 CGTGACCGTAGCAAAATGCGCAATAACAGAAAGAGCTTTAACTTTGACGAGGGCCATGCAC	840
841	Qy	 CAGAAATCCCATCCGGTTTCATTTCTTCTACATCTTTGAACCGGCATGACAAACAGAAACCTCAG	900
841	Db	 CAGAAATCCCATCCGGTTTCATTTCTTCTACATCTTTGAACCGGCATGACAAACAGAAACCTCAG	900
901	Qy	 AGTAGCTTAAATCTCCATGTCGGTTTAAACACACCGGCGCAGTTTGAGGATTTCTTCCGGC	960
901	Db	 AGTAGCTTAAATCTCCATGTCGGTTTAAACACACCGGCGCAGTTTGAGGATTTCTTCCGGC	960
961	Qy	 GAGCAGCCGAGACCAATCATCTTACTTTGACGGGCTTCAGCAGGAATACGTTGAGAGCCGC	1020
961	Db	 GAGCAGCCGAGACCAATCATCTTACTTTGACGGGCTTCAGCAGGAATACGTTGAGAGCCGC	1020
1021	Qy	 CTTCAATGCGGAATTTCAATGAGATACGAGAGGTGCTGTTAGAGAGAAATCAGAGAGGTGA	1080
1021	Db	 CTTCAATGCGGAATTTCAATGAGATACGAGAGGTGCTGTTAGAGAGAAATCAGAGAGGTGA	1080
1081	Qy	 GCAAGAGGAGAGGGGACAGAGGCGATCGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGT	1140
1081	Db	 GCAAGAGGAGAGGGGACAGAGGCGATCGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGT	1140
1141	Qy	 GATAGTCAAAAGTGTCAAAGGAGCAGCTTGAGAACTTACTAAGCAGCTAAATCCCGTCTC	1200
1141	Db	 GATAGTCAAAAGTGTCAAAGGAGCAGCTTGAGAACTTACTAAGCAGCTAAATCCCGTCTC	1200
1201	Qy	 AAGAAAGGCTCCGAGAGAGAGGAGATATCAACAACCCAATCAACTTGAGAGAGGCGA	1260
1201	Db	 AAGAAAGGCTCCGAGAGAGAGGAGATATCAACAACCCAATCAACTTGAGAGAGGCGA	1260
1261	Qy	 GCCGATCTTCTAACAACTTTGGGAAGTTATTGAGGTGAGCCAGCACAAGAGAACCC	1320
1261	Db	 GCCGATCTTCTAACAACTTTGGGAAGTTATTGAGGTGAGCCAGCACAAGAGAACCC	1320
1321	Qy	 CCAGCTTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAGAAGGAGCTTTGAT	1380
1321	Db	 CCAGCTTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAGAAGGAGCTTTGAT	1380
1381	Qy	 GCTCCCACTTTCAACTCAAGGCCATGTTTATCGTCGTCTGTCNAACAAAGAACTGGAAA	1440
1381	Db	 GCTCCCACTTTCAACTCAAGGCCATGTTTATCGTCGTCTGTCNAACAAAGAACTGGAAA	1440
1441	Qy	 CCTTGAACCTCGTGCTGTAGAAAGAGAACAAACAGAGGGGACGGCGGAAGAGGGA	1500
1441	Db	 CCTTGAACCTCGTGCTGTAGAAAGAGAACAAACAGAGGGGACGGCGGAAGAGGGA	1500
1501	Qy	 GGACGAAGAAGAAAGAGGAGGGAAGTAAACAGAGAGTTCGTAGGTATACACGCGAGTT	1560

[illegible]

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361 CCCTCAACCCGAGAGAGAGGAGCGGATGGGACACAGCTGGACCGAGGGAGCGTGA 420  
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661 GCAGTTTCAGAAATTCAGAAATCAACAGAAAGAGCTTTAATCTTGAACGAGGCAATCACTCT 720  
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1021 CTTCAATCGGAAATCAATGAGATACGAGGAGCTTGTAGAGAGAAATGCGAGGAGTGA 1080  
1021 CTTCAATCGGAAATCAATGAGATACGAGGAGCTTGTAGAGAGAAATGCGAGGAGTGA 1080  
1081 GCAAGAGGAGAGAGGAGGAGGAGGAGTCTCGAGTCTGAGGAGTCTGAGGAGTCTGAGGAG 1140  
1081 GCAAGAGGAGAGAGGAGGAGGAGGAGTCTCGAGTCTGAGGAGTCTGAGGAGTCTGAGGAG 1140  
1141 GATAGTCAAAAGTCAAAAGGAGCAGCTTGAAGAACTTACTTAAGACCGCTAAATCCGCTCTC 1200  
1141 GATAGTCAAAAGTCAAAAGGAGCAGCTTGAAGAACTTACTTAAGACCGCTAAATCCGCTCTC 1200  
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1261 GCCCGATCTTTCTAAACAATTTGGGAGTTATTTGAGTGAAGCCAGACAGAGAACCC 1320  
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1321 CCAGCTTCAGGACCTGGACATGATGCTCAGCTGTGTAGAGATCAAAAGAGAGCTTTGAT 1380  
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1381 GCTCCACACCTTCAACTCAAAAGGCCATGTTATCGTGTGTAGAGATCAAAAGAGAGCTTTGAT 1440  
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1501 GGACGAGAGAGAGAGAGAGGAGGAAAGTAAACAGAGAGGTCGCTAGGTACACAGCGAGTT 1560  
1561 GAAGGAGGCGATGTTTATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
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1621 CGAATCTCCATCTGCTTGGCTTCCGTTATCAACGCTGAAACCAACACAGAGATCTTCTTGC 1680  
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1741 TGGGTCGGGTGAACAAGTTGAGAGGCTCATCAAAAAACAGAGAGGATCTCACTTTGTGAG 1800  
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1801 TGCTCGTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT 1860  
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1861 AGAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920  
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1921 TTTTAACTGA 1930

## RESULT 6

US-09-106-872A-19

; Sequence 19, Application US/09106872A

; Patent No. 6486311

; GENERAL INFORMATION:

; APPLICANT: Burks Jr., A. Wesley

; APPLICANT: Stanley, J. Steven

; APPLICANT: Cockrell, Gael

; APPLICANT: King, Nina E.

; APPLICANT: Sampson, Hugh A.

; APPLICANT: Helm, Ricki M.

; APPLICANT: Bannon, Gary A.

; TITLE OF INVENTION: Peanut Allergens and Methods

; FILE REFERENCE: HS 103 CIP

; CURRENT APPLICATION NUMBER: US/09/106,872A

; CURRENT FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: PCT/US96/15222

; PRIOR FILING DATE: 1996-09-23

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patent Ver. 2.1

; SEQ ID NO 19

; LENGTH: 1949									
; TYPE: DNA									
; ORGANISM: Arachis hypogaea									
US-09-106-872A-19									
Query Match 86.2%; Score 1752.4; DB 3; Length 1949;									
Best Local Similarity 95.0%; Pred. No. 0;									
Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;									
QY	48	CAATGAGAGGGGGTTCTCCACTGATGCTGTGTCTAGGGATCCCTTGCTCGCTTCAG	107	1008	CGTTGGAGCCCGCTTCAATGCGGAATTC	1067	1009	CGTTGGAGCCCGCTTCAATGCGGAATTC	1067
DB	1	CAATGAGAGGGGGTTCTCCACTGATGCTGTGTCTAGGGATCCCTTGCTCGCTTCAG	60	943	CTTTGGAGCCCGCTTCAATGCGGAATTC	1002	1010	CTTTGGAGCCCGCTTCAATGCGGAATTC	1002
QY	108	TTTCTGCAACGATGCAAGTCACTTACAGAGAAACAGAGAACCCCTGCGCC	167	1068	ATGTCAGGAGGTGAGCAAGAGGAGAGGCGGATGGAGTACTCGGAGTAGTGAGA	1127	1011	ATGTCAGGAGGTGAGCAAGAGGAGAGGCGGATGGAGTACTCGGAGTAGTGAGA	1127
DB	61	TTTCTGCAACGAGGCAAGTCACTTACAGAGAAACAGAGAACCCCTGCGCC	114	1003	ATGTCAGGAGGAGCAAGAGGAGAGGCGGAGGCGGATGGAGTACTCGGAGTAGTG---	1059	1012	ATGTCAGGAGGAGCAAGAGGAGAGGCGGAGGCGGATGGAGTACTCGGAGTAGTG---	1059
QY	168	AGAGGTGCTCCAGAGTTGTCAACAGAAACCGGATGACTTGAAGCAAAAGGCATGCGAGT	227	1128	ACAATGAAGGAGTGATAGTCAAAAGTCTCAAAAGGAGCACGTTTGAAGAACTTACTAAGCACG	1187	1013	ACAATGAAGGAGTGATAGTCAAAAGTCTCAAAAGGAGCACGTTTGAAGAACTTACTAAGCACG	1187
DB	115	AGAGGTGCTCCAGAGTTGTCAACAGAAACCGGATGACTTGAAGCAAAAGGCATGCGAGT	174	1060	ATAATCAAGGAGTGATAGTCAAAAGTCTCAAAAGGAGCACGTTTGAAGAACTTACTAAGCACG	1119	1014	ATAATCAAGGAGTGATAGTCAAAAGTCTCAAAAGGAGCACGTTTGAAGAACTTACTAAGCACG	1119
QY	228	CTCGCTGCAACCAAGCTCGAGTATGATCTCTGTTGTCTATGATCCTCGAGGACACACTG	287	1188	CTAAATCCGTCTCAAAAGAAAGGCTCCGAAGAGAGAGGAGATATCAACCAACCCCAATCAACT	1247	1015	CTAAATCCGTCTCAAAAGAAAGGCTCCGAAGAGAGAGGAGATATCAACCAACCCCAATCAACT	1247
DB	175	CTCGCTGCAACCAAGCTCGAGTATGATCTCTGTTGTCTATG-----ACACTG	222	1120	CTAAATCCGTCTCAAAAGAAAGGCTCC---GAAGAGGAAGATATCAACCAACCCCAATCAACT	1176	1016	CTAAATCCGTCTCAAAAGAAAGGCTCC---GAAGAGGAAGATATCAACCAACCCCAATCAACT	1176
QY	288	GCACCAACCAACCAAGTTCCCTCCAGGGAGCGGACACGCTGCGCCCAACCCGGAGACT	347	1248	TGAGAGAGGCGAGCCCGGATCTTTCTAAACAACTTTGGGAAGTTATTTGAGGTTGAAGCCAG	1307	1017	TGAGAGAGGCGAGCCCGGATCTTTCTAAACAACTTTGGGAAGTTATTTGAGGTTGAAGCCAG	1307
DB	223	GGCCCAACCAACCAAGTTCCCTCCAGGGAGCGGACACGCTGCGCCCAACCCGGAGACT	282	1177	TGAGAGATGCGGAGCCCGATCTTTCTAAACAACTTTGGGAAGTTATTTGAGGTTGAAGCCAG	1236	1018	TGAGAGATGCGGAGCCCGATCTTTCTAAACAACTTTGGGAAGTTATTTGAGGTTGAAGCCAG	1236
QY	348	ACGATGATGACCGCGTCAACCCGAGAGAGAGGAGCGGATGGGACACAGCTGGAC	407	1308	ACAAGAAACCCCGAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAG	1367	1019	ACAAGAAACCCCGAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAG	1367
DB	283	ACGATGATGACCGCGTCAACCCGAGAGAGAGGAGCGGATGGGACACAGCTGAAC	342	1237	ACAAGAAACCCCGAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAG	1296	1020	ACAAGAAACCCCGAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAG	1296
QY	408	CGAGGAGCGGTGAAGAGAGAGAGACTGGAGACAACCAAGAGAGATTTGGAGCGACCAA	467	1368	AAGGAGCTTTGATGCTCCACACTTCAACTCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGG	1427	1021	AAGGAGCTTTGATGCTCCACACTTCAACTCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGG	1427
DB	343	CGAGGAGCGGTGAAGAGAGAGAGACTGGAGACAACCAAGAGAGATTTGGAGCGACCAA	402	1297	AAGGAGCTTTGATGCTCCACACTTCAACTCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGG	1356	1022	AAGGAGCTTTGATGCTCCACACTTCAACTCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGG	1356
QY	468	GTATCAGAGCCACGGAAATTAAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	527	1428	AAGGAACTGGAAACCTTGAACCTCGTAGCTGAAGAAAGAGCAACCAACAGAGGGGACGGC	1487	1023	AAGGAACTGGAAACCTTGAACCTCGTAGCTGAAGAAAGAGCAACCAACAGAGGGGACGGC	1487
DB	403	GTATCAGAGCCACGGAAATTAAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	462	1357	AAGGAACTGGAAACCTTGAACCTCGTAGCTGAAGAAAGAGCAACCAACAGAGGGGACGGC	1416	1024	AAGGAACTGGAAACCTTGAACCTCGTAGCTGAAGAAAGAGCAACCAACAGAGGGGACGGC	1416
QY	528	CACAGGTAGCCATGTGAGGAGAGAAACATCTCGGAACCAACCTTTCTACTTCCCGTCAA	587	1488	GGGAA-----GAAGAGGAGGAGCAAGACGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG	1538	1025	GGGAA-----GAAGAGGAGGAGCAAGACGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG	1538
DB	463	CACAGGTAGCCATGTGAGGAGAGAAACATCTCGGAACCAACCTTTCTACTTCCCGTCAA	522	1417	GGGAA-----GAAGAGGAGGAGCAAGACGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG	1476	1026	GGGAA-----GAAGAGGAGGAGCAAGACGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG	1476
QY	588	GGCGGTTTAGCACCCGCTACGGGAACCAAAACCGGTAGGATCCGGGTCCTGAGAGGTTTG	647	1539	TGCGTAGGTACACAGCGAGGTTGAAGGAGGCGGATGTTTCAATCATGCCAGAGCTCATC	1598	1027	TGCGTAGGTACACAGCGAGGTTGAAGGAGGCGGATGTTTCAATCATGCCAGAGCTCATC	1598
DB	523	GGCGGTTTAGCACCCGCTACGGGAACCAAAACCGGTAGGATCCGGTCTTGCAGAGGTTTG	582	1477	TGCGTAGGTACACAGCGAGGTTGAAGGAGGCGGATGTTTCAATCATGCCAGAGCTCATC	1536	1028	TGCGTAGGTACACAGCGAGGTTGAAGGAGGCGGATGTTTCAATCATGCCAGAGCTCATC	1536
QY	648	ACCAAGGTCMAGGCGATTCAGAACTCCAGAACTCCAGAACTCCAGAACTCCAGAACTCCAG	707	1599	CAGTAGCCATCAACCGCTTCTCCGAACTCCATCTCGTTGGCTTTCGGTATCAACCGCTGAAA	1658	1029	CAGTAGCCATCAACCGCTTCTCCGAACTCCATCTCGTTGGCTTTCGGTATCAACCGCTGAAA	1658
DB	583	ACCAAGGTCMAGGCGATTCAGAACTCCAGAACTCCAGAACTCCAGAACTCCAGAACTCCAG	642	1537	CAGTAGCCATCAACCGCTTCTCCGAACTCCATCTCGTTGGCTTTCGGTATCAACCGCTGAAA	1596	1030	CAGTAGCCATCAACCGCTTCTCCGAACTCCATCTCGTTGGCTTTCGGTATCAACCGCTGAAA	1596
QY	708	AACCTAACACTCTTGTCTTCCCAAGCAGCGCTGATGCTGATAACATCTTGTATCCAGC	767	1659	ACAAACACAGAACTTCTTCTTCAGGTGATAAGGACAACTGTGTAGACCCAGATAGAGAAGC	1718	1031	ACAAACACAGAACTTCTTCTTCAGGTGATAAGGACAACTGTGTAGACCCAGATAGAGAAGC	1718
DB	643	GACCTAACACTCTTGTCTTCCCAAGCAGCGCTGATGCTGATAACATCTTGTATCCAGC	702	1597	ACAACACACAGAACTTCTTCTTCAGGTGATAAGGACAACTGTGTAGACCCAGATAGAGAAGC	1656	1032	ACAACACACAGAACTTCTTCTTCAGGTGATAAGGACAACTGTGTAGACCCAGATAGAGAAGC	1656
QY	768	AAGGCAAGCCCGTGACCGTGAAGCAATGGCAATTAACAGAAAGAGCTTTAATCTTTGAGC	827	1719	AAGCGAAGGATTTAGCATTTCCCTGGGTCGAAACAAAGTTGAGAAAGCTCATCAAAAACC	1778	1033	AAGCGAAGGATTTAGCATTTCCCTGGGTCGAAACAAAGTTGAGAAAGCTCATCAAAAACC	1778
DB	703	AAGGCAAGCCCGTGACCGTGAAGCAATGGCAATTAACAGAAAGAGCTTTAATCTTTGAGC	762	1657	AAGCGAAGGATTTAGCATTTCCCTGGGTCGAAACAAAGTTGAGAAAGCTCATCAAAAACC	1716	1034	AAGCGAAGGATTTAGCATTTCCCTGGGTCGAAACAAAGTTGAGAAAGCTCATCAAAAACC	1716
QY	828	AGGGCCATGCACCTCAGAACTCCGTTTCAATTTCTTACATCTTGAACCCGATGACA	887	1779	AGAGGAATCTCACTTTGTGAGTGTCTCTCAATCTCAATCTCAATCTCCGTCGTC	1838	1035	AGAGGAATCTCACTTTGTGAGTGTCTCTCAATCTCAATCTCAATCTCCGTCGTC	1838
DB	763	AGGGCCATGCACCTCAGAACTCCGTTTCAATTTCTTACATCTTGAACCCGATGACA	822	1717	AGAGGAGTCTCACTTTGTGAGTGTCTCTCAATCTCAATCTCAATCTCCGTC	1765	1036	AGAGGAGTCTCACTTTGTGAGTGTCTCTCAATCTCAATCTCAATCTCCGTC	1765
QY	888	ACCAGAACCTCAGAGTAGCTTAAATCTCCATGCGCGTTAAACACACCCGCGGCTTTGAGG	947	1839	CTGAGAAAGAGTCTCTCTGAGAAAGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGAGGTC	1898	1037	CTGAGAAAGAGTCTCTCTGAGAAAGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGAGGTC	1898
DB	823	ACCAGAACCTCAGAGTAGCTTAAATCTCCATGCGCGTTAAACACACCCGCGGCTTTGAGG	882	1766	-----GTCTCTCGAAAGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGAGGTC	1815	1038	-----GTCTCTCGAAAGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGAGGTC	1815
QY	948	ATTTCTTCCGGCGAGCGGAGCAACATCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1007	1899	CACTCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGAACTTGTATGTATCCAT	1958	1039	CACTCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGAACTTGTATGTATCCAT	1958
DB	883	ATTTCTTCCGGCGAGCGGAGCAACATCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	942	1816	CACTCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGAACTTGTATGTATCCAT	1875	1040	CACTCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGAACTTGTATGTATCCAT	1875
QY				1959	AATAAGATCACGCTTTTGTACTCTACTATCCAAAAAATTATCAATAAATAAAAAAGTTTG	2018	1041	AATAAGATCACGCTTTTGTACTCTACTATCCAAAAAATTATCAATAAATAAAAAAGTTTG	2018
DB				1876	AATAAGATCACGCTTTTGTAACTTACTATCCAAAAAATTATCAATAAATAAAAAAGTTTG	1935	1042	AATAAGATCACGCTTTTGTAACTTACTATCCAAAAAATTATCAATAAATAAAAAAGTTTG	1935
QY				2019	TGCGTTGTTTCTCC 2032		1043	TGCGTTGTTTCTCC 2032	
DB				1936	TGCGTTGTTTCTCC 1949		1044	TGCGTTGTTTCTCC 1949	

RESULT 7  
US-09-191-593-4  
; Sequence 4, Application US/09191593  
; Patent No. 6835824  
; GENERAL INFORMATION:  
; APPLICANT: BURKS, A Wesley, HELM, Ricki M,  
; APPLICANT: COCKRELL, Gael, STANLEY, J Steven,  
; APPLICANT: BANNON, Gary A  
; TITLE OF INVENTION: PEANUT ALLERGENS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Head, Johnson & Kachigian  
; STREET: 112 W. Center St., Suite 230  
; CITY: Fayetteville  
; STATE: Arkansas AR  
; COUNTRY: United States of America  
; ZIP: 72701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 6.2  
; SOFTWARE: Wordperfect 6.0C  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/191,593  
; FILING DATE: 13 NOVEMBER 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/717,933  
; FILING DATE: 23 SEPTEMBER 1996  
; APPLICATION NUMBER: US 07/998,377  
; FILING DATE: 30 DECEMBER 1992  
; APPLICATION NUMBER: US 08/158,704  
; FILING DATE: 29 NOVEMBER 1993  
; APPLICATION NUMBER: US 60/009,455  
; FILING DATE: 29 DECEMBER 1995  
; APPLICATION NUMBER: US 08/610,424  
; FILING DATE: 04 MARCH 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ALEXANDER, DANIEL R  
; REGISTRATION NUMBER: 32,604  
; REFERENCE/DOCKET NUMBER: ARK00895601B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (501) 582-9111  
; TELEFAX: (501) 521-4931  
; TELEX: No. 6835824 applicable  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1949 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; DESCRIPTION: identified as Ara h I Alpha P17  
; HYPOTHEtical: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE: No. 6835824 applicable  
; ORIGINAL SOURCE:  
; ORGANISM: Arachis hypogaea  
; STRAIN: Florunner  
; INDIVIDUAL ISOLATE: Clone P17  
; DEVELOPMENTAL STAGE: Seed  
; HAPLOTYPE: No. 6835824 applicable  
; TISSUE TYPE: Seed mRNA, cDNA library  
; CELL TYPE: No. 6835824 applicable  
; CELL LINE: No. 6835824 applicable  
; ORGANELLE: No. 6835824 applicable  
; IMMEDIATE SOURCE:  
; LIBRARY: Florunner seed cDNA expression  
; LIBRARY: library in Uni-ZAP XR vector  
; CLONE: P17  
; POSITION IN GENOME:

; CHROMOSOME/SEGMENT: No. 6835824 applicable  
; MAP POSITION: No. 6835824 applicable  
; UNITS: No. 6835824 applicable  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1847  
; IDENTIFICATION METHOD: By agreement with  
; IDENTIFICATION METHOD: protein information and established  
; IDENTIFICATION METHOD: consensus sequence  
; OTHER INFORMATION: Seed storage protein and  
; OTHER INFORMATION: allergen  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-09-191-593-4  
Query Match 86.2%; Score 1752.4; DB 3; Length 1949;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;  
Qy 48 CAATGAGGGAGGGTTTCTCCACTGATGCTGTGTAGGGATCCTTGTCTGGCTTCAG 107  
Db 1 CAATGAGGGAGGGTTTCTCCACTGATGCTGTGTGGGATCCTTGTCTGGCTTCAG 60  
Qy 108 TTCTCGCAACGCGATGCCAAGTGCATCACCTTACCAGAAAGAAAACAGAGAACCCCTGCCGCC 167  
Db 61 TTCTCGCAACGCGAGGCCAAGTGCATCACCTTACCAGAAAGAAAACAGAGAACCCCTGCCGCC 114  
Qy 168 AGAGGTGCTCTCCAGAGTTGTCAACAGGAACCCGATGACTTTGAAGCAAAAGGCGATGCGAGT 227  
Db 115 AGAGGTGCTCTCCAGAGTTGTCAACAGGAACCCGATGACTTTGAAGCAAAAGGCGATGCGAGT 174  
Qy 228 CTCGCTGCACCAAGCTCGAGTATGATCCTCGTGTGTCTATGATCCTCGAGGACACACTG 287  
Db 175 CTCGCTGCACCAAGCTCGAGTATGATCCTCGTGTGTCTATG-----ACACTG 222  
Qy 288 GCACCAACCAACCAACGTTCCCTCCAGGGAGCGGACACGTCGCGCCCAACCCGAGACT 347  
Db 223 GCGCCACCAACCAACGTTCCCTCCAGGGAGCGGACACGTCGCGCCCAACCCGAGACT 282  
Qy 348 ACGATGATGACCGCCGCTCAACCCCGAAGAGAGGAAGGCCGATGGGACCAAGCTGGAC 407  
Db 283 ACGATGATGACCGCCGCTCAACCCCGAAGAGAGGAAGGCCGATGGGACCAAGCTGAAC 342  
Qy 408 CGAGGGAGCGTGAAGAGAAAGACTGGAGACAAACAGAGAAAGATTGGAGGGACCAA 467  
Db 343 CGAGGGAGCGTGAAGAGAAAGACTGGAGACAAACAGAGAAAGATTGGAGGGACCAA 402  
Qy 468 GTCATCAGCAGCCACCGAAAATAAGCCCGAAGAGAGAAAGAGAAAGAGTGGGGAA 527  
Db 403 GTCATCAGCAGCCACCGAAAATAAGCCCGAAGAGAGAAAGAGAGAAAGAGTGGGGAA 462  
Qy 528 CACCGGTAGCCATGTGAGGGAAGAAACATCTCGGAACAAACCCCTTCTACTTCCCGTCAA 587  
Db 463 CACCGGTAGCCATGTGAGGGAAGAAACATCTCGGAACAAACCCCTTCTACTTCCCGTCAA 522  
Qy 588 GCGGTTTACGACCCCTACGGGAACCAAAACGGTAGGATCCGGGTCTCTGACAGGTTG 647  
Db 523 GCGGTTTACGACCCGCTACGGGAACCAAAACGGTAGGATCCGGGTCTCTGACAGGTTG 582  
Qy 648 ACCAAGGTCAAGGCGATTTTCAAGATCTCCAGAAATCACCGTATTTGTCAGATCGAGCCA 707  
Db 583 ACCAAGGTCAAGGCGATTTTCAAGATCTCCAGAAATCACCGTATTTGTCAGATCGAGCCA 642

QY 708 AACCTAACACTCTTGTCTTCCCAAGCAGCTGATGCTGATACATCCTTGTATCCAGC 767  
Db 643 GACCTTAACACTCTTGTCTTCCCAAGCAGCTGATGCTGATACATCCTTGTATCCAGC 702  
QY 768 AAGGGCAAGCCACCGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTGACG 827  
Db 703 AAGGACAGCCACCGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTGACG 762  
QY 828 AGGGCCATGCACCTCAGAAATCCCATCCGTTTCAATCTTCTACATCTTTGAACCCGCATGACA 887  
Db 763 AGGGCCATGCACCTCAGAAATCCCATCCGTTTCAATCTTCTACATCTTTGAATCGACATGACA 822  
QY 888 ACCAGAACCTCAGAGTAGCTAAATCTCCATGCCGTTAAACACACCGGCCAGTTTGAGG 947  
Db 823 ACCAGAACCTCAGAGTAGCTAAATCTCCATGCCGTTAAACACACCGGCCAGTTTGAGG 882  
QY 948 ATTCTCTCCGGCGAGCAGCGGAGACCAATCATCTTACTTGCAGGGCTTCAGCAGGAATA 1007  
Db 883 ATTCTCTCCGGCGAGCAGCGGAGACCAATCATCTTACTTGCAGGGATTCAGCAGGAATA 942  
QY 1008 CGTTGAGCGCGCTTCAATGCGGAATTCATGAGATACGAGGGTCTGTTAGAAAGAGA 1067  
Db 943 CTTTGAGGCGCGCTTCAATGCGGAATTCATGAGATACGAGGGTCTGTTAGAAAGAGA 1002  
QY 1068 ATCGAGAGGTGAGCAAGAGGAGAGGCGAGGCGATGGAGTACTCGGAGTAGTGAGA 1127  
Db 1003 ATCGAGAGGAGAGCAAGAGGAGAGGCGAGGCGAGGAGTACTCGGAGTAGTG--- 1059  
QY 1128 ACAATGAAGGAGTGATAGTCAAAAGTGTCAAAGGAGCAGCTTTGAAGAACTTACTAAGCAGC 1187  
Db 1060 ATAAATGAAGGAGTGATAGTCAAAAGTGTCAAAGGAGCAGCTTCAAGAACTTACTAAGCAGC 1119  
QY 1188 CTAATTCCTGCTTCAAAGAAAGGCTCCGAAGAAGAGGGAGATATCAACCAACCCCAATCAACT 1247  
Db 1120 CTAATTCCTGCTTCAAAGAAAGGCTCC---GAAGAGGAAGATATCAACCAACCCCAATCAACT 1176  
QY 1248 TGAGAGAGGCGAGCGGATCTTCTTCAAACCTTTGGGAAGTTATTTGAGGTGAAGCCAG 1307  
Db 1177 TGAGAGATGCGAGCGGATCTTCTTCAAACACTTTGGGAAGTTATTTGAGGTGAAGCCAG 1236  
QY 1308 ACAAGAAGAACCCCGAGCTTCAGGACCTGGACATGATGCTCACTGTGTAGAGATCAAAAG 1367  
Db 1237 ACAAGAAGAACCCCGAGCTTCAGGACCTGGACATGATGCTCACTGTGTAGAGATCAAG 1296  
QY 1368 AAGGAGCTTTGATGCTCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCAACA 1427  
Db 1297 AAGGAGCTTTGATGCTCCACACTTCAACTCAAAGGCCATGGTCACTCGTCGTCAACA 1356  
QY 1428 AAGGAACTGGAAACCTTGAACTCGTGTGTAAGAAAGAGCAACACAGAGGGGACGGC 1487  
Db 1357 AAGGAACTGGAAACCTTGAACTCGTGTGTAAGAAAGAGCAACACAGAGGGGACGGC 1416  
QY 1488 GGGAA-----GAAGAGGAGGACGAAGACCAAGAGAGGAGGAAAGTAAACAGAGAGG 1538  
Db 1417 GGGAAACAGAGTGGGAAGAGAGAGGAGAGATGAAGAGAGGAGGAAAGTAAACAGAGAGG 1476  
QY 1539 TCGGTAGGTACACAGCGAGGTTGAAGAAAGGCGATGTGTTCATCATGCGACGAGCTCATC 1598  
Db 1477 TCGGTAGGTACACAGCGAGGTTGAAGAAAGGCGATGTGTTCATCATGCGACGAGCTCATC 1536  
QY 1599 CAGTAGCCATCAACGCTTCTCCGAATCCATCTGCTTGGCTTCGGTATCAGCTGAAG 1658  
Db 1537 CAGTAGCCATCAACGCTTCTCCGAATCCATCTGCTTGGCTTCGGTATCAGCTGAAG 1596  
QY 1659 ACAACACACAGAACTCTTCTTGCAGGTGATAAGGACAAATGTGTAGACCAGATAGAGAAGC 1718  
Db 1597 ACAACACACAGAACTCTTCTTGCAGGTGATAAGGACAAATGTGTAGACCAGATAGAGAAGC 1656  
QY 1719 AAGCGAAGGATTTAGCATTCCTCGGTCGGGTGAACAAGTTGAGAGAGCTCATCAAAAACC 1778  
Db 1657 AAGCGAAGGATTTAGCATTCCTCGGTCGGGTGAACAAGTTGAGAGAGCTCATCAAAAACC 1716  
QY 1779 AGAAGGAATCTCACTTTGTGAGTGTCTCTCAATCTCAATCTCAATCTCCGTCGCTC 1838

Db 1717 AGAGGAGAGTCTCACCTTTGTGAGTGTCTCGCTCAATCTCAATCTCCGTC----- 1765  
QY 1839 CTGAGAAAAGAGTCTCTCTGAGAAAAGAGATCAAGAGAGGAGAAAACCAAGAGGGAAGGGTC 1898  
Db 1766 -----GTCTCTCTGAAAAGAGGATCAAGAGGAGGAAAACCAAGAGGGAAGGGTC 1815  
QY 1899 CACTCCTTTCAATTTTGAAGGCTTTTAACTGAGAAATGGAGGCAACTTTGTATGTATCGAT 1958  
Db 1816 CACTCCTTTCAATTTTGAAGGCTTTTAACTGAGAAATGGAGGAACTTTGTATGTATCCAT 1875  
QY 1959 AATAAGATCACGCTTTTGTACTCTACTATCCAAAACCTTATCAATAAATAAAACCGTTTG 2018  
Db 1876 AATAAGATCACGCTTTTGTAACTACTATCCAAAACCTTATCAATAAATAAAACCGTTTG 1935  
QY 2019 TCGCTTTGTTTCTCC 2032  
Db 1936 TCGCTTTGTTTCTCC 1949

RESULT 8  
US-09-106-872A-18  
; Sequence 18, Application US/09106872A  
; Patent No. 6496311  
; GENERAL INFORMATION:  
; APPLICANT: Burks Jr., A. Wesley  
; APPLICANT: Stanley, J. Steven  
; APPLICANT: Cockrell, Gael  
; APPLICANT: King, Nina E.  
; APPLICANT: Sampson, Hugh A.  
; APPLICANT: Helm, Ricki M.  
; APPLICANT: Bannon, Gary A.  
; TITLE OF INVENTION: Peanut Allergens and Methods  
; FILE REFERENCE: HS 103 CIP  
; CURRENT APPLICATION NUMBER: US/09/106,872A  
; CURRENT FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: PCT/US96/15222  
; PRIOR FILING DATE: 1996-09-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 750  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea  
US-09-106-872A-18

Query Match 36.9%; Score 750; DB 3; Length 750;  
Best Local Similarity 100.0%; Pred. No. 2.3e-217;  
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 687 GTATTGTGCAGATCGAGGCCAAACCTTAACACTCTTGTCTTCCCAAGCAGCTGATGCTG 746  
Db 1 GTATTGTGCAGATCGAGGCCAAACCTTAACACTCTTGTCTTCCCAAGCAGCTGATGCTG 60  
QY 747 ATAAACATCTTGTATTCAGCAAGGCAAGCCAGCCGTGACCGTAGCAAAATGGCAATAACA 806  
Db 61 ATAAACATCTTGTATTCAGCAAGGCAAGCCAGCCGTGACCGTAGCAAAATGGCAATAACA 120  
QY 807 GAAAGAGCTTTAATCTTTCAGAGGGCCATGCAATCCCATCCCGTTTCATTTCTCT 866  
Db 121 GAAAGAGCTTTAATCTTTCAGAGGGCCATGCAATCCCATCCCGTTTCATTTCTCT 180  
QY 867 ACATCTTGAACCGCCATGACAACCGAACCTCAGAGTAGCTAAATCTCCATGCCCGTTA 926  
Db 181 ACATCTTGAACCGCCATGACAACCGAACCTCAGAGTAGCTAAATCTCCATGCCCGTTA 240  
QY 927 ACACACCCCGCCAGTTTGGAGGATTTCTCCCGCGAGCAGCCGAGACCAATCATCTTCT 986  
Db 241 ACACACCCCGCCAGTTTGGAGGATTTCTCCCGCGAGCAGCCGAGACCAATCATCTTCT 300  
QY 987 TCGAGGGCTTCAGCAGGAATACTGTGGAGGCCGCTTCAATGCGGAATTCATAGATAC 1046  
Db 301 TCGAGGGCTTCAGCAGGAATACTGTGGAGGCCGCTTCAATGCGGAATTCATAGATAC 360

QY 1047 GGAGGGTCTGTTTGAAGAAGATCGAGGAGGTGAGCAAGAGGAGAGGAGGCGAGAGGGCAT 1106  
DB 361 GGAGGGTCTGTTTGAAGAAGATCGAGGAGGTGAGCAAGAGGAGAGGAGGCGAGAGGGCAT 420  
QY 1107 GGAGTACTCGAGTAGTGAGAACAAATGAAGAGGTAGTAGTCAAAAGTGTCAAAAGAGCACG 1166  
DB 421 GGAGTACTCGAGTAGTGAGAACAAATGAAGAGGTAGTAGTCAAAAGTGTCAAAAGAGCACG 480  
QY 1167 TTGAAGAACTTACTTAAGCAGCTAAATCCGCTCTCAAAAGAAAGGCTCCGAAAGAGAGGGAG 1226  
DB 481 TTGAAGAACTTACTTAAGCAGCTAAATCCGCTCTCAAAAGAAAGGCTCCGAAAGAGAGGGAG 540  
QY 1227 ATATCAACCAACCCCAATCAACTTTGAGAAGAGCGAGCCCGATCTTTCTAAACAATTTTGGGA 1286  
DB 541 ATATCAACCAACCCCAATCAACTTTGAGAAGAGCGAGCCCGATCTTTCTAAACAATTTTGGGA 600  
QY 1287 AGTTATTTGAGGTGAAGCCAGACAAGAAAGAACCCCAAGCTTTCAGGACCTGGACATGATGC 1346  
DB 601 AGTTATTTGAGGTGAAGCCAGACAAGAAAGAACCCCAAGCTTTCAGGACCTGGACATGATGC 660  
QY 1347 TCACCTGTGTAGAGATCAAGAGAGGAGCTTTGTGCTCCCACTTCAACTCAAAAGGCCA 1406  
DB 661 TCACCTGTGTAGAGATCAAGAGAGGAGCTTTGTGCTCCCACTTCAACTCAAAAGGCCA 720  
QY 1407 TGGTTATCGTCTGCTCAACAAAGGAACTG 1436  
DB 721 TGGTTATCGTCTGCTCAACAAAGGAACTG 750

## RESULT 9

US-10-245-227D-84  
; Sequence 84, Application US/10245227D  
; Patent No. 6936696  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; APPLICANT: Rapp, William D.  
; APPLICANT: Peng, Jieixin  
; APPLICANT: Nadig, Gautham  
; APPLICANT: Venkatesh, Tyamagondlu  
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use  
; FILE REFERENCE: REN-00-087 US  
; CURRENT APPLICATION NUMBER: US/10/245, 227D  
; CURRENT FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 84  
; LENGTH: 1350  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-245-227D-84

Query Match 20.1%; Score 408.4; DB 3; Length 1350;  
Best Local Similarity 62.2%; Pred. No. 3e-113;  
Matches 780; Conservative 0; Mismatches 381; Indels 93; Gaps 5;

QY 562 GAACAACCTTCTACTT---CCCGTCAAGCGGTTTAGCACCGCTACGGGACCAAAA 618  
DB 120 GAATAACCTTCTACTTGAGAGCTTAAACGCTTCCAAACTCTCTTTGAGAACCAAAA 179  
QY 619 CGGTAGGATCCGGGTCTCTGAGAGGTTTGACCAAAAGGTCAAGGCAGTTTCAGAAATCTCCA 678  
DB 180 CGGTGCGATTCGCTCATTCAGAGATTCAACAAACGCTCCCACTTTCAGAAACCTTCG 239  
QY 679 GAATACCGTATTTGTGAGATCGAGGCCAAACCTTAACACTTCTTTGTTCTTCCCAAGCAGC 738  
DB 240 AGACTACCGATTTGTCAGTTTCAGTCAAAACCCCAACAAATCAATCTTCCCCCAACCATGC 299  
QY 739 TGATGCTGATAACATCTCTGTTATCCAGCAAGGCAAGCCACCGTGACCGTACCAATG 798  
DB 300 TGACGGCGATTTCAATTAATTAATTTCTAGCGGGAGGCCATACTTACCTTTGTGAAACAA 359  
QY 799 CAATAACAGAAAGAGCTTTAATCTTGACGAGGCGCATGCACTCAGAAATCCCATCCGGTTT 858

DB 360 CGACGACAGAGACTCTCTACAACATTTACCTCGCGATGTCACAGAGAAATCCAGCTGGAAC 419  
QY 859 CATTTCTTACATCTTTGAAACCGCATGACAACACAGAACTCAGAGTAGCTAAATCTCCAT 918  
DB 420 CACTTACTATATTATTAAACCTTCACGACCAACAGAAATCTCAAAATAATCAAAATTTGCCAT 479  
QY 919 GCCCGTTAAACACACCCCGGCGAGTTTGAAGATTTCTTCCCGCGAGAGCGGAGACCAATC 978  
DB 480 ACCCGTCAACAAACCTTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 539  
QY 979 ATCTTACTTCCAGGGCTTTCAGCAGGAATACGTTGGAGCGCGCTTCAATCGGAATTTCAA 1038  
DB 540 GTCTTACTTCAAGGGCTTCAGCCATAATAATTTAGAGACCTCTCTTCCATAGCGAAATTCGA 599  
QY 1039 TGAGATACGAGGGTCTGTTTGAAGAGAAATGCAAGAGGTGAGCAAGAGGAGAGAGGCA 1098  
DB 600 GGAGATAAACAGGGTTTGTGGAGAGGAAGAGGACGAGGCGCAAGAG----- 651  
QY 1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAAATGAAGGAGTAGTAGTCAAAAGTGTCAAA 1158  
DB 652 -----GGAGTGATCTGGAACTCTCAAA 674  
QY 1159 GGAGCAGCTTTGAAGAACTTACTAAGCACGCTAAATCCGTCTCAAAAGAAAGGCTCCGAAGA 1218  
DB 675 GGAACAAATTCGGCAACTGAGCAGACGTCGCAAAATCTAGTTCAAGGAAACCACTTCTCTC 734  
QY 1219 AGAGGAGATATCACCAACCAATCACTTGAAGAGAGGCGAGCCCGATCTTTCTAAACA 1278  
DB 735 CGAAGATG-----AACCATTTCAACTTTGAGAAGCGCAACCCCATCTATTTCACAA 785  
QY 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAACCCCGAGCTTCAGGACCTGGA 1338  
DB 786 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAACCCACAGCTTCGGNACTTTGGA 842  
QY 1339 CATGATGCTCACTGTTGTAGAGATCAAAAGAGAGCTTTGATGCTCCCACTTTCAACTC 1398  
DB 843 TATCTTCTCAGTTCTGTGGATATCAACGAAGAGAGCTTCTTCTTACCACTTTCAATTC 902  
QY 1399 AAGGGCATGGTTATCGTCTGCTCAACAAAGAACTGGAAACCTTGAACCTCGGCTGT 1458  
DB 903 AAGGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 962  
QY 1459 AAGAAAGAGCAACAACAGAGGGGCGCGGGGAAAGAGAGGAGGAGCAACGACGAAGAAGA 1518  
DB 963 TAAAGAACACACACAGAGCAAGAAACAGGAGAGGAACTTTG----- 1005  
QY 1519 GGAGGAAAGTAAACAGAGAGGTGCTAGGTACACAGCGAGGTTGAAGGAAGCGGATGTT 1578  
DB 1006 -----GAAGTGCAAGGTACAGAGCTGAATTTGCTGAAGACGATGATTT 1049  
QY 1579 CATCATGCCAGAGCTCATCCAGTACCGATCAACGCTTCTCCGAACCTCATCTGCTTG 1638  
DB 1050 TGTAATTCAGCAGCTTATCCATTTTGTGCTCAACGCTACCTCAAACTTCAATTTCTTGC 1109  
QY 1639 CTTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCTTTCAGGTTGATGAAGCAATGT 1698  
DB 1110 TTTTGGTATCAATGCTGAGAACCAACAGAGAACTTCTTTCAGGCGGAGAAACAAATGT 1169  
QY 1699 GATAGACAGATAGAGAAGCAAGCGAAGGATTTAGCAATTTCCCTGGGTGCGGTGAACAAGT 1758  
DB 1170 GGTAAAGCAGATAGAAAGACAAGTGCAGGAGCTTGGCTTCCCTGGGTCTGCACAAGATGT 1229  
QY 1759 TGAGAGCTCATCAAAACCAACAGAGAAATCTCACTTTGTGAGTGTGCTGCTCTCA 1812  
DB 1230 TGAGAGGCTATTAAAGAGCAGAGGGAATCTCACTTTGTGATGCTGCTCAGCTCA 1283

## RESULT 10

US-10-245-227D-88  
; Sequence 88, Application US/10245227D  
; Patent No. 6936696  
; GENERAL INFORMATION:



APPLICANT: Monsanto Company  
; APPLICANT: Rapp, William D.  
; APPLICANT: Peng, Jieixin  
; APPLICANT: Nadi, Gautham  
; APPLICANT: Venkatesh, Tyamagondlu  
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use  
; FILE REFERENCE: REN-00-087 US  
; CURRENT APPLICATION NUMBER: US/10/245,227D  
; CURRENT FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 88  
; LENGTH: 3808  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-245-227D-88

Query Match 20.1%; Score 408.4; DB 3; Length 3808;  
Best Local Similarity 62.2%; Pred. No. 6e-113;  
Matches 780; Conservative 0; Mismatches 381; Indels 93; Gaps 5;

QY 562 GAACAAACCCCTTCTACTTT---CCCGTCAAGGCGGTTTAGCACCCGCTACGGGAACCAAAA 618  
Db 1293 GAATAACCCCTTCTACTTTGAGAAGCTCTAACAGCTTCCAAACTCTCTTTGAGAAACCAAAA 1352

QY 619 CGGTAGATCCGGGCTCTGCAGAGGTTTGACCAAGGTCNAGGCAGTTTCAGAAATCTCCA 678  
Db 1353 CGGTGCAATTCGCTCTCTCCAGAGATTCACAAACGCTCCCCAACACTTTGAGAAACCTTCG 1412

QY 679 GAATACCGGATTTGTGCAGATCAGGCGCAAAACCTTAACACTTTGTTCTTCCCAAGCACGC 738  
Db 1413 AGACTACCGGATTTGTGCAGTTTCAGTTTCAGTCAAAACCCCAACACAACTCTCTCCCCACCATGC 1472

QY 739 TGATGCTGATAACATCTTGTATTCCAGCAAGGCGCAAGCCGTCGACCGGTAGCAAAATGG 798  
Db 1473 TGACGCGGATTTCTCTCTCTTGTCTTAGCGGAGAGCCATCTACTTACCTTTGGTGAACAA 1532

QY 799 CAATAACAGAAAGCTTTTAATCTTGACGAGGCGCATGCACTCAGAAATCCCATCCGGTTT 858  
Db 1533 CGACGACAGAGACTCTCTACAACTTCCACCTTGGCGATGCGCCAGAGAAATCCAGCTGGAAC 1592

QY 859 CATTTCTTACATCTTGAACCGGCATGACAAACCAAGCACTCAGAGTAGCTAAAAATCTCCAT 918  
Db 1593 CACTTACTATTGGTTAACTTACCTCAGACCAACAGATCTCAAAATATCAAACTTGGCAT 1652

QY 919 GCCCGTTAACACACCCGCGCAGTTTGAGGATTTCTTCCGCGGAGCAGCGCAGACCAATC 978  
Db 1653 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 1712

QY 979 ATCTACTTTCAGGCTTCAGAGGATACGTTTGGAGCGCGCTTCAATGCGGAATTCAA 1038  
Db 1713 GTCCCTACTTGAAGGCTTCAGCCATTAATTTCTAGAGACCTCTCTTCCATAGCGAATTCGA 1772

QY 1039 TGAGATACGAGGCGTGTCTTTAGAAAGAAATGCAAGAGGTGAGCAAGAGAGAGAGAGGCA 1098  
Db 1773 GGAATAAACAGGTTTGTGGAGAGGAGAGGAGCAGCAGCAAGAG-----1824

QY 1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGTGATAGTCAAAATGTCAAA 1158  
Db 1825 -----GGAGTGATCGTGGAACTCTCAAA 1847

QY 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCGTAAATCGTCTCAAGAAAGGCTCCGAAGA 1218  
Db 1848 GGAACAAATTCGGCACTAGCAGAGCGTGCCTCAATCTAGTTCAAGAAACCAATTTCTCTC 1907

QY 1219 AGAGGAGATATCAACAAACCAATCAACTTTGAGAGAGGCGAGCGCGATCTTTCTAACAA 1278  
Db 1908 CGAAGATG-----AACCAATCACTTTGAGAGCGCAACCCCATCTATTTCACAA 1958

QY 1279 CTTTGGGAAGTTATTGAGGTGAAGCCAGACAGAAACCCCGCAGCTTCAGAACCTGGA 1338  
Db 1959 CTTTGGAAAGTTCTTTGAGATCAACCCCTG---AGAAACCCCAAGCTTCGGGACTTGA 2015

QY 1339 CATGATGCTCACCTGTGTAGAGATCAAGAAGGAGCTTTTGATGCTCCCACTTCAACTC 1398  
Db 2016 TATCTTCTTCAGTTCTGTGGATATCAACGAAGAGCTCTTCTTACCACACTTCAATTC 2075

QY 1399 AAAGGCCATGGTTTATCGTCTGCTCAACAAAGGAACTGGAAACCTTTGAACTCTGTGGCTGT 1458  
Db 2076 AAAGGCCATAGTGATAGTACTAGTGAATTAATGAAGGAGATGCAAAACATTGAACTTTGGCAT 2135

QY 1459 AAGAAAGAGCAACAAACAGAGGAGCGGCGGAGAAAGAGAGGAGGAGCAAGACGAAGA 1518  
Db 2136 TAAAGAAACAAACAGAGAGCAGAAACAGGAAGAGGAAACCTTTG-----2178

QY 1519 GGAGGGAAGTAAACAGAGAGGTGCTAGGTACACAGCGAGGTTGAAGAAAGGCGATGTGT 1578  
Db 2179 -----GAAGTGCMAAGGTACAGAGCTGAATTTGTCTGAAGACGATGTATT 2222

QY 1579 CATCATGCGCAGCTCATCCAGTAGCCATCAACCGTTCTCTCGAACTCAATCTGTGTGG 1638  
Db 2223 TGTAAATTCAGCAGCTTATCCATTTTGTCTCAACGCTACCTCAAACTCAATTTCTTCTG 2282

QY 1639 CTTGCGTATCAACGCTGAAACCAACACAGAAATCTTCTTGCAGGTGATAAGGACAATGT 1698  
Db 2283 TTTTGGTATCAATGCTGGAACCAACAGAGAACTTCTTTCAGGCGAGAAACAATGT 2342

QY 1699 GATAGACCATAGAGAGCAAGCAAGGATTTAGCATTTCCCTGGGTGCAACAAGT 1758  
Db 2343 GGTAAAGCAGATAGAAAGCAAGTGCGAGGCTTGGTTCCTTGGGTCTGCACAAGATGT 2402

QY 1759 TGAGAAAGCTCATCAAAACCAAGAGAAATCTCACTTTGTGAGTGTCTCTCA 1812  
Db 2403 TGAGAGGCTATTAAAGAGCAGAGGGAATCTACTTTGTGTGATGCTCAGCCTCA 2456

RESULT 11  
US-10-245-227D-90  
; Sequence 90, Application US/10245227D  
; Patent No. 6936696  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; APPLICANT: Rapp, William D.  
; APPLICANT: Peng, Jieixin  
; APPLICANT: Nadi, Gautham  
; APPLICANT: Venkatesh, Tyamagondlu  
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use  
; FILE REFERENCE: REN-00-087 US  
; CURRENT APPLICATION NUMBER: US/10/245,227D  
; CURRENT FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 90  
; LENGTH: 3808  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-245-227D-90

Query Match 20.1%; Score 408.4; DB 3; Length 3808;  
Best Local Similarity 62.2%; Pred. No. 6e-113;  
Matches 780; Conservative 0; Mismatches 381; Indels 93; Gaps 5;

QY 562 GAACAAACCCCTTCTACTTT---CCCGTCAAGGCGGTTTAGCACCCGCTACGGGAACCAAAA 618  
Db 1293 GAATAACCCCTTCTACTTTGAGAAGCTCTAACAGCTTCCAAACTCTCTTTGAGAAACCAAAA 1352

QY 619 CGGTAGATCCGGGCTCTGCAGAGGTTTGACCAAGGTCNAGGCAGTTTCAGAAATCTCCA 678  
Db 1353 CGGTGCAATTCGCTCTCTCCAGAGATTCACAAACGCTCCCCAACACTTTGAGAAACCTTCG 1412

QY 679 GAATACCGGATTTGTGCAGATCAGGCGCAAAACCTTAACACTTTGTTCTTCCCAAGCACGC 738  
Db 1413 AGACTACCGGATTTGTCCAGTTTCAGTCAAAACCCCAACAACTATCTTCCCCACCATGC 1472

QY 739 TGATGCTGATAACATCTTGTATTCCAGCAAGGCGCAAGCCGTCGACCGGTAGCAAAATGG 798  
Db 1473 TGACGCGGATTTCTCTCTCTTGTCTTAGCGGAGAGCCATCTACTTACCTTTGGTGAACAA 1532

QY 799 CAATAACAGAAAGCTTTTAATCTTGACGAGGCGCATGCACTCAGAAATCCCATCCGGTTT 858  
Db 1533 CGACGACAGAGACTCTCTACAACTTCCACCTTGGCGATGCGCCAGAGAAATCCAGCTGGAAC 1592

QY 859 CATTTCTTACATCTTGAACCGGCATGACAAACCAAGCACTCAGAGTAGCTAAAAATCTCCAT 918  
Db 1593 CACTTACTATTGGTTAACTTACCTCAGACCAACAGATCTCAAAATATCAAACTTGGCAT 1652

QY 919 GCCCGTTAACACACCCGCGCAGTTTGAGGATTTCTTCCGCGGAGCAGCGCAGACCAATC 978  
Db 1653 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 1712

QY 979 ATCTACTTTCAGGCTTCAGAGGATACGTTTGGAGCGCGCTTCAATGCGGAATTCAA 1038  
Db 1713 GTCCCTACTTGAAGGCTTCAGCCATTAATTTCTAGAGACCTCTCTTCCATAGCGAATTCGA 1772

QY 1039 TGAGATACGAGGCGTGTCTTTAGAAAGAAATGCAAGAGGTGAGCAAGAGAGAGAGGCA 1098  
Db 1773 GGAATAAACAGGTTTGTGGAGAGGAGAGGAGCAGCAGCAAGAG-----1824

QY 1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGTGATAGTCAAAATGTCAAA 1158  
Db 1825 -----GGAGTGATCGTGGAACTCTCAAA 1847

QY 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCGTAAATCGTCTCAAGAAAGGCTCCGAAGA 1218  
Db 1848 GGAACAAATTCGGCACTAGCAGAGCGTGCCTCAATCTAGTTCAAGAAACCAATTTCTCTC 1907

QY 1219 AGAGGAGATATCAACAAACCAATCAACTTTGAGAGAGGCGAGCGCGATCTTTCTAACAA 1278  
Db 1908 CGAAGATG-----AACCAATCACTTTGAGAGCGCAACCCCATCTATTTCACAA 1958

QY 1279 CTTTGGGAAGTTATTGAGGTGAAGCCAGACAGAAACCCCGCAGCTTCAGAACCTGGA 1338  
Db 1959 CTTTGGAAAGTTCTTTGAGATCAACCCCTG---AGAAACCCCAAGCTTCGGGACTTGA 2015



Db 1473 TGAGCGCGATTTCATTATTATTATTCTTAGCGGAGAGCCATACTTACCTTGGTGAACAA 1532  
Qy 799 CAATAACAGAAAGAGCTTTTAACTCTGACGAGGCGCATGCACTCAGAAATCCCATCCGGTTT 858  
Db 1533 CGAGCAGAGACTCTTACAACTTTCACCTGGCGATGCCAGAGAAATCCAGTGAAC 1592  
Qy 859 CATTCTCTACATCTTGAAACCGCCATGACAAACCAAGCTTCAGAGTAGCTAAAATCTCCAT 918  
Db 1593 CACTTACTATATTATTAACTCTCAGACACCAAGACTCTCAAAATATCAAAATTTGCCAT 1652  
Qy 919 GCCGGTTAAACACACCGCGCAGTTTGGAGATTTCTTCCCGGAGAGCGGAGACCAATC 978  
Db 1653 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 1712  
Qy 979 ATCTCTCTCAGGGCTTCAGCAGGAATACGTTGGAGGCGCCTTCAATCGGAATTCAA 1038  
Db 1713 GTCTCTCTGCAAGGCTTCAGCCATAATATCTTAGAGACCTCTTCCATAGCAATTCGA 1772  
Qy 1039 TGAGATACGGAGGTGCTGTTAGAGAGAAATGCAAGGAGGTGAGCAAGAGAGAGAGGCA 1098  
Db 1773 GGAGATAAACAGGGTTTGTGGAGAGGAAGAGGAGCAGAGGTCAGCAAG----- 1824  
Qy 1099 GAGCGATGAGTACTCGGAGTAGTGAGAACATGAAGGAGTAGTAGTCAAGTGTCAAA 1158  
Db 1825 -----GGAGTGTATCGTGAACCTCTCAA 1847  
Qy 1159 GGAGCAGGTTGAAGACTTACTAAGCAGCGTAAATCGTCTCAAGAAAGGCTCCGAAGA 1218  
Db 1848 GGAACAAATTCGGCAACTGAGCAGAGCTGCAAAATCTAGTTCAAGGAAACCAATTTCCCTC 1907  
Qy 1219 AGAGGGAGATATCACCAACCCAACTCACTTTGAGAGAGGCGGAGCCGATCTTTCTAACAA 1278  
Db 1908 CGAAGATG-----AACCACTTCACTTTGAGAAGCGGCAACCCCACTCTATTTCCAAACA 1958  
Qy 1279 CTTTGGGAAGTTATTTAGGTGAAGCCAGACAGAGAAACCCCGAGCTTCAGAGACCTGA 1338  
Db 1959 CTTTGGAAAGTTCTTTGAGATACCCCTG---AGAAAAACCCACAGCTTCGGAGCTTGA 2015  
Qy 1339 CATGATGCTCACCTGTGTAGATCAAGAGAGGCTTTGATGCTCCACACTTCAACTC 1398  
Db 2016 TATCTTCTCAGTTCTGTGATATCAACGAAGAGCTCTTCTTACCACTTCAATTC 2075  
Qy 1399 AAAGGCCATGTTATCGTCTGCTGCAACAAAGGAATGGAACCTTTGAATCTGTGGCTGT 1458  
Db 2076 AAAGGCCATGATGATCTAGTATTAATGAAGGAGATGCAACATTTGAATCTGTGGCAT 2135  
Qy 1459 AAGAAAGAGCAACACAGAGGGGACGGCGGGAAGAGAGGAGGAGCAAGAACGAAGA 1518  
Db 2136 TAAAGAAACAAACAGAGAGCAGAAACAGGAAGAGGAACCTTTG----- 2178  
Qy 1519 GGAGGGAAGTAAACAGAGAGTGCCTAGGTACACAGCGAGGTTGAAGGAAGCGATGTGT 1578  
Db 2179 -----GAGTGAAGGTACAGAGCTGAATTTGTCTGAAGACGATGATT 2222  
Qy 1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCATCTGCTTGG 1638  
Db 2223 TGTAATTTCCAGCAGCTTATCCATTTGTCTGCTCAAGCTTACCTCAACCTCAATTTCTTGC 2282  
Qy 1639 CTTTCGGTATCAACGCTGAAACCAACACAGAACTTCTTCTGAGGTGATGAAGACATGT 1698  
Db 2283 TTTTGGTATCAATGCTGAGAACCAACAGAGGAACCTTCTTTCGAGGCGAAGAACATGT 2342  
Qy 1699 GATAGACCATAGAGAGCAAGGAGGATTTAGCAATTCCTGGGTCCGGTCAACAAGT 1758  
Db 2343 GGTAGGCGATAGAAAGACAAGTGCAGGAGCTTTCGTTCCCTGGGTCTGCACAAGATGT 2402  
Qy 1759 TGAGAGCTCATCAAAACAGAGGAATCTCACTTTTGTGAGTGTCTGCTCTCA 1812  
Db 2403 TGAGAGGCTATTAAAGAGCAGAGGGAATCTTACTTTTGTGATGCTCAGCCTCA 2456

RESULT 12

US-10-245-227D-15

; Sequence 15, Application US/10245227D  
; Patent No. 6936696  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; APPLICANT: Rapp, William D.  
; APPLICANT: Peng, Jieixin  
; APPLICANT: Nadi, Gautham  
; APPLICANT: Venkatesh, Tyamagondlu  
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use  
; FILE REFERENCE: REN-00-087 US  
; CURRENT APPLICATION NUMBER: US/10/245, 227D  
; CURRENT FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15  
; LENGTH: 1254  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: mature form of beta-conglycinin beta-subunit  
US-10-245-227D-15

Query Match 20.0%; Score 406.8; DB 3; Length 1254;  
Best Local Similarity 62.1%; Pred. No. 8.9e-113;  
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;  
Qy 562 GAACAAACCCCTTTCTACTT---CCGTCAGGGCGGTTTAGCACCCGCTACGGGAACCAAAA 618  
Db 24 GAATAACCCCTTTCTACTTTGAGAAGCTCTAACAGCTTCCAAACTCTCTTTGAGAACCAAAA 83  
Qy 619 CGGTAGGATCCGGGTCTCTCAGAGGTTTGACAAAGGTCAAGGAGTTTCAGAAATCTCCA 678  
Db 84 CGGTGCACTTCGTCTCTCTCAGAGATTCAACAAACGCTCCCAACAACCTTGAGAACCTTCG 143  
Qy 679 GAATCACCATTATGTGCGAGATCGAGGCCAAACCTTAACACTCTTTGTTCTTCCCAAGCAGC 738  
Db 144 AGACTACCGGATTTGTCCAGTTTCAGTCAAAACCCCAACAACCTTCTTCCCAACCATGC 203  
Qy 739 TGATGCTGATAACATCTTGTATCCAGCAAGGCAAGCCAGCCGTCGACCTAGCAATGG 798  
Db 204 TGAGCGGATTTCTCTCTCTTTGCTTTAGCGGAGAGCCATACTTACCTTGGTGAACAA 263  
Qy 799 CAATAACAGAAAGAGCTTTAATCTTGACGAGGCCATGCACTCAGAAATCCCATCCGGTTT 858  
Db 264 CGACGACAGAGACTCTCTAACCTTCAACCTTCCCTGCGATGCCAGAGAATCCAGCTGGAAC 323  
Qy 859 CATTTCTCTACATCTTGAACCGCCATGACAAACCAAGCTTCAGAGTAGTAAATCTCCAT 918  
Db 324 CACTTACTATTGGTTTAAACCTTCAACCAACCAAGAAATCTCAAAATATATCAAACTTGCAT 383  
Qy 919 GCCGGTTAAACACACCCCGCAGTTTGAGGATTTCTTCCCGGAGAGCGGAGACCAATC 978  
Db 384 ACCGTCACAAACCTTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 443  
Qy 979 ATCTTACTTTCAGGGCTTTCAGAGGAATACGTTGGAGGCGCCTTCAATCGGAATTCAA 1038  
Db 444 GTCTTACTTTCAGAGGCTTCAGCCATAATATCTTAGAGACCTCTCTCATAGCAATTCGA 503  
Qy 1039 TGAGATACGGAGGTCTGTGTAGAGAGAAATGCAAGAGGTGAGCAAGAGAGAGAGGCA 1098  
Db 504 GGAGATAAACAGGGTTTGTGGGAGGAAGAGGAGCAGAGGAGCAAG----- 555  
Qy 1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAACAAATGAAGGAGTAGTAGTCAAGTGTCAAA 1158  
Db 556 -----GGAGTGTCTGGAACCTCTCAA 578  
Qy 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCGTAAATCCGTTCTCAAGAAAGGCTCCGAAGA 1218  
Db 579 GGAACAAATTCGGCAACTGAGCAGAGCTGCAAAATCTAGTTCAAGGAAACCAATTTCCCTC 638  
Qy 1219 AGAGGAGATATCACCAACCCCAATCACTTGAGAGAGGCGGAGCCGATCTTTCTAACAA 1278  
Db 639 CGAAGATG-----AACCACTTCAACTTGAGAAAGCCGCAACCCCATCTATTTCACAA 689

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QY 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAAGAACCCCGAGCTTCAGACCTGGA 1338
Db 690 CTTTGGAAAGTTCTTTTGAGATCACCCCTG---AGAAACCCACAGACTTCGGGACTTGA 746
QY 1339 CATGATGCTCACCTGTGTAGAGATCAAAAGAGAGCTTTGATGCTCCACACTTCAACTC 1398
Db 747 TATCTTCTCAGTCTGTGGATATCAACGAGAGCTTCTTCTTACCACACTTCAATTC 806
QY 1399 AAAGGCCATGGTTATCGTGTCTGTCAACAAAGGAACTGGAAACCTTGAACCTGTGCTGT 1458
Db 807 AAAGGCCATAGTGTACTAGTATTAATGAAGGAGATGCAAAACATTTGAACCTTGTGGCAT 866
QY 1459 AAGAAAGACACACACAGAGGGGCGCGGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1518
Db 867 TAAAGAACCAACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 909
QY 1519 GGAGGGAAGTAAACAGAGAGTGGTGTAGGTACACAGCGAGGTTGAAGGAAGGCGATGTGT 1578
Db 910 -----GAAGTGAAGGTACAGAGCTGAATGTCTGAAGACGATGTATT 953
QY 1579 CATCATGCCAGCAGCTATCCAGTAGCCATCAACGGTTCTTCGAACTCCATCTGCTTGG 1638
Db 954 TGTAAATTCAGCAGCTTATCCATTTGTGTCAACGCTACCTCAACCTCAATTTCTCTGC 1013
QY 1639 CTTTGGTATCAACGCTGAAACCAACACACAGAAATCTTCTTGCAGGTGATAAGGACAATGT 1698
Db 1014 TTTTGGTATCAATGCTGTAGAACCAACAGAGGAACTTCTTTCGAGGCGAAGAACAAATGT 1073
QY 1699 GATAGACCATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1758
Db 1074 GGTAAAGCAGATAGAAAGACAACTGACGAGCTTGGTTCCTTGGGTCTGACACAGATGT 1133
QY 1759 TGAGAGCTCATCAAAACACAGAGGAATCTCAATTTGTGAGTGTCTGCTCCTCA 1812
Db 1134 TGAGAGGCTATTAAAGACAGAGGGAATCCTACTTTGTGTGCTCAGCCTCA 1187

RESULT 13
US-10-245-227D-13
; Sequence 13, Application US/10245227D
; Patent No. 6936696
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; APPLICANT: Rapp, William D.
; APPLICANT: Peng, Jieixin
; APPLICANT: Nadiq, Gautham
; APPLICANT: Venkatesh, Tyamagondlu
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use
; FILE REFERENCE: REN-00-087 US
; CURRENT APPLICATION NUMBER: US/10/245, 227D
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: epitope form of beta-conglycinin beta-subunit
US-10-245-227D-13

Query Match 20.0%; Score 406.8; DB 3; Length 1278;
Best Local Similarity 62.1%; Pred. No. 9e-113;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAACCCCTTCTACTT---CCCGTCAAGCGGTTTAGCACCCGCTACGGGAACCAAAA 618
Db 48 GAATAACCCCTTCTACTTTGAGAGCTCTAACAGCTTCCAACTCTCTTTGAGAACCAAAA 107
QY 619 CGGTAGATCCGGGTCTCTCAGAGGTTTGAACAAAGGTCAAGCGATTTTCAGAAATCTCCA 678
Db 108 CGGTGCAATTCGTCTCTCTCAGAGATTCACAAACGCTCCCAACAACTTGAGAACCTTCG 167
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QY 679 GAATCACCGTATTGTGCAGATCGAGCCCAAACTTAACACTCTTGTTCTTCCCAAGCACGC 738
Db 168 AGACTACCCGGATTGTCTCAGTTTCAGTCAAAACCCCAACAACAACTTCTTCCCAAGCACGC 227
QY 739 TGATGCTGATAACATCTCTTGTATCCAGCAAGGGCAAGCCACCGTACCGTAGCAAAATGG 798
Db 228 TGACGCCGATTTCCTCTCTTGTCTTAGCGGGAGAGCCATACCTTACCTTGGTGAACAA 287
QY 799 CAATAACAGAAAGAGCTTTAAATCTTGAAGGGGCCATGCACTCAGAAATCCCATCCGGTTT 858
Db 288 CGACGACAGAGACTCTCTACAACCTTCAACCTTGGCGATGGCCAGAGAAATCCCAAGTGAAC 347
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QY 919 GCCCGTTAAACACACCCCGCCAGTTTGAGGATTTCTTCCCGGCGAGCAGCGAGACCAATC 978
Db 408 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 467
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QY 1039 TGAGATACGAGGGTCTGTTAGAGAGAAATGCAGAGGTGAGCAAGAGAGAGAGAGGCA 1098
Db 528 GGAGATAAAACAGGGTTTGTGGGAGAGGAAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 579
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QY 1399 AAAGGCCATGGTTATCGTGTCTGTCAACAAAGGAACTGGAAACCTTGAACCTCGTGGCTGT 1458
Db 831 AAAGGCCATAGTGTACTAGTATTAATGAAGGAGATGCAACATTTGAACCTTGTGGCAT 890
QY 1459 AAGAAAGAGCAACAAACAGAGGGGCGCGGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1518
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QY 1519 GGAGGGAAGTAAACAGAGAGTGGTGTAGGTACACAGCGAGGTTGAAGGAAGGCGATGTGT 1578
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QY 1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTTCCGAACTCCATCTGCTTGG 1638
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Db 1038 TTTTGGTATCAATGCTGTAGAACCAACCAAGAGGAACTTCTTTCGAGGCGGAGAAAGACAATGT 1097
QY 1699 GATAGACCATAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1758
Db 1098 GGTAGGCGAGATAGAAAGACAAAGTCAGGAGCTTGGCTTCCCTTGGGTCTGCAACAGATGT 1157
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QY 1759 TGAGAGCTCATCAAAACCAAGAGGAATCTACTTTGTGAGTCTCGTCTCA 1812  
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Db 1158 TGAGAGGCTATTAAGAGCAGAGGAATCTACTTTGTGATGCTCAGCCTCA 1211  
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## RESULT 14

US-09-108-0108-3  
; Sequence 3, Application US/091080108  
; Patent No. 6362399  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD 7.0A

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/108,0108  
; FILING DATE: 30-Jun-1998

; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/019,940

; FILING DATE: JUNE 14, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LYNN M. CHRISTENBURY

; REGISTRATION NUMBER: 30,971  
; REFERENCE/DOCKET NUMBER: BB-1071-A

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-5481  
; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1320 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-108-0108-3

Query Match 20.0%; Score 406.8; DB 3; Length 1320;  
Best Local Similarity 62.1%; Pred. No. 9.2e-113;  
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

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; Sequence 3, Application US/09758652  
; Patent No. 6703544  
; GENERAL INFORMATION:

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APPLICANT: ANTHONY JOHN KINNEY  
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC CLASSES OF SOYBEAN SEED PROTEIN GENES  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WINDOWS 95  
SOFTWARE: MICROSOFT WORD 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,652  
FILING DATE: 11-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/019,940  
FILING DATE: JUNE 14,1996  
ATTORNEY/AGENT INFORMATION:  
NAME: LYNN M. CHRISTENBURY  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1071-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1320 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-758-652-3

Query Match 20.0%; Score 406.8; DB 3; Length 1320;  
Best Local Similarity 62.1%; Pred.No. 9.2e-113;  
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

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Job time : 326.712 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC  
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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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23	404	19.9	2260	8	US-10-424-599-10353	Sequence 10353, A
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ALIGNMENTS

RESULT 1

US-09-731-375A-1

; Sequence 1, Application US/09731375A

; Publication No. US20030035810A1

; GENERAL INFORMATION:

; APPLICANT: Caplan, Michael

; TITLE OF INVENTION: Microbial Delivery System

; FILE REFERENCE: 2002834-0100

; CURRENT APPLICATION NUMBER: US/09/731,375A

; PRIOR FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 60/195,035

; PRIOR FILING DATE: 2000-04-06

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2032

; TYPE: DNA

; ORGANISM: Arachis hypogaea

US-09-731-375A-1

Query Match 100.0%; Score 2032; DB 3; Length 2032;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1321 CCAGCTTCAGGACCTGACATGATGCTCACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT 1380
QY 1381 GTTCCACACTTTCAACTCAAAGGCCATGGTTATTCGTGTCGTCAACAAAGGAACTGGA 1440
Db 1381 GCTCCACACTTTCAACTCAAAGGCCATGGTTATTCGTGTCGTCAACAAAGGAACTGGA 1440
QY 1441 CTTTGAATCTGCTGCTGTAAAGAAAGAGCAACACAGAGGGGACGGCGGGAAGAGGA 1500
Db 1441 CTTTGAATCTGCTGCTGTAAAGAAAGAGCAACACAGAGGGGACGGCGGGAAGAGGA 1500
QY 1501 GACGGAAGACGAGAGAGAGGAGTAACAGAGAGGTCGTAGGTACACACGCGAGGTT 1560
Db 1501 GACGGAAGACGAGAGAGAGGAGTAACAGAGAGGTCGTAGGTACACACGCGAGGTT 1560
QY 1561 GAAGGAAGCGGATGTTTCATCATGTCAGCAGCTCATCCAGTAGCCATCAACGCTTCTC 1620
Db 1561 GAAGGAAGCGGATGTTTCATCATGTCAGCAGCTCATCCAGTAGCCATCAACGCTTCTC 1620
QY 1621 CGAATCTCATCTGCTTGGCTTCGGTATCAACCGTGAACCAACACAGAACTCTTCTTGC 1680
Db 1621 CGAATCTCATCTGCTTGGCTTCGGTATCAACCGTGAACCAACACAGAACTCTTCTTGC 1680
QY 1681 AGTGATTAAGGACAAATGTCATGACAGATAGAGAGCAAGCGAAGATTTAGCATTTCC 1740
Db 1681 AGTGATTAAGGACAAATGTCATGACAGATAGAGAGCAAGCGAAGATTTAGCATTTCC 1740
QY 1741 TGGTTCGGGTGAACAAATTTGAGAAGCTCATCAAAAACCAAGAGAAATCTCCTTGTGAG 1800
Db 1741 TGGTTCGGGTGAACAAATTTGAGAAGCTCATCAAAAACCAAGAGAAATCTCCTTGTGAG 1800
QY 1801 TGCTGCTCCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAAAGAGTCTCTCTGAGAA 1860
Db 1801 TGCTGCTCCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAAAGAGTCTCTCTGAGAA 1860
QY 1861 AGAGGATCAAGAGGAGGAGAAACCAAGGAGGAGGAGGTCCTCTTCAATTTTGAAGGC 1920
Db 1861 AGAGGATCAAGAGGAGGAGAAACCAAGGAGGAGGAGGTCCTCTTCAATTTTGAAGGC 1920
QY 1921 TTTTAACTCAGAAATGAGGCAACTTGTATGATATGATATGATATGATATGATATGATATGAT 1980
Db 1921 TTTTAACTCAGAAATGAGGCAACTTGTATGATATGATATGATATGATATGATATGATATGAT 1980
QY 1981 CTACTATCAAAAACCTTATCAATAAATAAAAGCTTTGTGCGTTGTTCTCC 2032
Db 1981 CTACTATCAAAAACCTTATCAATAAATAAAAGCTTTGTGCGTTGTTCTCC 2032
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## RESULT 2

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US-10-228-806-1
; Sequence 1, Application US/10228806
; Publication No. US20030049237A1
; GENERAL INFORMATION:
; APPLICANT: Bannan, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions
; TITLE OF INVENTION: to Allergy
; FILE REFERENCE: 2002834-0043
; CURRENT APPLICATION NUMBER: US/10/228,806
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2032
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-228-806-1
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Query Match 100.0%; Score 2032; DB 6; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATAATCATATATATTTTCATCAATCATCTATATATAGTAGTAGCAGGAGCAATGAGAGGAG 60
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Db 1 AATAATCATATATATTATCATCAATATATATAGTAGTAGCAGGAGCAATAGAGGGAG 60  
Qy 61 GGTTCCTCCACTGATGCTGTGTAGGATCCTTGTCTCGCTTCAGTTCTGCAACGCA 120  
Db 61 GGTTCCTCCACTGATGCTGTGTAGGATCCTTGTCTCGCTTCAGTTCTGCAACGCA 120  
Qy 121 TGCAAGTATCATCTTACAGAGAAAGAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180  
Db 121 TGCAAGTATCATCTTACAGAGAAAGAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180  
Qy 181 GAGTTCTCAACAGAACCGGATGACTTGAAGCAAAAGGATCGAGTCTCGTGCACCA 240  
Db 181 GAGTTCTCAACAGAACCGGATGACTTGAAGCAAAAGGATCGAGTCTCGTGCACCA 240  
Qy 241 GCTCGAGTATGATCCTCGTGTGTATGATCCTCGAGGACACACTGGCACCAACCA 300  
Db 241 GCTCGAGTATGATCCTCGTGTGTATGATCCTCGAGGACACACTGGCACCAACCA 300  
Qy 301 ACCTTCCCTCCAGGGAGCGGACACGTGCGCGCAACCCGGAGACTACGATGATGACCG 360  
Db 301 ACCTTCCCTCCAGGGAGCGGACACGTGCGCGCAACCCGGAGACTACGATGATGACCG 360  
Qy 361 CCCTCAACCCGAGAGAGAGAGGCGCGATGGGACAGCTGGACCGAGGAGCGTGA 420  
Db 361 CCCTCAACCCGAGAGAGAGAGGCGCGATGGGACAGCTGGACCGAGGAGCGTGA 420  
Qy 421 AAGAGAAAGAGACTGGAGACAAACAGAGAAAGATTGGAGCGACCAAGTCAACAGAGCC 480  
Db 421 AAGAGAAAGAGACTGGAGACAAACAGAGAAAGATTGGAGCGACCAAGTCAACAGAGCC 480  
Qy 481 ACAGAAATTAAGCCCGAAGAGAGAGAGAGAGAAAGAGTGGGGACACACAGGTAGCCA 540  
Db 481 ACAGAAATTAAGCCCGAAGAGAGAGAGAGAGAAAGAGTGGGGACACACAGGTAGCCA 540  
Qy 541 TGTGAGGAGAAACACTCTCGGACACCCCTTCTACTCTCCCTCAAGGCGTTTAGCAC 600  
Db 541 TGTGAGGAGAAACACTCTCGGACACCCCTTCTACTCTCCCTCAAGGCGTTTAGCAC 600  
Qy 601 CCCTACGGGAAACAAAACGGTAGGATCCGGGTCTCGCAGAGGTTTGACCAAGGTCAAG 660  
Db 601 CCCTACGGGAAACAAAACGGTAGGATCCGGGTCTCGCAGAGGTTTGACCAAGGTCAAG 660  
Qy 661 GCAGTTTCAGAACTCCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTTAACACTCT 720  
Db 661 GCAGTTTCAGAACTCCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTTAACACTCT 720  
Qy 721 TGTCTCTCCAGACGCTGATGCTGATACATCTTGTATCCAGCAAGGGCAAGCCAC 780  
Db 721 TGTCTCTCCAGACGCTGATGCTGATACATCTTGTATCCAGCAAGGGCAAGCCAC 780  
Qy 781 CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTAACTTTGACGAGGGCCATGCAC 840  
Db 781 CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTAACTTTGACGAGGGCCATGCAC 840  
Qy 841 CAGAAATCCCATCCGGTTTCATTTCTACATCTTGAACCGCCATGACAAACAGAAACCTCAG 900  
Db 841 CAGAAATCCCATCCGGTTTCATTTCTACATCTTGAACCGCCATGACAAACAGAAACCTCAG 900  
Qy 901 AGTAGCTTAAATCTCCATGCCCGTTTAAACACCCGGCCAGTTTGAGGATTTCTTCCGGC 960  
Db 901 AGTAGCTTAAATCTCCATGCCCGTTTAAACACCCGGCCAGTTTGAGGATTTCTTCCGGC 960  
Qy 961 GAGCAGCCGAGACCAATCATCTTACTTTCAGGGCTTCAGCAGGAATACGTTGGAGCGCG 1020  
Db 961 GAGCAGCCGAGACCAATCATCTTACTTTCAGGGCTTCAGCAGGAATACGTTGGAGCGCG 1020  
Qy 1021 CTTCAATGCGGAATTCATAGAGATCGAGGGTGTCTTTAGAGAGAAATCGCAGAGGTGA 1080  
Db 1021 CTTCAATGCGGAATTCATAGAGATCGAGGGTGTCTTTAGAGAGAAATCGCAGAGGTGA 1080  
Qy 1081 GCAGAGGAGAGAGGCGAGGCGATGAGTACTCGGAGTGTGAGCAACAACTGAAGGAGT 1140  
Db 1081 GCAAGAGGAGAGAGGCGAGGCGATGAGTACTCGGAGTGTGAGCAACAACTGAAGGAGT 1140

Qy 1141 GATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACGCTAAATCCGTC 1200  
Db 1141 GATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACGCTAAATCCGTC 1200  
Qy 1201 AAAGAAGGCTCCGAAGAAGAGAGGAGATATCACAAACCCCAATCAACTTTGAGAGAGCGGA 1260  
Db 1201 AAAGAAGGCTCCGAAGAAGAGAGGAGATATCACAAACCCCAATCAACTTTGAGAGAGCGGA 1260  
Qy 1261 GCCCGATCTTTCTAAACAACCTTTTCGGGAAGTTATTTGAGGTGAAGCCAGCAAGAAGAACC 1320  
Db 1261 GCCCGATCTTTCTAAACAACCTTTTCGGGAAGTTATTTGAGGTGAAGCCAGCAAGAAGAACC 1320  
Qy 1321 CCAGCTTCAGGACCTCGACATGATGCTCACCTGTGTAGAGATCAAAAGAAGAGCTTTGAT 1380  
Db 1321 CCAGCTTCAGGACCTCGACATGATGCTCACCTGTGTAGAGATCAAAAGAAGAGCTTTGAT 1380  
Qy 1381 GCTCCACACTTCAACTCAAGGCCATGGTTATTCGTCTGCTCAACAAAGAACTGAAA 1440  
Db 1381 GCTCCACACTTCAACTCAAGGCCATGGTTATTCGTCTGCTCAACAAAGAACTGAAA 1440  
Qy 1441 CCTTGAACCTCGTGTGAAGAAAGAGCAACACAGAGGGGACGCGGGAAGAAGAGGA 1500  
Db 1441 CCTTGAACCTCGTGTGAAGAAAGAGCAACACAGAGGGGACGCGGGAAGAAGAGGA 1500  
Qy 1501 GGAAGAGAGAGAGAGAGGAGGAAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGTT 1560  
Db 1501 GGAAGAGAGAGAGAGAGGAGGAAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGTT 1560  
Qy 1561 GAAGGAGGCGATGTTGTTATCATGCGCAGCAGCTCATCCAGTAGCCATCAACGTTCTC 1620  
Db 1561 GAAGGAGGCGATGTTGTTATCATGCGCAGCAGCTCATCCAGTAGCCATCAACGTTCTC 1620  
Qy 1621 CGAATCTCAATCTCGTTCGGTTCGATCAACGCTGAAACAAACACAGAACTTCTCTTC 1680  
Db 1621 CGAATCTCAATCTCGTTCGGTTCGATCAACGCTGAAACAAACACAGAACTTCTCTTC 1680  
Qy 1681 AGGTGATAAGGACAACTGTATAGACAGATAGAGAAAGCAAGCGAAGGATTTAGCATTTCC 1740  
Db 1681 AGGTGATAAGGACAACTGTATAGACAGATAGAGAAAGCAAGCGAAGGATTTAGCATTTCC 1740  
Qy 1741 TGGTCGGGTGAACAAAGTTGAGAGCTCATCAAAAACAGAGAGAAATCTCAGTTGTGAG 1800  
Db 1741 TGGTCGGGTGAACAAAGTTGAGAGCTCATCAAAAACAGAGAGAAATCTCAGTTGTGAG 1800  
Qy 1801 TGCTCGTCTCAATCTCAATCTCGCTCGTCTCAATCTCGCTCGTCTCTGAGAAAGAGTCT 1860  
Db 1801 TGCTCGTCTCAATCTCAATCTCGCTCGTCTCAATCTCGCTCGTCTCTGAGAAAGAGTCT 1860  
Qy 1861 AGAGGATCAAGAGGAGGAGAAACCAAGGAGGAAAGGTTCCACTCTTTCATTTTGAAGGC 1920  
Db 1861 AGAGGATCAAGAGGAGGAGAAACCAAGGAGGAAAGGTTCCACTCTTTCATTTTGAAGGC 1920  
Qy 1921 TTTTAACTCAGAAATGAGGCAACTTGTATGATTCGATTAATAGATCAACGCTTTGTACT 1980  
Db 1921 TTTTAACTCAGAAATGAGGCAACTTGTATGATTCGATTAATAGATCAACGCTTTGTACT 1980  
Qy 1981 CTACTATCAAAAACCTTATCAATAAATAAAAACGTTTGTGCGTTGTTCTCC 2032  
Db 1981 CTACTATCAAAAACCTTATCAATAAATAAAAACGTTTGTGCGTTGTTCTCC 2032

## RESULT 3

US-10-100-303A-5  
; Sequence 5, Application us/10100303A  
; Publication No. US20030202980A1  
; GENERAL INFORMATION:  
; APPLICANT: Caplan, et al.  
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction  
; TITLE OF INVENTION: to Allergy  
; FILE REFERENCE: 2002834-0166  
; CURRENT APPLICATION NUMBER: US/10/100,303A  
; CURRENT FILING DATE: 2002-03-18



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; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2032
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-100-303A-5

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Query Match		100.0%	Score 2032;	DB 7;	Length 2032;			
Best Local Similarity		100.0%	Pred. No. 0;					
Matches 2032;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGACGAATGAGAGGGAG	60					
Db	1	AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGACGAATGAGAGGGAG	60					
Qy	61	GGTTTCTCCACTGATGCTGTGTGCTAGGGATCCTTGTCTCGCTTTCAGTTTCTGCAACGCA	120					
Db	61	GGTTTCTCCACTGATGCTGTGTGCTAGGGATCCTTGTCTCGCTTTCAGTTTCTGCAACGCA	120					
Qy	121	TGCCAAGTCATCACCTTACNAGAAAGAAAACAGAGAAACCCCTGCGCCACAGAGTGCTTCCA	180					
Db	121	TGCCAAGTCATCACCTTACNAGAAAGAAAACAGAGAAACCCCTGCGCCACAGAGTGCTTCCA	180					
Qy	181	GAGTTGTCAACAGGAAACCGGATGACTTTGAAGCAAAAGGCATGCGAGTCTCGCTGCACCAA	240					
Db	181	GAGTTGTCAACAGGAAACCGGATGACTTTGAAGCAAAAGGCATGCGAGTCTCGCTGCACCAA	240					
Qy	241	GCTCGAGTATGATCCTCGTTGTGTCTATGATCTCGAGGACACACTGGCACCAACCAACCA	300					
Db	241	GCTCGAGTATGATCCTCGTTGTGTCTATGATCTCGAGGACACACTGGCACCAACCAACCA	300					
Qy	301	ACGTTCCCTCCAGGGAGCGGACACGTTGGCGCGCAACCCGGAGACTACGATGATGACCG	360					
Db	301	ACGTTCCCTCCAGGGAGCGGACACGTTGGCGCGCAACCCGGAGACTACGATGATGACCG	360					
Qy	361	CCGTCAACCCGGAAGAGAGGAGGCGGATGGGACCACTGGAGCCAGCTCGACCGAGGGACGTGA	420					
Db	361	CCGTCAACCCGGAAGAGAGGAGGCGGATGGGACCACTGGAGCCAGCTCGACCGAGGGACGTGA	420					
Qy	421	AAGAGAAAGAGACTGGAGACAAACCAAGAGAAAGATTGGAGGCGCACCAAGTCTATCAGCAGCC	480					
Db	421	AAGAGAAAGAGACTGGAGACAAACCAAGAGAAAGATTGGAGGCGCACCAAGTCTATCAGCAGCC	480					
Qy	481	ACGGAATAAAGGCCCGAAGGAAGAGAGAGACAGAGTGGGGACACACCAAGTACCAAGGTAGCCA	540					
Db	481	ACGGAATAAAGGCCCGAAGGAAGAGAGAGACAGAGTGGGGACACACCAAGTACCAAGGTAGCCA	540					
Qy	541	TGTGAGGGAAGAAACATCTCGGAACAAACCCCTTCTACTTCCCGTCAAGGCGGTTTAGCAC	600					
Db	541	TGTGAGGGAAGAAACATCTCGGAACAAACCCCTTCTACTTCCCGTCAAGGCGGTTTAGCAC	600					
Qy	601	CCGCTACGGGAACCAAAACCGTAGGATCCCGGTCTTCAGAGGTTTGACAAAGGTCAAG	660					
Db	601	CCGCTACGGGAACCAAAACCGTAGGATCCCGGTCTTCAGAGGTTTGACAAAGGTCAAG	660					
Qy	661	GCAGTTTCAGNATCTCCAGATCACCGTATTGTGCGAGNATCAGGCCAAACCTTACACTCT	720					
Db	661	GCAGTTTCAGNATCTCCAGATCACCGTATTGTGCGAGNATCAGGCCAAACCTTACACTCT	720					
Qy	721	TGTTCTTTCCCAAGCAGCTGATGCTGATAACATCCTTGTATTACAGCAAGGCGCAAGCCAC	780					
Db	721	TGTTCTTTCCCAAGCAGCTGATGCTGATAACATCCTTGTATTACAGCAAGGCGCAAGCCAC	780					
Qy	781	CGTGACCGGTAGCAAAATGGCAATAACAGAAAGAGCTTTAATCTTGACGAGGGCCATGCACT	840					
Db	781	CGTGACCGGTAGCAAAATGGCAATAACAGAAAGAGCTTTAATCTTGACGAGGGCCATGCACT	840					
Qy	841	CAGNAATCCCATCCGGTTTCATTTTCCCTACATCTTGAAACCGCCATGACACACCAAGACCTCAG	900					
Db	841	CAGNAATCCCATCCGGTTTCATTTTCCCTACATCTTGAAACCGCCATGACACACCAAGACCTCAG	900					
Qy	901	AGTAGCTAAATCTCCATGCGCGTTAAACACACCCGGCCAGTTTCAGGATTTCTTCCCGGC	960					



Db 1981 C TACTATCCAAACTTATCAATAATAAAACGTTTGTCGTTGTTCTCC 2032

## RESULT 4

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US-10-728-323-1
; Sequence 1, Application US/10728323
; Publication No. US20040208894A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0232
; CURRENT APPLICATION NUMBER: US/10728,323
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/731,375
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2032
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-323-1

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[illegible]

Qy	601	CCGCTACGGAAACCAAAACGGTAGATCCGGGTCCTGCAGAGGTTTTGACCAAAAGGTCAAG	660
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Qy	661	GCAGTTTCCAGATCTCCAGAACTCACGTAATTGTGCAGATCGAGGCCAAACCTTAACACTCT	720
Db	661	GCAGTTTCCAGATCTCCAGAACTCACGTAATTGTGCAGATCGAGGCCAAACCTTAACACTCT	720
Qy	721	TGTTCTTCCAAAGCAGCTGATCTGATAACATCTTTGTTATTCAGCAAGGGCAAGCCAC	780
Db	721	TGTTCTTCCAAAGCAGCTGATCTGATAACATCTTTGTTATTCAGCAAGGGCAAGCCAC	780
Qy	781	CGTGACCGTAGCAAAATGGCNAATACAGAAAGAGCTTTAATCTTGACAGAGGCCATGCAC	840
Db	781	CGTGACCGTAGCAAAATGGCNAATACAGAAAGAGCTTTAATCTTGACAGAGGCCATGCAC	840
Qy	841	CAGAACTCCCATCCGGTTTCATTTCTTACATCTTTGAACCGCCATGACAAACAGAACTCAG	900
Db	841	CAGAACTCCCATCCGGTTTCATTTCTTACATCTTTGAACCGCCATGACAAACAGAACTCAG	900
Qy	901	AGTAGCTAAATCTCCATGCCGTTAAACACACCCGGCCAGTTTGTAGGATTTCTTCCCGGC	960
Db	901	AGTAGCTAAATCTCCATGCCGTTAAACACACCCGGCCAGTTTGTAGGATTTCTTCCCGGC	960
Qy	961	GAGAGCGAGACCAATCATCTTATCTTGAGGCTTTCAGCAGGAATACGTTGGAGGCCGC	1020
Db	961	GAGAGCGAGACCAATCATCTTATCTTGAGGCTTTCAGCAGGAATACGTTGGAGGCCGC	1020
Qy	1021	CTTCAATGCGGAATTCAAATGAGATACGGAGGTCGTTTAGAGAGAAATGCAGGAGGTGA	1080
Db	1021	CTTCAATGCGGAATTCAAATGAGATACGGAGGTCGTTTAGAGAGAAATGCAGGAGGTGA	1080
Qy	1081	GCAAGAGGAGAGAGGCGAGCGATGGAGTACTCGGAGTAGTGAGAACTTAAGAGGAGT	1140
Db	1081	GCAAGAGGAGAGAGGCGAGCGATGGAGTACTCGGAGTAGTGAGAACTTAAGAGGAGT	1140
Qy	1141	GATAGTCAAAGTGTCAAAGGAGCAGTTGGAAGAACTTACTAAGCAGCTTAATTCGTCCTC	1200
Db	1141	GATAGTCAAAGTGTCAAAGGAGCAGTTGGAAGAACTTACTAAGCAGCTTAATTCGTCCTC	1200
Qy	1201	AAAGAAAGCTCCGAGAGAGGGAGATATCACCAACCAATCAACTTGAGAGAGGCGA	1260
Db	1201	AAAGAAAGCTCCGAGAGAGGGAGATATCACCAACCAATCAACTTGAGAGAGGCGA	1260
Qy	1261	GCCCGATCTTTCTAACTTTGGGAAGTTATTGTAGGTGAAGCCAGACAGAAAGAACCC	1320
Db	1261	GCCCGATCTTTCTAACTTTGGGAAGTTATTGTAGGTGAAGCCAGACAGAAAGAACCC	1320
Qy	1321	CCAGCTTACGACCTGGACATGATGCTCACTGTGTAGAGATCAAGAAAGGAGCTTTGAT	1380
Db	1321	CCAGCTTACGACCTGGACATGATGCTCACTGTGTAGAGATCAAGAAAGGAGCTTTGAT	1380
Qy	1381	GCTCCACACTTCAACTCAAGGCCATGGTTATCGTCTGTCGTCACAAAGGAACCTGGAAA	1440
Db	1381	GCTCCACACTTCAACTCAAGGCCATGGTTATCGTCTGTCGTCACAAAGGAACCTGGAAA	1440
Qy	1441	CCTTTGAATCTCGTGGCTGTAAAGAAAAGAGCAACACAGAGGGGACGGCGGGAAGAGAGGA	1500
Db	1441	CCTTTGAATCTCGTGGCTGTAAAGAAAAGAGCAACACAGAGGGGACGGCGGGAAGAGAGGA	1500
Qy	1501	GGAAGGAGCGAAGAGAGGGGGAAGTAAACAGAGAGGTGCGTAGGTATACACAGCAGGTT	1560
Db	1501	GGAAGGAGCGAAGAGAGGGGGAAGTAAACAGAGAGGTGCGTAGGTATACACAGCAGGTT	1560
Qy	1561	GAAGGAAGCGATGTGTTTCATCATGCGCAGCAGCTCATCCAGTAGCCATCAACGCTTCTC	1620
Db	1561	GAAGGAAGCGATGTGTTTCATCATGCGCAGCAGCTCATCCAGTAGCCATCAACGCTTCTC	1620
Qy	1621	CGAACTCCATCTGCTTGGCTTCGGGTATCAACGCTCAAAACACACAGAACTCTCTTGC	1680
Db	1621	CGAACTCCATCTGCTTGGCTTCGGGTATCAACGCTCAAAACACACAGAACTCTCTTGC	1680
Qy	1681	AGGTGATAAGGCAATGTGTATAGACCAAGATAGAGAGCAAGCAAGGATTTAGCATTC	1740

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Db 1681 AGGTGATAGGACAAATGTGATAGACAGATAGAGAAAGCAAGCAAGATTTAGCATTC 1740
Qy 1741 TGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAAGAAATCTCAGTTGTGAG 1800
Db 1741 TGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAAGAAATCTCAGTTGTGAG 1800
Qy 1801 TGTCTGCTCAATCTCAATCTCAATCTCGTGTCTCTGAGAAAGAGTCTCTCGAGAA 1860
Db 1801 TGTCTGCTCAATCTCAATCTCAATCTCGTGTCTCTGAGAAAGAGTCTCTCGAGAA 1860
Qy 1861 AGAGGATCAAGAGAGGAGAAACCAAGGAGGAGAGGTCCACTCTCTTCAATTTGAAGGC 1920
Db 1861 AGAGGATCAAGAGAGGAGAAACCAAGAGGAGAGGTCCACTCTCTTCAATTTGAAGGC 1920
Qy 1921 TTTTAACTGAGAAATGGAGGCAACTTGTATGATCGATAATAAGATCAAGCTTTTGTACT 1980
Db 1921 TTTTAACTGAGAAATGGAGGCAACTTGTATGATCGATAATAAGATCAAGCTTTTGTACT 1980
Qy 1981 CTACTATCCAAAACCTTATCAATAAATAAAAACGTTTGTGCGTTGTTCTCC 2032
Db 1981 CTACTATCCAAAACCTTATCAATAAATAAAAACGTTTGTGCGTTGTTCTCC 2032

RESULT 5
US-10-728-051-1
; Sequence 1, Application US/10728051
; Publication No. US20040234548A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0222
; CURRENT APPLICATION NUMBER: US/10/728,051
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/731,375
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2032
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-051-1

Query Match 100.0%; Score 2032; DB 9; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATAATCATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGAG 60
Db 1 AATAATCATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGAG 60
Qy 61 GGTTCCTCCACTGATGCTGTGTGCTAGGGATCCTTGTCTCGCTTCAGTTTCTGCAAGCA 120
Db 61 GGTTCCTCCACTGATGCTGTGTGCTAGGGATCCTTGTCTCGCTTCAGTTTCTGCAAGCA 120
Qy 121 TGCAAGTATCATCTTACAGAGAAACCAAGAGAACCCCTGGCCAGAGAGTGCCTCCA 180
Db 121 TGCAAGTATCATCTTACAGAGAAACCAAGAGAACCCCTGGCCAGAGAGTGCCTCCA 180
Qy 181 GAGTTGTCAACAGAACCGGATGACTTGAAGCAAAAGGCGATCGAGTCTCGCTGCACAA 240
Db 181 GAGTTGTCAACAGAACCGGATGACTTGAAGCAAAAGGCGATCGAGTCTCGCTGCACAA 240
Qy 241 GCTCGAGTATGATCCTCGTTGTGTCTATGATCTCTCGAGGACACATGCGCACCAACCA 300
Db 241 GCTCGAGTATGATCCTCGTTGTGTCTATGATCTCTCGAGGACACATGCGCACCAACCA 300
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Qy 301 AGTTTCCCTCCAGGGAGCGGACACGTGGCCGCCAACCCGGAGACTACGATGATGACCG 360
Db 301 AGTTTCCCTCCAGGGAGCGGACACGTGGCCGCCAACCCGGAGACTACGATGATGACCG 360
Qy 361 CCGTCAACCCCAAGAGAGAGGAGGCGCATGGGGACCCAGCTGGACCCAGCTGGAGGAGCGTGA 420
Db 361 CCGTCAACCCCAAGAGAGAGGAGGCGCATGGGGACCCAGCTGGAGGAGGAGCGTGA 420
Qy 421 AAGAGAAGAGACTGTGAGACAACCAAGAGAAGATTGGAGGCGCACCAAGTCAATCAGCAGCC 480
Db 421 AAGAGAAGAGACTGTGAGACAACCAAGAGAAGATTGGAGGCGCACCAAGTCAATCAGCAGCC 480
Qy 481 ACGGAAAAATAAGCCCCGAAGAGAGACAAGAGAAACAGAGTGGGGAAACACACAGGTAGCCA 540
Db 481 ACGGAAAAATAAGCCCCGAAGAGAGACAAGAGAAACAGAGTGGGGAAACACACAGGTAGCCA 540
Qy 541 TGTGAGGGAAGAAAACATCTCGGAAACAAACCTTTTACTTTCCCTCAAGGCGGTTTAGCAC 600
Db 541 TGTGAGGGAAGAAAACATCTCGGAAACAAACCTTTTACTTTCCCTCAAGGCGGTTTAGCAC 600
Qy 601 CCGCTACGGGAAACAAAACCGTAGAGATCCGGGTCCTGCGAGAGGTTTGAACAAAGGTCAAG 660
Db 601 CCGCTACGGGAAACAAAACCGTAGAGATCCGGGTCCTGCGAGAGGTTTGAACAAAGGTCAAG 660
Qy 661 GCAGTTTTCAGAAATCTCCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTAACACTCT 720
Db 661 GCAGTTTTCAGAAATCTCCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTAACACTCT 720
Qy 721 TGTTCCTTCCCAAGCACGCTGATGATAACATCTTTGTATCCAGCAAGGCGAACCCAC 780
Db 721 TGTTCCTTCCCAAGCACGCTGATGATAACATCTTTGTATCCAGCAAGGCGAACCCAC 780
Qy 781 CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTTAATCTTGACGAGGCGCATGCAC 840
Db 781 CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTTAATCTTGACGAGGCGCATGCAC 840
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Qy 901 AGTAGCTAAAATCTCCATGCCCTTAAACACACCCGGCCAGTTTGAAGATTTCTCCCGGC 960
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Qy 961 GAGCAGCCGAGACCAATCATCTTCTTACATCTTGAAGGCTTTCAGCAGGAATACGTTGGAGCGCG 1020
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QY 1261 GCCCGATCTTTCTAAACAACCTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAAGAACCC 1320
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Db 1801 TGCTCGTCTCAATCTCAATCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCG 1860
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RESULT 7
US-10-958-324-5
; Sequence 5, Application US/10958324
; Publication No. US20050114924A1
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIQUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN TRANSGENIC PEANUT SEEDS
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; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/10/958,324
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/715,036
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2032
; TYPE: DNA
; ORGANISM: Arachis hypogaea
; US-10-958-324-5
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Query Match 100.0%; Score 2032; DB 10; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 781 CGTGACCGTAGCAAAATGGCAATAACAGAAAAGAGCTTTAAATCTTGACGAGGCCCATGCACCT 840  
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Qy 1861 AGAGGATCAAGAGGAGGAAACCAAGAGGGAAGGTTCCACTCTTTCAATTTTGAAGGC 1920  
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Qy 1921 TTTTAATCAGAAATGAGGCAACTTGTATGTATCGATAATAGATCAGCCTTTTGTACT 1980  
Db 1921 TTTTAATCAGAAATGAGGCAACTTGTATGTATCGATAATAGATCAGCCTTTTGTACT 1980  
Qy 1981 CTACTATCAAAAACCTTATCAATAAATAAAAACGTTTGTGCGTTGTTTCTCC 2032  
Db 1981 CTACTATCAAAAACCTTATCAATAAATAAAAACGTTTGTGCGTTGTTTCTCC 2032

RESULT 8

US-10-100-303A-6  
; Sequence 6, Application US/10100303A  
; Publication No. US20030202980A1  
; GENERAL INFORMATION:

; APPLICANT: Caplan, et al.  
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction  
; FILE REFERENCE: 2002834-0166  
; CURRENT APPLICATION NUMBER: US/10/100,303A  
; CURRENT FILING DATE: 2002-03-18  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; TYPE: DNA  
; ORGANISM: Atachis hypogaea, Prot/Nucleo-Ara h 1  
US-10-100-303A-6

Query Match 86.2%; Score 1752.4; DB 7; Length 1949;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;

Qy 48 CAATGAGAGGGAGGGTTTCTCCACTGATGCTGTGTCTAGGGATCCTTGTCTGGCTTCAG 107  
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Db 61 TTTCTGCAACGAGGCCAAGTCAC-----TTACCGGAAACAGAGAACCCCTGGCCCC 114  
Qy 168 AGAGGTGCTCCAGAGTTGTCAACAGGAACCGGATCACTTGAAGCAAAAAGGCATGCGAGT 227  
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Qy 228 CTCGCTGCAACGAGCTCGAGTATGATCCTGTTGTCTGTATGATCCTCGAGGACACACTG 287  
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QY 1657 AAGCGAAGATTTAGCATTCCTGGTTCCGGTGAACAAGTTGAGAGCTCATCAAAAACC 1716  
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QY 1779 AGAAGAAATCTCACTTTGTGAGTGTCTGCCTCAATCTCAATCTCAATCTCGTCTGCTC 1838  
Db |||  
QY 1717 AGAGGAGTCTCACTTTGTGAGTGTCTGCCTCAATCTCAATCTCAATCTCGTCTC----- 1765  
QY 1839 CTGAGAAAGAGTCTCTCTGAGAAAGAGGATCAAGAGGAGGAGAAACCAAGAGGAGGAGGTC 1898  
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QY 1766 -----GTCTCTCTGAAAAGAGGATCAAGAGGAGGAGAAACCAAGAGGAGGAGGTC 1815  
QY 1899 CACTCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTTGTATGTATCGAT 1958  
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QY 1816 CACTCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGAAACTTTGTATGTATCCAT 1875  
QY 1959 AATAAGATCACGCTTTTGTACTTACTATCCAAAAAATTTATCAATAAATAAAACGTTTG 2018  
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QY 1876 AATAAGATCACGCTTTTGTAACTACTATCCAAAAAATTTATCAATAAATAAAACGTTTG 1935  
QY 2019 TCGGTTGTTTCTCC 2032  
Db |||  
QY 1936 TCGGTTGTTTCTCC 1949  
RESULT 9  
US-10-245-227B-15  
; Sequence 15, Application US/10245227B  
; Publication No. US20030200558A1  
; GENERAL INFORMATION:  
; APPLICANT: Peng, William  
; APPLICANT: Rapp, Jieixin  
; APPLICANT: Nadig, Gautham  
; APPLICANT: Venkatesh, T  
; TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR THEIR USE  
; FILE REFERENCE: REN-00-087-US  
; CURRENT APPLICATION NUMBER: US/10/245,227B  
; CURRENT FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 1254  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: mature form of beta-conglycinin beta-subunit  
US-10-245-227B-15  
Query Match 20.0%; Score 406.8; DB 7; Length 1254;  
Best Local Similarity 62.1%; Pred. No. 4.2e-115;  
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;  
QY 562 GAACAACCCCTTCTACTT---CCCGTCAAGGCGGTTTAGCACCCGCTACGGNACCAAAA 618  
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QY 24 GAATAACCCCTTCTACTTGAAGAAGCTTAACAGCTTCCAAGCTCTCTTTGAGAAACCAAAA 83  
QY 619 CGGTAGGATCCGGTCTCGCAGAGGTTTCACCAAGGTCAAGGCGAGTTTTCAGAATCTCA 678  
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QY 84 CGGTGCATTCGTCTCTCCAGAGATTCAACAAAACGCTCCCAACACTTTGAGNACCTTGC 143  
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QY 204 TGACGCGGATTCTCTCTCTTTGCTTAGCGGAGAGCCATACCTTACCTTGGTGAACAA 263  
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Db 324 CACTTACTATTGGTTAAACCTCAGACCCAGAAATCTCAAAATAATCAAACTGCCAT 383
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Qy 979 ATCTTACTTTCAGGGCTTTCAGCAGGAATACGTTGGAGCCGCTTCAATCGGAATTCAA 1038
Db 444 GTCTTACTTTCAGGGCTTTCAGCAGGAATATTTCTAGAGACCTCTCTCCATAGCGAATTCGA 503
Qy 1039 TGAGATACGAGGGTGTCTGTAGAGAGAAATGACGAGGAGTGCACAGAGGAGAGGGCA 1098
Db 504 GGAGATAAACAGGGTTTGTGGAGAGGAAGAGCAGAGGAGCAGCAAG----- 555
Qy 1099 GAGGCGATGAGTACTCGGAGTAGTGAGAAATGAAGGAGTGTAGTCAAGTGTCAAA 1158
Db 556 -----GGAGTGTCTGTGAATCTCAAA 578
Qy 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCTTAATTCGTCTCAAGAAAGGCTCCGAGA 1218
Db 579 GGAACAAATTCGGCAACTGAGCAGACGTGCCAAATCTAGTTCAAGGAAACCAATTCCTC 638
Qy 1219 AGAGGGAGATATCACCACCAATCAACTTTCAGAGAGGCGAGCCGATCTTTCTAACAA 1278
Db 639 CGAAGATG-----AACCATTTCAACTTGAAGCGCCGCAACCCCATCTATTTCCAA 689
Qy 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAAACCCCGAGCTTCAGGACCTGGA 1338
Db 690 CTTTGGGAAGTTCTTGGAGTACCCCTG---AGAAACCCACAGCTTCGGAGCTTGG 746
Qy 1339 CATGATGCTCAGCTGTGTAGAGATCAAGAGAGGCTTTGATGCTCCCACTTCAACTC 1398
Db 747 TATCTTCTCAGTCTGTGATATCAACGAAGGAGCTCTTCTTACCACTTCAATTC 806
Qy 1399 AAAGGCCATGGTTATCTGCTGTCTCAACAAAGNACTGGAAACCTTGAATCTGTGGCTGT 1458
Db 807 AAAGGCCATAGTATCTAGTGTATTAATGAAGGAGATGCAAACTTGAATCTGTGGCAT 866
Qy 1459 AAGAAAGAGCAACACAGAGGGGAGCGCGGGAAGAGAGGAGGAGCAAGACGCAAGAAGA 1518
Db 867 TAAAGAACACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 909
Qy 1519 GGAGGGAAGTAAACAGAGAGGTCGTAGGTACACAGCAGAGTTTGAAGAGGCGATGTT 1578
Db 910 -----GAGTGCAAGAGGTACAGAGCTGAAATTTGTCTGAAGACGATGATT 953
Qy 1579 CATCATGCGAGAGCTCATCCAGTAGCCATCAAGCTTCTCCGAACTCATCTGCTTGG 1638
Db 954 TGTAAATTCAGAGCTTATCTCATTTGTCTCAAGCTTACCTCAAACTCAATTTCTCTGC 1013
Qy 1639 CTTTCGGTATCAACGCTGAAACCAACACAGAACTTCTTCTGCGAGGTGATAAGGACAATGT 1698
Db 1014 TTTTGGTATCAATGCTGAGAAACACAGAGGAACTTCTTTCAGGCGAGGAAAGCAATGT 1073
Qy 1699 GATAGACCATAGAGAGCAAGCAGAGGATTTAGCATTTCCCTGGGTGGGTGAACAAGT 1758
Db 1074 GGTAAAGSCAGATAGAAGACAAAGTGCAGGAGCTTGCCTTCCCTGGGTCTGCAAGATGT 1133
Qy 1759 TGAGAGCTCATCAAAACACAGAGGAACTCTACTTTGTGAGTGTCTGCTCTCA 1812
Db 1134 TGAGAGGCTATTAAGAGAGGAGGAACTCTACTTTTGTGATGCTCAGGCTCA 1187

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RESULT 10

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US-10-245-227B-13
; Sequence 13, Application US/10245227B
; Publication No. US20030200558A1
; GENERAL INFORMATION:
; APPLICANT: Rapp, William
; APPLICANT: Peng, Jiexin
; APPLICANT: Nadi, Gautham
; APPLICANT: Venkatesh, T
; TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR THEIR USE

```

```

; FILE REFERENCE: REN-00-087-US
; CURRENT APPLICATION NUMBER: US/10/245,227B
; FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: epitope form of beta-conglycinin beta-subunit
US-10-245-227B-13

```

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Query Match 20.0%; Score 406.8; DB 7; Length 1278;
Best Local Similarity 62.1%; Pred. No. 4.3e-115;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

Qy 562 GAACAACCCCTTCTACTT---CCGTCAGGCGGTTTAGCACCCGCTACGGAGCAACAAA 618
Db 48 GAATAACCCCTTCTACTTGAGAGCTTAACAGCTTCCAAACTCTCTTTGAGAACCAAAA 107
Qy 619 CGGTAGATCCGGGTCTTCAGAGGTTTGACCAAGGTCAAGCAGTTTCAGAACTCTCCA 678
Db 108 CGGTGCAATTCGTCTCTCCAGAGATTCAACAAACGCTCCCAACACTTGAGAACCTTCG 167
Qy 679 GAATCAACCCGTTTGTGCAGATCGAGGCCAAACCTTAACACTCTTTGTTCTTCCCAAGCAGC 738
Db 168 AGACTACCGGATTCCTAGTTTCAGTCAAAACCCCAACACAATCTTCTCCCCACCACATGC 227
Qy 739 TGATGCTATAACATCTTGTGTTATCAGCAAGGGCAAGCCAGCTGACCGTAGCAATGG 798
Db 228 TGACGCGGATTTCTCTCTCTTTGTCCTTTAGCGGAGAGGCACTACTTACCTTGGTGAACA 287
Qy 799 CAATAACAGAAAGAGCTTTAACTCTTCAGAGGGCCATGCACTCAGAAATCCCATCCGGTTT 858
Db 288 CGAGCAGAGACTCTCTACAACTTCACCTTGGCGATGCCAGAGAAATCCAGCTGGAAC 347
Qy 859 CATTTCTCTACATCTGAACCCGCTATGACAAACCAAGAACTTCAGAGTAGTCTTCAATCTCCAT 918
Db 348 CACTTACTATTGTTTAACTTACCTCAGCCACCAAGAAATCTCAAAATAATCAAACTTGCCAT 407
Qy 919 GCCGTTTAAACACACCCCGCAGTTTGAGGATTTCTCCCGCGAGCAGCCGAGACCAATC 978
Db 408 ACCCGTCAACAAACCTTGGCAGATATGATGATTTCTTTATCTAGCACTCAAGCCCAACA 467
Qy 979 ATCTTACTTTCAGGGCTTTCAGAGGAAATACGTTGGAGGGCGCTTCAATCGCGAATTCAA 1038
Db 468 GTCCTACTTTCAGAGGCTTCAGCCATTAATTTCTAGAGACTCTCTTCCATAGCGAATTCGA 527
Qy 1039 TGAGATACGAGGGTCTGTGTAGAGAGAAATGACAGAGGTGAGCAAGAGAGAGAGGGCA 1098
Db 528 GGAGATAAACAGGGTTTGTTCGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 579
Qy 1099 GAGGCGATGAGTACTCGGAGTAGTGAGAACTTAAGAGAGTGTAGTCAAGTGTCAAA 1158
Db 580 -----GGAGTGTCTGTGAATCTCAAA 602
Qy 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCTTAATCCGTCTCAAGAAAGGCTCCGAGA 1218
Db 603 GGAACAAATTCGGCAACTGAGCAGACGTGCCAAATCTAGTTCAAGGAAACCAATTTCTCTC 662
Qy 1219 AGAGGGAGATATCAACCAACCCCAATCACTTTCAGAGAGGCGAGCCGCTCTTTCTAACAA 1278
Db 663 CGAGATG-----AACCATTTCACTTGAGAACCCGCAACCCCATCTATTTCCAACAA 713
Qy 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAAAGAAACCCCGAGCTTCAGAGCTTGA 1338
Db 714 CTTTGGGAAGTTCTTTGAGATCACCCCTG---AGAAACCCCAACAGCTTCGGAGCTTGA 770
Qy 1339 CATGATGCTCAGCTGTGTAGATCAAGAGAGGCTTTGATGCTCCCACTTCAACTC 1398
Db 771 TATCTTCTCAGTCTGTGGATATCAAGAGGAGCTCTTCTTCTACCACACTTCAATTC 830

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Db 976 -----GAAGTGAAGGTACAGAGCTGAATTTGTCTGAAGACCATGTATT 1019  
QY 1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACCGCTTCTCGAAGCTCCATCTGCTTGG 1638  
Db 1020 TGTAAATTCAGCAGCTTATCCATTTGTCTCAACGCTTACCTCAAACTCAATTTCTTGC 1079  
QY 1639 CTTGGGTATCAACGCTGAAACCAACACAGAAATCTTCTTGCAGGTGATAAGGACAATGT 1698  
Db 1080 TTTTGGTATCAATGCTGAGAACCAACAGAGAACTTCTTGCAGGCGAGAAAGACAATGT 1139  
QY 1699 GATAGACAGATAGAGAGCAAGCAAGGAGGATTTAGCAATCCCTGGGTCCGGTGAACAAT 1758  
Db 1140 GGTAAAGCAGATAGAAAGCAAGTGCAGAGCTTGCCTTCCCTGGGTCTGCACAAGATGT 1199  
QY 1759 TGAGAACTCATCAAAACAGAGGAAATCTCACTTTGTGAGTCTCGTCTCA 1812  
Db 1200 TGAGAGCTATTAAAGAGCAGAGGGAATCCTACTTTGTTGATGCTCAGCCTCA 1253

## RESULT 12

US-10-245-227B-3

; Sequence 3, Application US/10245227B

; Publication No. US20030200558A1

; GENERAL INFORMATION:

; APPLICANT: Rapp, William

; APPLICANT: Peng, Jieixin

; APPLICANT: Nadiq, Gautham

; APPLICANT: Venkatesh, T

; TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR THEIR USE

; FILE REFERENCE: REN-00-087-US

; CURRENT APPLICATION NUMBER: US/10/245, 227B

; CURRENT FILING DATE: 2002-09-17

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1320

; TYPE: DNA

; ORGANISM: Glycine max

US-10-245-227B-3

Query Match 20.08; Score 406.8; DB 7; Length 1320;  
Best Local Similarity 62.14; Pred. No. 4.3e-115;  
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;  
QY 562 GAACAAACCTTTCTACTTT---CCGCTCAAGCGGTCTTAGCACCGCTTACCGGGAACCAAAA 618  
Db 90 GAATACCTTTCTACTTTGAGAAGCTCTAAGAGCTTCCAACTCTCTTTGAGAACCAAAA 149  
QY 619 CGGTAGATCCGGTCTCTGAGAGTTTGACCAAGGTCAAGGAGTTTCAGAAATCTCCA 678  
Db 150 CGGTGCGATTCGTCTCTCCAGAGATTCAACAAACGCTCCCAACAACTTGAGAACCTTCG 209  
QY 679 GAATACCGTATTGTGAGATCGAGCCCAACCTTAACACTTTGTTCTTCCCAAGCAGC 738  
Db 210 AGACTACCGGATTTGTCAGTTTCAGTCAAAACCAACCAACAACTCTTCTCCCCACCATGC 269  
QY 739 TGATGCTGATAACATCTCTGTTATCCAGCAAGGCAAGCCACCGTGACCGTAGCAATGG 798  
Db 270 TGAGCGGATTTCTCTCTTTGCTTCTTACGGGAGAGCCATCTACTTCTTGTGTAACA 329  
QY 799 CAATAACAGAAAGAGCTTTTAATCTTGACAGGGCCATGCACTCAGAAATCCCATCCGGTTT 858  
Db 330 CGAGCAGAGAGCTCTTCAACCTTACCCCTGGGATGCCAGAGAAATCCAGCTGGAAC 389  
QY 859 CATTTCTACATCTTGACCGCCATGACACCCAGAACTCAGAGTAGCTTAAATCTCCAT 918  
Db 390 CACTTACTATTGTTTAACTTCAACCTCAGACCAACCAAGAAATCTCAAAATTAATCAAACTTCCAT 449  
QY 919 GCCGTTTAAACACACCCCGGCTTTGAGGATTTCTTCCCGGCGAGAGCGGAGCAACAATC 978  
Db 450 ACCGTCACAAACCTGGGAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 509  
QY 979 ATCCTACTTGCAGGGCTTACAGAGGAATACGTTGGAGGCGGCTTCAATGCGGAATTCAA 1038

Db 510 GTCTACTTGCAGAGGCTTCAAGCATATAATTTCTAGAGACCTCTCTCATAGCAATTCGA 569  
QY 1039 TGAGATACGAGAGGCTCTGTTAAGAGAGATGACAGAGGTGACAGAGAGAGAGAGGCA 1098  
Db 570 GGAGATAAACACAGAGGTTTGTGGGAGAGGAAGAGGAGCAGAGGCAAGAG----- 621  
QY 1099 GAGCGATGAGAGTACTCGGAGTAGTGAGAACAAATGAAGGAGTAGTAGTCAAGTGTCAAA 1158  
Db 622 -----GGAGTGTATCGTGAACCTCTCAAA 644  
QY 1159 GGAGCAGCTTGAAGAACTTACTAAGCACGCTAAATCGTCTCAAGAAAGGCTCCGAAGA 1218  
Db 645 GGAACAAATTCGCAACTGACGAGAGCTGCAAAATCTAGTTCAAGGAAAAACCAATTTCTC 704  
QY 1219 AGAGGAGATATCACCAACCAATCAATTTGAGAGAGGCGCGCGATCTTTCTTAACAA 1278  
Db 705 CGAAGATG-----AACCATTTCACTTTGAGAGCGCAACCCATCTATTTCCAAACA 755  
QY 1279 CTTTGGGAAAGTTATTTGAGGTGAAGCCAGACAAGAAAGACCCCGAGCTTCAGGACCTGGA 1338  
Db 756 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAACCCACAGCTTCGGGACTTGA 812  
QY 1339 CATGATGCTCACCTGTGTAGAGATCAAAGAGAGCTTTGATGCTCCACACTTTCAACTC 1398  
Db 813 TATCTTCTCAGTTCTGTGATATCAACGAAGAGGCTCTTTCTTACCACACTTCAATTC 872  
QY 1399 AAAGCGCATGCTTATCGTCTGCTCAACAAAGAACTTGAAGAACTTGAACCTCTGCTGT 1458  
Db 873 AAAGCGCATAGTGATACTAGTGATTAATGAAGAGAGATGCAACATTTGAACCTTGTG 932  
QY 1459 AAGAAAGAGCAACACAGAGGCGCGCGGGAAGAGAGGAGGAGGAGCAAGACGAAGAAGA 1518  
Db 933 TAAAGAAACAAACACAGACAGAAACAGGAAGAGAACTTTG----- 975  
QY 1519 GGAGGAAAGTAAACAGAGAGGTGCTAGGTACACAGCAGAGTTTGAAGAGGCGCATGTGT 1578  
Db 976 -----GAAAGTCAAGAGGTACAGAGCTGAATTTGCTCAAGACGATGTATT 1019  
QY 1579 CATCATGCCAGAGCTCATCCAGTACCATCAACGCTTCTCTCGAACTCCATCTGCTTGG 1638  
Db 1020 TGTAAATTCAGCAGCTTATCCATTTGTGCTCAACGCTACTCTAAACCTCAATTTCTTGC 1079  
QY 1639 CTTTGGTATCAACGCTGAAACCAACCAAGAACTTCTTCTTGCAGGTGATAAGGACAATGT 1698  
Db 1080 TTTTGGTATCAATGCTGAGAACCAACCAAGAGAACTTCTTTCAGGCGAGAAACAAATGT 1139  
QY 1699 GATAGACAGATAGAGAACCAAGGAGATTTAGCATTTCCCTGGGTCCGGTGAACAAGT 1758  
Db 1140 GGTAAAGCAGATAGAAAGACAAGTGCAGAGCTTGGCTTCCCTGGGTCTGCACAAGATGT 1199  
QY 1759 TGAGAGGCTCATCAAAACCAAGAGGAATCTCACTTTGTGAGTGTCTGCTCTCA 1812  
Db 1200 TGAGAGGCTATTAAAGAACAGAGGGAATCTTACTTTGTTGATGCTCAGCCTCA 1253

## RESULT 13

US-10-684-651-3

; Sequence 3, Application US/10684651

; Publication No. US20040064858A1

; GENERAL INFORMATION:

; APPLICANT: GARY MICHAEL FADER

; APPLICANT: ANTHONY JOHN KINNEY

; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC

; CLASSES OF SOYBEAN SEED

; PROTEIN GENES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WINDOWS 95  
SOFTWARE: MICROSOFT WORD 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/684,651  
FILING DATE: 14-Oct-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,652  
FILING DATE: 11-Jan-2001  
APPLICATION NUMBER: 60/019,940  
FILING DATE: JUNE 14,1996  
ATTORNEY/AGENT INFORMATION:  
NAME: LYNNE M. CHRISTENBURY  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1071-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1320 base pairs  
TYPE: nucleic acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-684-651-3

Query Match 20.0%; Score 406.8; DB 8; Length 1320;  
Best Local Similarity 62.1%; Pred. No. 4.3e-115;  
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAAACCTTCTACTT---CCGTCAGGCGGTTTAGCACCCGCTACGGGAACCAAAA 618  
DB 90 GAATAACCTTCTACTTTAGAGCTCTAACAGCTTCCAACTCTCTTTGAGAACCAAAA 149  
QY 619 CGGTAGATCCGGGTCCTCGAGAGTTTGACAAAGGTCAGGAGCTTTTCAGAAATCTCCA 678  
DB 150 CGTTCGATTCGTCCTCTCAGAGATTCAACAAACGCTCCCAACACTTGAGAACCTCG 209  
QY 679 GAATACCGATTGTGCAGATCAGGCAACCTAACACTCTGTCTTCTCCCAAGCACGC 738  
DB 210 AGACTACCGGATTGTCCAGTTTCAGTCAAAACCCAAACAACTCTCTCCCAACCATGC 269  
QY 739 TGATGCTGATAACATCCTTGTATTCCAGCAAGGCAAGCCACCGTCGACCGTAGCAAAATGG 798  
DB 270 TGACGCGATTCTCTCTCTTTGCTTAGCGGAGAGCCATACCTTGTGTGAACAA 329  
QY 799 CAATAACAGAAAGAGCTTTAATCTTGACGAGGCCATGCACTCAGAAATCCCATCCGGTTT 858  
DB 330 CGACGACAGAGACTCTTCAACCTTCACCTGCGGATGCCAGAGAAATCCAGCTGGAAC 389  
QY 859 CATTTCTACATCTTGAACCGCCATGACACAGAACCTTCAGATAGCTAAATCTCCAT 918  
DB 390 CACTTACTATTGTGTTAAACCTCAGCACCAACCAAGAACTCTCAAAATTAATCAAACTTCCCAT 449  
QY 919 GCCCGTTAACACACCGCGGCTTTGAGGATTTCTCCCGGCGAGCGGAGACCAATC 978  
DB 450 ACCCGTCAACAAACCTTGGGAGATATGATGTTCTTCTATCTAGCACTCAAGCCCAACA 509  
QY 979 ATCTTACTTGCAGGGCTTCAGCAGGAATAGTTGGAGGCGCTTCAATCGGGAATCAA 1038  
DB 510 GTCTTACTTGCAGGGCTTCAGCAGGAATATTTCTAGAGACCTCTCCATAGCGAATTCGA 569  
QY 1039 TGAGATACGAGGGTCTGTTAGAGAGATGAGGAGGTGACAGAGGAGAGAGGCA 1098  
DB 570 GGAGATAAACAGGGGTTTGTGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 621  
QY 1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGTAGTAGTCAAAAGTGTCAA 1158

DB 622 -----GGAGTGATCGTGAACCTCTCAA 644  
QY 1159 GGAGCAGCTTGAAGAACTTACTAAGCAGCGTAAATCCGTCTCAAGAAAGGCTCCGAAGA 1218  
DB 645 GGAACAAATTCGCAACTCAGCAGCGTCCCAAATCTAGTTCAAGGAAACCAATTTCTC 704  
QY 1219 AGAGGAGATATCACCAACCCAACTCAACTTGAGAGAGGCGGAGCCGATCTTTCTAACAA 1278  
DB 705 CGAAGATG-----AACCAATTCAACTTGAGAGCCGCAACCCCATCTTATTTCCAAACA 755  
QY 1279 CTTTGGGAAGTTATTGAGGTGAAGCAGACAGAAAGAAACCCCACTTTCAAGACCTGGA 1338  
DB 756 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAACCCACACAGCTTCGGGACTTGA 812  
QY 1339 CATGATGCTCACTGTGTAGATCAAGAGAGCTTTGATGCTCCCACTTCAACTC 1398  
DB 813 TATCTTCCTCAGTTCTGTGATATCAACGAAGAGCTCTTCTTACCACACTTCAATTC 872  
QY 1399 AAAGCCATGTTATCGTCTGTCGTCACAAAGGAACTGAAACCTTGAACCTCGTGGCTGT 1458  
DB 873 AAAGCCATAGTGATAGTATGATTAAAGAGAGATGCAAAACATTGAACTTGTTCGCAT 932  
QY 1459 AAGAAAGAGCAACACAGAGGGGCGCGGAAAGAGAGGAGGAGCAAGAGCAAGAAGA 1518  
DB 933 TAAAGNACAAACAGACAGAAACAGAAAGGAACTTTG----- 975  
QY 1519 GGAGGAAAGTAACAGAGAGGTGCTAGGTACACAGGAGGTTGAAGAGAGGCGATGTGTT 1578  
DB 976 -----GAAAGTCAAAAGGTACAGAGCTGAAATTTCTCTGAAGAGCGATGTAAT 1019  
QY 1579 CATCTGCCAGCAGCTCCAGTAGCCATCAACGCTTCCCTCGAACTCCATCTGCTCG 1638  
DB 1020 TGTAAATTCAGCAGCTTATCCATTTGTCTCAACGCTACTCAAACTCAATTTCTCTG 1079  
QY 1639 CTTTGGTATCAACGCTGAAACCAACACAGAAATCTTCTTTCAGAGTGATAAGGACAATGT 1698  
DB 1080 TTTTGTATCAATGCTGAGACAAACAGAGGAATCTTCTTTCAGGCGGAGAAAGACAATGT 1139  
QY 1699 GATAGACAGATAGAGAGCAAGCGAGGATTTAGCAATTCCTTGGGTCGGGTGAACAAGT 1758  
DB 1140 GGTAAAGCAGATAGAAAGCAAGTGCAGAGCTTGGCTTCCCTGGGTCTGCAACAAGATGT 1199  
QY 1759 TCAGAGGCTCATCAAAACCAAGAAATCTCACTTTGTGAGTGTCTGCTCTCA 1812  
DB 1200 TGAGAGGCTATTAAAGAACAGAGGAATCTTCTTGTGATGCTCAGCCTCA 1253

## RESULT 14

US-10-757-074-3  
; Sequence 3, Application US/10757074  
; Publication No. US20040139502A1  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; GARY MICHAEL FADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/757,074

; FILING DATE: 14-Jan-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/758,652  
; FILING DATE: 11-Jan-2001  
; APPLICATION NUMBER: 60/019,940  
; FILING DATE: JUNE 14, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LYNNE M. CHRISTENBURY  
; REGISTRATION NUMBER: 30,971  
; REFERENCE/DOCKET NUMBER: BB-1071-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-5481  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1320 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-757-074-3  
  
Query Match 20.0%; Score 406.8; DB 8; Length 1320;  
Best Local Similarity 62.1%; Pred. No. 4.3e-115;  
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;  
  
QY 562 GAACAACTTCTACTT---CCGTCAGCGGTTTAGCACCGCTACCGGACCAAAA 618  
DB 90 GAATAACCTTCTACTTTAGAGCTCTAACAGCTTCCAAACTCTCTTTGAGAACCAAAA 149  
QY 619 CGGTAGGATCCGGTCTCGAGAGGTTTGACCAAGGTCAAGGCAGTTTCAGAAATCTCCA 678  
DB 150 CGTTCGATTCGTCTCTCCAGAGATTCAACAAACGCTCCCAACTTCGAGAACCTTCG 209  
QY 679 GAATACCGTATTGTGAGATCGAGGCCAAACCTTAACACTCTTTGTTTCCCAAGCAGC 738  
DB 210 AGACTACCGATTGTCAGTTTCAGTCAAAACCAACACAACTCTTCTCCCCACCATGC 269  
QY 739 TGATGCTGATAACATCTTGTATTCCAGCAAGGCGACCGTAGCCGTAGCAATGG 798  
DB 270 TGACGCGGATTCTCTCTCTTTGTCCTTAGCGGAGAGCCATCTTACCTTGTGACAA 329  
QY 799 CAATAACAGAAAGCTTTAATCTTGACAGGCGCATGCACTCAGAAATCCCATCCGTTT 858  
DB 330 CGAGCAGAGACTCTTACAACTTTCACCTGGCGATGCCAGAGAAATCCAGCTGGAAC 389  
QY 859 CATTTCTCATCTTTGAACCGCCATGACAAACGAACTTCAGAGTAGCTAAATCTCCAT 918  
DB 390 CACTTACTATTGTTTAACTTCACTCAGCACCAGAACTCTCAAAATATCAAACTTGCCAT 449  
QY 919 GCCGTTAAACACACCGGCGAGTTTGGAGATTCTTCCCGGAGAGCGGAGACCAATC 978  
DB 450 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTATAGCACTCAAGCCCAACA 509  
QY 979 ATCTACTTCAGCGCTTCAGCAGGAATACGTTGAGGCGCGCTTCAATCGGAATTCAA 1038  
DB 510 GTCTTCTTGAAGGCTTCAGCCATATATCTAGAACCTCTTCCATAGCGAATTCGA 569  
QY 1039 TGAGATACGAGGCTGCTGTTAGAGAGAAATGCAAGGAGGTGACAGAGAGAGAGGCA 1098  
DB 570 GGAGATAACAGGCTTTGTTGGAGAGGAAGAGGACGAGGACGCAAG----- 621  
QY 1099 GAGCGATGAGGACTCGGAGTAGTGAGAAATGAAGGAGTAGTAGTCAAGTGTCAA 1158  
DB 622 -----GGAGTGTCTGTGGAATCTCAA 644  
QY 1159 GGAGCAGTTGAGAACTTACTAGCAGCGTTAAATCGTCTCAAGAAAGGCTCCGAAGA 1218  
DB 645 GGAACAAATTCGGCAATCTAGCAGACGTGCAAACTTAGTTCAAGGAAACCAATTTCTC 704  
QY 1219 AGAGGAGATATACCAACCAATCAACTTTGAGAGAGGCGAGCCGATCTTTCTAACAA 1278

DB 705 CGAAGATG-----AAACCATTTCAAGCGCGCAACCCCATCTTATTTCAACAA 755  
QY 1279 CTTTGGAAAGTTATTTGAGTGAAGCAGACAAGAAAGAACCCCGAGCTTCAGGACCTGGA 1338  
DB 756 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAAAACCCACAGCTTCGGAGCTTGA 812  
QY 1339 CATGATGCTCACCTGTGTAGAGATCAAGAAGGAGCTTTTGAATGCTCCACACTTCAATC 1398  
DB 813 TATCTTCTCAGTTCTGTGATATCAACGAAGGAGCTCTTCTTCTACCACTTCAATTC 872  
QY 1399 AAAGGCATGTTATCGTGTCTCAACAAAGAACTGGAACCTTGAACCTTGGCTGT 1458  
DB 873 AAAGGCATAGTATAGTACTAGTATTAAATGAAGGAGATGCAAAACATTTGAACCTTGTGGCAT 932  
QY 1459 AAGAAAAGAGCAACACAGAGGCGCGCGGGAAGAGAGGAGGAGCAAGACGAAGAAGA 1518  
DB 933 TAAAGAACACACACAGAGCAAGAAACAGGAGAGGAACTTTG----- 975  
QY 1519 GGAGGGAAGTAAACAGAGAGGTGCTAGGTACACAGCGAGGTTGAAGAAAGCGCATGTT 1578  
DB 976 -----GAAGTGCAAGGTACAGAGCTGAATTTCTCTGAAGACCATGTTAT 1019  
QY 1579 CATCATGCCAGAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACCTCATCTGCTTG 1638  
DB 1020 TGTAAATTCAGCAGCTTATCCATTTGTCTCAACGCTACCTCAAACTTCAATTTCTCTGC 1079  
QY 1639 CTTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCTTTCAGGAGTGATAAGGACAATGT 1698  
DB 1080 TTTTGTATCAATGCTGTAGAACCAACAGAGGAACTTCTTTCAGGCGGAGAAACAATGT 1139  
QY 1699 GATAGACCATAGAGAGCAAGCAAGAGGATTTAGCAATTCCTTGGGTGCGGTGAACAAGT 1758  
DB 1140 GGTAAAGCAGATAGAAAGACAGTGCGAGAGCTTGGTTCCCTGGGTCTGCACAAGATGT 1199  
QY 1759 TGAGAAGCTCATCAAAACCAAGAGGAATCTCACTTTGTGAGTGTCTGCTCTCA 1812  
DB 1200 TGAGAGGCTATTAAAGAGCAGAGGGAATCTACTTTGTGTGATGCTCAGCCTCA 1253  
  
RESULT 15  
US-10-757-155-3  
; Sequence 3, Application US/10757155  
; Publication No. US20040139503A1  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/757,155  
; FILING DATE: 14-Jan-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/758,652  
; FILING DATE: 11-Jan-2001  
; APPLICATION NUMBER: 60/019,940  
; FILING DATE: JUNE 14, 1996  
; ATTORNEY/AGENT INFORMATION:

```
; NAME: LYNNE M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1320 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-757-155-3

Query Match      20.0%; Score 406.8; DB 8; Length 1320;
Best Local Similarity 62.1%; Pred. No. 4.3e-115;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAACCTTTCTACTT-----CCCGTCAAGCGGTTTAGACCCGCTAGCGGGAACCAAAA 618
Db 90 GAATAACCTTTCTACTTTAGAAGCTCTAACAGCTTCCAAACTCTCTTTGAGAACCAAAA 149
QY 619 CGGTAGATCCGGTCTCTGAGAGGTTTGACCAAGGTCAAGGCAAGTTTCAGBAATCTCA 678
Db 150 CGTTCGCAATTCGTCCTCTCAGAGATTCAACAAACGCTCCCACTTGTGAGAACCTTCG 209
QY 679 GAATACCGTATTGTGAGATCGAGGCCAAACCTTAACACTTCTTGTCTTCCCAAGCACGC 738
Db 210 AGACTACCGATTGTTCAGTTTCAGTCAAAACCCCAACACAATCTTCTCCCAACCATGC 269
QY 739 TGATGTGATAACATCTCTGTTATCCAGCAAGGGCAAGCCACGTCAGCTAGCAATGG 798
Db 270 TGACGGCGATTTCCTCTCTTTCCTTAGCGGAGGCCATATCTTACCTTGTGTAACAA 329
QY 799 CAATAACAGAGAGCTTTAATCTTGACGAGGCCATGCACTCAGATCCCATCCCGGTTT 858
Db 330 CGACGACAGAGACTCTCTACAACTTTCACCTGGCGATGCCAGAGATCCAGCTGGAAC 389
QY 859 CATTCCTTACATCTTGAACCGCCATGACAAACAGAACCTCAGAGTAGCTAAATCTCCAT 918
Db 390 CACTTACTATTGTGTTAACTTCAACCCACACAGATCTCAAAATTAATCAAACTTGCAT 449
QY 919 GCCGTTTAAACACCCGGCCAGTTTGAGGATTTCTCCCGGCGAGCAGCGGAGACCAATC 978
Db 450 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTTATCTAGCACTCAAGCCCAACA 509
QY 979 ATCCTACTTGCAGGCTTCAAGCAGGAATAGTTGGAGGCGCCCTTCAATGCGGAATTCAA 1038
Db 510 GTCTTACTTGAAGGCTTACGCCATTAATTTCTAGAGACCTCTTCCATAGCGAATTCGA 569
QY 1039 TGAGATACGGAGGTTGCTGTTAGAGAGAAATGAGGAGGTGAGCAAGAGAGAGAGGGCA 1098
Db 570 GGAGATAAACACAGGTTTGTGTTGAGAGGAAGAGGAGCAGGACCAAGAG----- 621
QY 1099 GAGCGATGGAGTACTCGGAGTAGTGAGAAATGAGAGGTGATAGTCAAAGTGTCAA 1158
Db 622 -----GGAGTGTCTGTGGAACCTCTCAA 644
QY 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCGTAAATCCGTCTCAAGAAAGGCTCCGAAGA 1218
Db 645 GGAAACAAATTCGGCAACTGAGCAGACGTGCCAAATCTAGTTCAAGGAAACCAATTCCTC 704
QY 1219 AGAGGAGATATCAACCAACCAATCAACTTGAGAGAGGCGAGCCCGATCTTTTAAACAA 1278
Db 705 CGAAGATG-----AACCAATTCACTTGAGAAGCGCAACCCCATCTATTCCAACAA 755
QY 1279 CTTTGGGAGTTATTTGAGGTGAAGCGACAGACAGAAACCCCGAGCTTCAGGACCTGGA 1338
Db 756 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAACCCACAGCTTCGGGACTTGA 812
QY 1339 CATGATGCTCACCTGTGTAGAGATCAAGAGAGGAGCTTTGATGCTCCCACTTCAACTC 1398
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Db 813 TATCTTCCTCAGTTCTGTGGATATCAACGAAGAGAGCTCTTCTTACCAACACTTCAATTC 872
QY 1399 AAAGGCCATGGTTTATCGTCTGTCCTCAACAAAGGAACTGGAACCTTTGAACTCGTGCTGT 1458
Db 873 AAAGGCCATAGTCATATACTAGTAGTATTATGAAGAGATGCAAAACATTGAACCTTGTTCGCAT 932
QY 1459 AAGAAAGAGCAACAAACAGAGGGGACGCGGGAAGAAAGAGGAGGACGAAGACGAAGAAGA 1518
Db 933 TAAAGAAACAAACACAGAGCAGAAAAACAGGAAGAGGAACCTTTG----- 975
QY 1519 GGAGGGAAGTAACACAGAGAGGTGCGTAGGTACACAGAGAGGTTGAAGGAAGGCGATGTT 1578
Db 976 -----GAAAGTGAAAGGTACAGAGCTGAATTTGTCTGAAGACGATGATT 1019
QY 1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCATCTGCTTGG 1638
Db 1020 TGTAAATTCAGCAGCTTATCCATTTGTCTCAACGCTACCTCAAAACCTCAATTTCTCTGC 1079
QY 1639 CTTTCGTTATCAACGCTGAAACAAACCAACAGAAATCTTCTTGCAGGTGATAAGGACAATGT 1698
Db 1080 TTTTGGTATCAATGCTGAGAACCAACCAAGAGAACTTCTTTCGAGGCGAGAAACAAATGT 1139
QY 1699 GATAGACCAGATAGAGAAGCAAGCGAAGGATTTAGCATTTCCCTGGGTGCGGTGAACAAGT 1758
Db 1140 GGTAAAGCAGATAGAAAGACAAAGTCAGAGAGCTTGGCTTCCCTGGGTCTGCACAAGATGT 1199
QY 1759 TGAGAAGCTCATCAAAACCAAGAGGAATCTCACTTTGTGAGTGTCTGCTCTCA 1812
Db 1200 TGAGAGGCTATTAAAGAGCAGAGGGAATCTTACTTTGTGATGCTCAGCTCA 1253
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Search completed: June 24, 2006, 01:56:13

Job time : 2781.65 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 18:21:18 ; Search time 44.2256 Seconds  
(without alignments)  
11014.453 Million cell updates/sec

Title: US-10-728-051-1

Perfect score: 2032

Sequence: 1 aataatcatatattcatc.....cgttgtgctgtttcttc 2032

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /EMC\_Celerra\_SID33/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SID33/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SID33/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SID33/prodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SID33/prodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SID33/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SID33/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SID33/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.6	2.9	1338	6	US-10-953-349-26870 Sequence 26870, A
2	46.6	2.3	1005	6	US-10-449-902-7999 Sequence 7999, Ap
3	43.4	2.1	1295	6	US-10-449-902-20667 Sequence 20667, A
4	42.2	2.1	1420	6	US-10-534-744-1 Sequence 1, Appli
5	42	2.1	726	6	US-10-953-349-34378 Sequence 34378, A
6	41.6	2.0	931	6	US-10-449-902-6550 Sequence 6550, Ap
7	41.4	2.0	1644	6	US-10-953-349-38190 Sequence 38190, A
8	40.8	2.0	3602	6	US-10-449-902-9830 Sequence 9830, Ap
9	40.4	2.0	615	7	US-11-217-529-77435 Sequence 77435, A
10	40.4	2.0	3489	7	US-11-106-014-93 Sequence 93, Appl
11	39.2	1.9	1962	6	US-10-486-020-52 Sequence 52, Appl
12	39.2	1.9	2824	6	US-10-486-020-48 Sequence 48, Appl
13	39.2	1.9	2906	6	US-10-486-020-54 Sequence 54, Appl
14	39.2	1.9	3005	6	US-10-486-020-53 Sequence 53, Appl
15	39.2	1.9	3495	7	US-11-217-529-5994 Sequence 5994, Ap
16	39	1.9	2140	6	US-10-449-902-25837 Sequence 25837, A
17	38.8	1.9	653	6	US-10-449-902-5672 Sequence 5672, Ap
18	38.6	1.9	42999	7	US-11-284-877-17 Sequence 17, Appl
19	38	1.9	151830	6	US-10-519-335-37 Sequence 37, Appl
20	37.6	1.9	1539	6	US-10-953-349-23883 Sequence 23883, A
21	37.6	1.9	2824	7	US-11-293-697-93 Sequence 93, Appl
22	37.4	1.8	735	6	US-10-449-902-10416 Sequence 10416, A
23	37.2	1.8	1045	6	US-10-953-349-26209 Sequence 26209, A
24	37	1.8	547	6	US-10-488-619-2599 Sequence 2599, Ap
25	37	1.8	776	6	US-10-488-619-1733 Sequence 1733, Ap

ALIGNMENTS

RESULT 1

US-10-953-349-26870  
; Sequence 26870, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26870  
; LENGTH: 1338  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; US-10-953-349-26870

Query Match 2.9%; Score 58.6; DB 6; Length 1338;  
Best Local Similarity 47.0%; Pred. No. 2.2e+07;  
Matches 181; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY	569	CCTTTCTACTCCCGTCAAGGGGTTTAGCACCCTAGCGGAACCAAAACGGTAGATC	628	Sequence 13170, A
DB	436	CGGTACGTGTTCCGCCCGCGCAGCTTCCCGCGCATCATCCGGAGCGACACCGGTTTCGTC	495	Sequence 25812, A
QY	629	CGGTCTCTCAGAGTTTTCACCAAGGTCAAGGCAGTTTCAGAAATCTCCAGATCACCGT	688	Sequence 18644, A
DB	496	AAGGCCCTTCCCGCGTTCCAGCAAGTGTCCAGGCTCCTCCGGGGCATCAGGAATACCGT	555	Sequence 9874, Ap
QY	689	ATTGTGCAGATCGAGGCCAAACCTAACACTTGTTCCTCCCAAGCACGCTGATGCTGAT	748	Sequence 8264, Ap
DB	556	GTCCGCATCATGAGGTGAACCCGCCGCGGTTCGTCTCCGGGATCTACGGAGCGAGAC	615	Sequence 22022, A
QY	749	AACATCCTTTTATCCAGCAAGGGCAAGCCCGTAGCCGATGCAAAATGGCAATAACAGA	808	Sequence 23827, A
DB	616	GGCGTCGGTACGTCTCAAGCGGAGGGGTGCTGACGGTGTATCAGAAACGGCGAGAAG	675	Sequence 17345, A
QY	809	AAGAGCTTTTAACTTTCAGCAGGGGCGCATGCACTCAGAAATCCATCCCGTTTCATTCTC	868	Sequence 5628, Ap
DB	676	CGGTCTCTACACCGTTCAGGAAGCGATGTGATCGTGGCCCGCGGGTCCCATCATGCAC	735	Sequence 17797, A
QY	869	ATCTTCAACCGGCATGACAACAGAACCTCAGAGTAGTGTAAATCTCCATGCCCGTTAAC	928	Sequence 1913, Ap
DB	736	CTGGCCAAACACGACCGCCGGAGGAAGCTGTGTCATCCCAAGATTTCTCCACACCATCTCC	795	Sequence 20711, A
QY	929	ACACCGGCCAGTTTGAGGATTCTT	953	Sequence 1916, Ap

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Db 796 GTCCCGGCAAGTTCAGTATTCT 820

RESULT 2
US-10-449-902-7999
; Sequence 7999, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7999
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK105347
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-7999

Query Match 2.3%; Score 46.6; DB 6; Length 1005;
Best Local Similarity 46.0%; Pred. No. 0.00068;
Matches 157; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 607 CGGGRACCAACGCTAGGATCGGCTCTGCAGAGGTTTGACCAAGGTCAGGCGATT 666
Db 396 CGCAGCGACCAAGGCTCGCTAGGCTCTCCCGCGCTTCCACAGGCTCCAGCTCCT 455
QY 667 TCAGAAATCTCCAGAAATCACCAGTATTGTGCAGATCGAGGGCCAAACCTTAACACTCTTGTCT 726
Db 456 GCGCGGCATCAAGAACTACCGCTCGGGTGTCTCGAGGGAACCCGCGCTCTTCTCAT 515
QY 727 TCCCAAGCAGCTGATGCTGATTAACATCTTGTATTCCAGCAAGGGCAAGCCAGTGC 786
Db 516 GCGGACCCACACGAGCGGCACTGCTACTGCTCGCCCAAGGCGAGGTGGTGGC 575
QY 787 CGTAGCAATGCGCAATAACAGAAAGAGCTTTAATCTTGACGGGCGCATGCACTCAGAAT 846
Db 576 GATCATCGAAGCGGAGAGTGGTGTGTAAGCCATCCGCAAGGCGACGTCTTCTGGC 635
QY 847 CCATCCGGTTTCATTTCCTACATCTTGAACCCGCCATGACCAACAGAACTCAGAGTAGC 906
Db 636 GCGCGGGGACGATCAATTAATCTTGGCAACACCGAGCGGCGGAGGAAGTGTCTTAC 695
QY 907 TAAATCTCATCCGCTTAAACACACCCGCGCAGTTTGGG 947
Db 696 CAAGATTCTCATACCATCTCTCCGCTCCGTCGCGCAGATCCAGG 736

RESULT 3
US-10-449-902-20667
; Sequence 20667, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902

Db 796 GTCCCGGCAAGTTCAGTATTCT 820

Query Match 2.1%; Score 43.4; DB 6; Length 1295;
Best Local Similarity 53.9%; Pred. No. 0.0071;
Matches 89; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 373 AAGAGAGGAAGAGCGCGATGGGACCACTGGACCGGAGGCGGTGAAGAGAAGAAGA 432
Db 543 AAGAAAAGAAAGAAAGACAAAGAGTGATAGAGGAAGAGGCAAGAAAAAGGATG 602
QY 433 CTGGAGACAAACCAAGAGAGATTGGAGGCGCAACAGTCATCAGCAGCCAGGAAATAAG 492
Db 603 ATGAGGAGGAAGGTAAAGAAAGAAAGAAAGAAAGAAAGATGCGGATGAGAAAGAAG 662
QY 493 GCCCGAAGGAAGAGAGGAGAAACAAGAGTGGGGACACCCAGGTAG 537
Db 663 GCAAGAAAGAGAAAGAAAGAAAGAAAGCAAGGACGGTGTATGAGGAGGAAG 707

RESULT 4
US-10-534-744-1
; Sequence 1, Application US/10534744
; Publication No. US2006012375A1
; GENERAL INFORMATION:
; APPLICANT: University of Saskatchewan Technologies Inc.
; TITLE OF INVENTION: PLANT STRESS TOLERANCE GENES, AND USES THEREFOR
; FILE REFERENCE: 47968-PT
; CURRENT APPLICATION NUMBER: US/10/534,744
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 60/426,012
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1420
; TYPE: DNA
; ORGANISM: Bromus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1212)..(1212)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (77)..(1231)
; OTHER INFORMATION:
US-10-534-744-1

Query Match 2.1%; Score 42.2; DB 6; Length 1420;
Best Local Similarity 50.5%; Pred. No. 0.017;
Matches 101; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 329 GCGCGCCAAACCGGAGACTACGATGATGACCCGCTCAACCCCGAAGAGAGAGGAGGC 388
Db 1030 GGACGCCACGTTGGAGAAGACCGAGTCCGCGAAGGACCGCTTGGAGACGCGGAGGC 1089
QY 389 CGATGGGGACCACTGGACCGGAGGCGGTGAAGAGAGAGAGACTGGAGACACCAAGA 448
Db 1090 GCCAAGGGCAAGGCTTAACGAGGGGTACGAGAAGGTGAAGGAGAGAGGACCGGACCAAGGA 1149
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Accession	Gene	Strain	Position	Sequence	Length
Qy	449	GAAGATTGGAGCCACCAAGT	CATCAGCAGCCGGA	AAATAGCCCGGAAGAA	508
Db	1150	AAAGCTCGCGAGGTGAAGG	ACAAGTCAACCGGCG	AGCATCCGACGGCAAGAA	1209
Qy	509	GGAGAACAAAGAGTGGG	GAAC		528
Db	1210	GCNCCGCAATGGCGAC	AGC		1229

## RESULT 5

US-10-953-349-34378  
; Sequence 34378, Application US/10953349  
; Publication No. US20060107345A1  
GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 34378  
; LENGTH: 726  
; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: {234}..(234)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: {281}..(281)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-953-349-34378

### Query Match

Query Match	2.1%;	Score 42;	DB 6;	Length 726;
Best Local Similarity	49.1%;	Pred. No. 0.013;		
Matches 111;	Conservative 0;	Mismatches 115;	Indels 0;	Gaps 0;
309	CTCCAGGAGCGGACAGTGGCGGCCCAACCGGAGACTACGATGATGATGACCGCCGTCAAC	368		
344	CTCCATATGGGGCGCACCAAGAAATGAAGGAGGAGGACCACAGAAGGCCGAGGAG	403		
369	CCCGAAGAGAGGAAGAGCGCCGATGGGGACCAAGTGGACCCAGGAGGCGGTGAAGAGAAG	428		
404	CACCACAAGAAAGGAGGGGGGAGCACCACAAGAAGGACCGCGGGGAGCACAGAAGAGGC	463		
429	AAGACTGGAGACAACCAAGAGAAGATTGGAGGCGCACCAAGTCATCAGCAGCCACCGAAAA	488		
464	ATCTGTGAGAGATCAAGACAAGATCACCGCGGAGCAGCGGCAAGTTCGGGCGACCAC	523		
489	TAAGCCCCGAAGAGGAAGGAGACAAGAGTGGGGNAACACCCAGG	534		
524	AAGGAAAAAGAGGACAAGAAAAAGAAAGCAAGCAGCGAGGGGCCACG	569		

## RESULT 6

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US-10-449-902-6550
; Sequence 6550, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y4-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-363870

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; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent ver. 2.1
; SEQ ID NO 6550
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK063700
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-6550

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## RESULT 7

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US-10-953-349-38190
; Sequence 38190, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38190
; LENGTH: 1644
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38190

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	Query Match	2.0%;	Score 41.4;	DB 6;	Length 1644;
	Best Local Similarity	46.8%;	Pred. No. 0.033;		
	Matches 166;	Conservative	0;	Mismatches 186;	Indels 3; Gaps 1;
Qy	675	TCCAGAAATCACCGTATTGTGCAGATCAGAGCCAAAACCTAACTACTCTGTGTTCTTCCCAAGC	733		
Db	256	TCGGCAACTACCGGTCCGAGCTGGAAACCGCGCGCGACGTTCTCGAGCCAGCC	315		
Qy	735	ACGCTGATGCTGATAACATCTCTTGTATTACAGCAAGGGCAAGCCACCGTGACCGTAGCAA	794		
Db	316	ACTACAGCGCGACGAGGTGATGTTCTGTGAAGAAAGCGAGGGCGTCATCGTGTGCTCC	375		
Qy	795	ATGCGAATACAGAAAGAGCTTTAACTTTGACAGAGGCCATGCACTCAGAAATCCCATCCG	854		
Db	376	CGCGCGGAGAGGGGAGTCGTTCTGCGTCAGGAGGGCGACGTCATGGTCATCCCCCGG	435		
Qy	855	GTTTTCATTTTCCCTACATCTTGAACCGGCATGACAAACAGAAACCTCAGAGTAGCTAAAAATCT	914		

Db 436 GCGCCGTCGTGTAAGTCTCGGCAACACGACCAAGTCGGAATGTTCCGGCTGTCATGCTCC 495  
QY 915 CCATGCC---CGTTAAACACACCCGCGCAGTTTTCAGGATTTCTTCCCGGCGAGCAGCCGAG 971  
Db 496 TCAGCCCGTCGTCTCCAGCTCTGGACGCTTCGAGGAGTCTTCCCGCCTCGGAGGCGAGA 555  
QY 972 ACCAATCATCTACTTTCGAGGGCTTCAGCAAGGAATAGTTGGAGCGCGCTTCAA 1026  
Db 556 GCGCCGAGTCTTCTCTCAGCGTCTTCAGCGACGACGCTTATCCAGGCGGTCTGTTCAA 610

## RESULT 8

US-10-449-902-9830  
; Sequence 9830, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9830  
; LENGTH: 3602  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK107178  
; DATABASE ENTRY DATE: 2002-08-28  
US-10-449-902-9830

Query Match 2.0%; Score 40.8; DB 6; Length 3602;  
Best Local Similarity 48.3%; Pred. No. 0.081;  
Matches 114; Conservative 0; Mismatches 122; Indels 0; Gaps 0;  
QY 269 GATCTCTGAGGACACACTGCGACCAACCAACAGTTCCTCCAGGGAGCGGACACGT 328  
Db 280 GAGGCTGGCGCCCAAGCGGCGGAAGCGCTCCATCTGTCGAGCTCTTCGCGCGCTGCCAA 339  
QY 329 GCGCGCCCAACCCGCGAGACTACGATGATGACCGCGTCAACCCCGAAGAGAGGAGGCG 388  
Db 340 GGTCTGTCGCGCCGCGCAGCGAGGGGCTCGGAGGGGAGCGTGTTCAGGAGGAGCTCGA 399  
QY 389 CGATGGGACCACTGCGACCGAGGCGGTGAAGAGAGAAGAGACTGGAGACACCAAGA 448  
Db 400 CRAAGGGGACCCCGCGGTGAGGCGGCGAAGAGAGGGTTTCAGGAAGCA 459  
QY 449 GAAGATTGAGGCGACCAAGTATCAGCAGCCACGGAATAAGGCCCGCAAGAG 504  
Db 460 GAAGTTCTAGTTGAGATCGGCTCAGAAAAAAGGGAATAATAGCAAGACAAAAG 515

## RESULT 9

US-11-217-529-77435/c  
; Sequence 77435, Application US/11217529  
; Publication No. US2006099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77435  
; LENGTH: 615  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (152)..(192)  
; OTHER INFORMATION: a, c, g, t, unknown, or other  
US-11-217-529-77435  
Query Match 2.0%; Score 40.4; DB 7; Length 615;  
Best Local Similarity 53.1%; Pred. No. 0.035;  
Matches 86; Conservative 0; Mismatches 76; Indels 0; Gaps 0;  
QY 373 AAGAGAGGAAGGAGCGCGATGGGACCGACCTGGACCGGAGCGGTGAAGAGAGAAGA 432  
Db 354 AAAAGAAGAAGGAAGAAGAAGGAAGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 295  
QY 433 CTGGACACCAACNAGAGAGATTGGAGGCGCACCAGTCTCAGCAGCCCGGAAAATAAG 492  
Db 294 AAGATGAAGAAAATAAAGAAAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAA 235  
QY 493 GCGCGAAGGAAGGAAGGAAGCAAGAGTGGGGAACACCCAGG 534  
Db 234 AAAGAAGCAGGAGGAGGAACNACNAGAAATGAAGATGAAG 193

## RESULT 10

US-11-106-014-93  
; Sequence 93, Application US/11106014  
; Publication No. US2006008846A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, Michele  
; APPLICANT: Chiau, Dah Sharim  
; APPLICANT: Latres, Esther  
; APPLICANT: Srivastava, Promod  
; APPLICANT: Chandawarkar, Rajiv  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT  
; FILE REFERENCE: 5914-106-999  
; CURRENT APPLICATION NUMBER: US/11/106,014  
; CURRENT FILING DATE: 2005-04-13  
; PRIOR APPLICATION NUMBER: 10/632,150  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: 10/042,417  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/385,219  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1997-03-15  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 93  
; LENGTH: 3489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human Fbx1 11 protein (NP\_036440.1)  
US-11-106-014-93  
Query Match 2.0%; Score 40.4; DB 7; Length 3489;  
Best Local Similarity 65.6%; Pred. No. 0.1;











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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 4184.37 Seconds  
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Title: US-10-728-051-2  
Perfect score: 717  
Sequence: 1 gctcaccatactagttagcccc.....taaaaagatcatgttttgtt 717

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	717	100.0	717	2	AR257468 Sequence
2	717	100.0	717	2	AR629099 Sequence
3	717	100.0	717	2	AR629100 Sequence
4	717	100.0	717	4	ARQALLII
5	713.8	99.6	743	2	AR257462 Sequence
6	705	98.3	810	4	AY722689
7	644.6	89.9	842	4	AY581853
8	598.8	83.5	678	4	AY581854
9	474	66.1	474	2	BD107899
10	472.4	65.9	474	2	AX155333
11	470.8	65.7	474	2	BD172108
12	462	64.4	472	4	AY007229
13	462	64.4	682	2	AR716327
14	462	64.4	682	2	AX148740
15	462	64.4	1162	2	AR716326 Sequence
16	462	64.4	1162	2	AX148738
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18	415.2	57.9	510	4	AY117434

19	404.8	56.5	502	4	AF366560	Arachis h
20	222	31.0	716	4	AY849314	Arachis h
21	220.8	30.8	634	4	AF366561	Arachis h
22	202.2	28.2	742	4	AY722690	Arachis h
23	197.8	27.6	627	4	AF092846	Arachis h
24	181.6	25.3	618	4	AY848699	Arachis h
25	162.6	22.7	375	4	AY871100	Arachis h
26	114.8	16.0	712	4	AF091737	Arachis h
27	108	15.1	581	4	AY722691	Arachis h
28	82	11.4	687	4	AM160790	Lupinus a
29	80	11.4	693	4	AM156845	Lupinus a
30	80	11.2	80	2	AR716331	Sequence
31	80	11.2	80	2	AX148744	Sequence
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33	65.6	9.1	777	2	AR066463	Sequence
34	65.6	9.1	777	4	GMU71195	U71195 Glycine max
35	64	8.9	777	2	AR066464	Sequence
36	63.4	8.8	770	2	AR107077	Sequence
37	63.4	8.8	770	2	BD075791	BD075791 Lunacin p
38	63.4	8.8	770	2	AR304633	Sequence
39	63.4	8.8	770	4	AF005030	AF005030 Glycine m
40	62	8.6	62	2	AR716332	Sequence
41	62	8.6	62	2	AX148745	Sequence
42	59.2	8.3	477	2	AX839974	Sequence
43	59.2	8.3	477	2	AX840499	Sequence
44	58.8	8.2	7218	2	I66494	166494 Sequence 14
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ALIGNMENTS

RESULT 1  
AR257468  
LOCUS AR257468 717 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 20 from patent US 6486311.  
ACCESSION AR257468  
VERSION AR257468.1 GI:27307481  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 717)  
AUTHORS Burks,A.W. Jr., Stanley,J.S., Cockrell,G., King,N.E., Sampson,H.A., Helm,R.M. and Bannon,G.A.  
TITLE Peanut allergens and methods  
JOURNAL Patent: US 6486311-A, 20 26-NOV-2002;  
NY Mc. Sinai School of Medicine and University of Arkansas; New York,  
NY  
FEATURES  
source Location/Qualifiers  
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/organism="unknown"  
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Query Match	100.0%;	Score 717;	DB 2;	Length 717;
Best Local Similarity	100.0%;	Pred. No. 9e-202;		
Matches 717;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCCGCCGATCTCGGAGGCA	60	
Db	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCCGCCGATCTCGGAGGCA	60	
QY	61	GCAGTGGGAACCTCCAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGCGCAACTGAG	120	
Db	61	GCAGTGGGAACCTCCAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGCGCAACTGAG	120	
QY	121	GCCTCGGAGCAACATCTTCATGCAGAAGATCCAACTGACGAGGATTCATATGAACGGGA	180	
Db	121	GCCTCGGAGCAACATCTTCATGCAGAAGATCCAACTGACGAGGATTCATATGAACGGGA	180	
QY	181	CCGCTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGAGCGCTGG	240	

Db 181 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 240  
Qy 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTGTGAGAACCAACAAAG 300  
Db 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTGTGAGAACCAACAAAG 300  
Qy 301 GTGCATGTGGAGGCATTGCAACAGATCATGGAGAACCAAGAGCGATAGGTTGCAGGGGAG 360  
Db 301 GTGCATGTGGAGGCATTGCAACAGATCATGGAGAACCAAGAGCGATAGGTTGCAGGGGAG 360  
Qy 361 GCAACAGGAGCAACAGTTCAGAGGAGGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
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Qy 421 GGCAACACAGCGTTGGCAGCTTGAGACGTCGAAAGTGGCGGCAGAGACAGATACCTAAACACC 480  
Db 421 GGCAACACAGCGTTGGCAGCTTGAGACGTCGAAAGTGGCGGCAGAGACAGATACCTAAACACC 480  
Qy 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 540  
Db 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 540  
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Db 541 GTTATGTTTGTAGTTTGGTAATAAAGATCATCACTATATGAATGTTGATCGTGTTA 600  
Qy 601 ACTAAGCAAGCTTAGGTTATATGAGCACCTTTAGAGTGCTTTTATGGCGTGTCTATGT 660  
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Qy 661 TTTGTTGCTCAGAGTTGAACCATCTTGAATAATAAAGATCATGTTTTGTT 717  
Db 661 TTTGTTGCTCAGAGTTGAACCATCTTGAATAATAAAGATCATGTTTTGTT 717

RESULT 2  
AR629099 LOCUS 717 bp mRNA linear PAT 14-FEB-2005  
DEFINITION Sequence 6 from patent US 6835824.  
ACCESSION AR629099  
VERSION AR629099.1 GI:59756575  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 717)  
AUTHORS Burks,A.W. Jr., Stanley,J.S., Bannon,G.A., Cockrell,G. and Helm,R.M.  
TITLE Peanut allergens and methods  
JOURNAL Patent: US 6835824-A 6 28-DEC-2004;  
LOCATION/Qualifiers University of Arkansas; Little Rock, AR  
FEATURES  
source 1. .717  
/organism="unknown"  
/mol\_type="mRNA"

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Query Match 100.0%; Score 717; DB 2; Length 717;  
Best Local Similarity 100.0%; Pred. No. 9e-202;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCGCTGCCCGCCACGCACTCGGAGGCA 60  
Db 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCGCTGCCCGCCACGCACTCGGAGGCA 60  
Qy 61 GCAGTGGGAATCTCAAGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120  
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Qy 121 GCCTTCGAGCAACATCTCATGCAAGAGATCCAACGTTGACGAGATTCATATGAACGGGA 180  
Db 121 GCCTTCGAGCAACATCTCATGCAAGAGATCCAACGTTGACGAGATTCATATGAACGGGA 180

Qy 181 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 240  
Db 181 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 240  
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Qy 361 GCAACAGGAGCAACAGTTCAGAGGAGGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
Db 361 GCAACAGGAGCAACAGTTCAGAGGAGGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
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Db 421 GGCAACACAGCGTTGGCAGCTTGAGACGTCGAAAGTGGCGGCAGAGACAGATACCTAAACACC 480  
Qy 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 540  
Db 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 540  
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Qy 661 TTTGTTGCTCAGAGTTGAACCATCTTGAATAATAAAGATCATGTTTTGTT 717  
Db 661 TTTGTTGCTCAGAGTTGAACCATCTTGAATAATAAAGATCATGTTTTGTT 717

RESULT 3  
AR629100 LOCUS 717 bp mRNA linear PAT 14-FEB-2005  
DEFINITION Sequence 9 from patent US 6835824.  
ACCESSION AR629100  
VERSION AR629100.1 GI:59756577  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 717)  
AUTHORS Burks,A.W. Jr., Stanley,J.S., Bannon,G.A., Cockrell,G. and Helm,R.M.  
TITLE Peanut allergens and methods  
JOURNAL Patent: US 6835824-A 9 28-DEC-2004;  
LOCATION/Qualifiers University of Arkansas; Little Rock, AR  
FEATURES  
source 1. .717  
/organism="unknown"  
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ORIGIN  
Query Match 100.0%; Score 717; DB 2; Length 717;  
Best Local Similarity 100.0%; Pred. No. 9e-202;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCGCTGCCCGCCACGCACTCGGAGGCA 60  
Db 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCGCTGCCCGCCACGCACTCGGAGGCA 60  
Qy 61 GCAGTGGGAATCTCAAGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120  
Db 61 GCAGTGGGAATCTCAAGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120  
Qy 121 GCCTTCGAGCAACATCTCATGCAAGAGATCCAACGTTGACGAGATTCATATGAACGGGA 180  
Db 121 GCCTTCGAGCAACATCTCATGCAAGAGATCCAACGTTGACGAGATTCATATGAACGGGA 180

Db 121 GCCCTGCGAGCAACATCTCATGCAAGAGATCCAACTGACGAGGATTCATATGAACGGGA 180  
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Db 181 CCGGTACAGCCCTAGTCAGGATCGTACAGCCCTAGTCCTATATGATCGGAGAGCGCTGG 240  
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Db 241 ATCCTCTCAGCACCAAGAGAGGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300  
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QY 421 GGCAACCAAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCGAGACAGATACCTAATG 540  
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QY 541 GTTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 717  
Db 541 GTTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 717

RESULT 4  
ARQALLII  
LOCUS Arachis hypogaea (clone Ara h II p38) allergen II gene, polyA  
DEFINITION signal.

ARQALLII 717 bp DNA linear PLN 28-MAR-1996  
L77197  
VERSION L77197.1 GI:1236995  
KEYWORDS allergen; conglutin; seed storage protein.  
SOURCE Arachis hypogaea (peanut)  
ORGANISM Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.

REFERENCE 1 (bases 1 to 717)  
AUTHORS Stanley,J.S.  
TITLE The major peanut allergen Ara h II is a seed storage protein with  
JOURNAL multiple IgE-binding epitopes  
COMMENT Unpublished (1996)  
Original source text: Arachis hypogaea (strain Florunner) (clone:  
Ara h II p38) DNA.

FEATURES  
source  
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Location/Qualifiers

polyA\_signal  
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ORIGIN  
100.0%; Score 717; DB 4; Length 717;  
Best Local Similarity 100.0%; Pred. No. 9e-202;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTGCGAGCA 60  
Db 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTGCGAGCA 60  
QY 61 GCAGTGGGAACTCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGGAACTCTGAG 120  
Db 61 GCAGTGGGAACTCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGGAACTCTGAG 120  
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QY 481 TATCTCAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 600  
Db 481 TATCTCAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 600  
QY 541 GTTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 660  
Db 541 GTTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 660  
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATGTTTTGTT 717  
Db 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATGTTTTGTT 717

RESULT 5  
AR257462

LOCUS AR257462 743 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 1 from patent US 6486311.  
ACCESSION AR257462  
VERSION AR257462.1 GI:27307475  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 743)  
AUTHORS Burks,A.W. Jr., Stanley,J.S., Cockrell,G., King,N.E., Sampson,H.A.,  
Helm,R.M. and Bannon,G.A.  
TITLE Peanut allergens and methods  
JOURNAL Patent: US 6486311-A 1 26-NOV-2002;  
Mc. Sinai School of Medicine and University of Arkansas; New York,  
NY

FEATURES  
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Location/Qualifiers  
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ORIGIN

Query Match	99.6%;	Score 713.8;	DB 2;	Length 743;	
Best Local Similarity	99.7%;	Pred. No. 8.1e-201;			
Matches 715;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCACGCGCATCTCGAGGCA	60		
Db	6	GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCACGCGCATCTCGAGGCA	65		
QY	61	GCAGTGGGAACCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTTGAG	120		
Db	66	GCAGTGGGAACCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTTGAG	125		
QY	121	GCCTCGAGCAACATCTCATGCAGAGATCCACGCTGACGAGGATTCATATGAACGGGA	180		
Db	126	GCCTCGAGCAACATCTCATGCAGAGATCCACGCTGACGAGGATTCATATGAACGGGA	185		
QY	181	CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG	240		
Db	186	CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG	245		
QY	241	ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAAACCAAG	300		
Db	246	ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAAACCAAG	305		
QY	301	GTGCATGTGCGAGGCAATTGCAACAGATCATGGAGAACGAGCGATAGTTGCAGGGGAG	360		
Db	306	GTGCATGTGCGAGGCAATTGCAACAGATCATGGAGAACGAGCGATAGTTGCAGGGGAG	365		
QY	361	GCAACAGGAGCAACAGTTCGAAGGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCTTAG	420		
Db	366	GCAACAGGAGCAACAGTTCGAAGGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCTTAG	425		
QY	421	GGCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCGAGACAGATACATAACACC	480		
Db	426	GGCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCGAGACAGATACATAACACC	485		
QY	481	TATCTCAAAAAAGAAAAGAAAAGAAAAGAAAAGTCTTATATATAGCTATTATCTATG	540		
Db	486	TATCTCAAAAAAGAAAAGAAAAGAAAAGAAAAGTCTTATATATAGCTATTATCTATG	545		
QY	541	GTTATGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA	600		
Db	546	GTTATGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA	605		
QY	601	ACTAAGCAAGCTTAGTTATATGAGCACTTTAGAGTGCTTTATGGGCTGCTATGT	660		
Db	606	ACTAAGCAAGCTTAGTTATATGAGCACTTTAGAGTGCTTTATGGGCTGCTATGT	665		
QY	661	TTTGTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT	717		
Db	666	TTTGTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT	722		
RESULT 6					
AY722689					
Arachis hypogaea 2S protein 1 mRNA, partial cds.					
AY722689					
AY722689.1 GI:52001226					
Arachis hypogaea (peanut)					
ORGANISM					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;					
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;					
Aeschynomeneae; Arachis.					
1 (bases 1 to 810)					
Van, Y. S., Lin, X. D., Zhang, Y. S., Wang, L., Wu, K. and Huang, S. Z.					
Isolation of peanut genes encoding arachins and conglutins by					
expressed sequence tags					
Plant Sci. 169 (2), 439-445 (2005)					
2 (bases 1 to 810)					
Van, Y., Wang, L. and Huang, S.					
TITLE					
CDNA clone of peanut seed storage protein gene					
Unpublished					
3 (bases 1 to 810)					
Yan, Y., Wang, L. and Huang, S.					
Direct Submission					
Submitted (30-JUL-2004) Department of Biology and Biotechnology,					
Sun Yat-sen University, Guangzhou, Guangdong 510275, China					
FEATURES					
source					
1..810					
/organism="Arachis hypogaea"					
/mol type="mRNA"					
/db xref="taxon:3818"					
<1..542					
/notes="seed storage protein"					
/codon_start=3					
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/protein_id="AAU21494.1"					
/db xref="GI:52001227"					
/translation="GRGKHHTLPNTHSIITTTTMAKLTLVALALFLAAHASARQW					
ELQDRRCOSQLERANLRFCEOHLMKIORDEDSYERDPYSQDPSYSPYDRRGAG					
SSOQBRCCNELNEFENNORCMCEALQQIMENQSDRLQGRQEQFQFRELRNLPQQCG					
LRAPQRCDLDVESGGRDRY"					
ORIGIN					
Query Match 98.3%; Score 705; DB 4; Length 810;					
Best Local Similarity 99.9%; Pred. No. 3.4e-198;					
Matches 716; Conservative 0; Mismatches 0; Indels 1; Gaps 1;					
QY	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCACGCGCATCTCGAGGCA	60		
Db	68	GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCACGCGCATCTCGAGGCA	127		
QY	61	GCAGTGGGAACCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAG	120		
Db	128	GCAGTGGGAACCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAG	187		
QY	121	GCCTCGAGCAACATCTCATGCAGAAAGATCCAACTGACGAGGATTCATATGAACGGGA	180		
Db	188	GCCTCGAGCAACATCTCATGCAGAAAGATCCAACTGACGAGGATTCATATGAACGGGA	247		
QY	181	CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG	240		
Db	248	CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG	307		
QY	241	ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAAACCAACAG	300		
Db	308	ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAAACCAACAG	367		
QY	301	GTGCATGTGCGAGGCAATTGCAACAGATCATGGAGAACGAGCGATAGTTGCAGGGGAG	360		
Db	368	GTGCATGTGCGAGGCAATTGCAACAGATCATGGAGAACGAGCGATAGTTGCAGGGGAG	427		
QY	361	GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACTTGCCTCAACAGTGGCGCTTAG	420		
Db	428	GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACTTGCCTCAACAGTGGCGCTTAG	487		
QY	421	GGCACCAAGCGTTGCGACTTGGACCTCGAAAGTGGCGGCGAGACAGATACATAACACC	480		
Db	488	GGCACCAAGCGTTGCGACTTGGACCTCGAAAGTGGCGGCGAGACAGATACATAACACC	547		
QY	481	TATCTCAAAAAAGAAAAGAAAAGAAAAGTCTTATATATAGCTATTATCTATG	540		
Db	548	TATCTCAAAAAAGAAAAGAAAAGAAAAGTCTTATATATAGCTATTATCTATG	607		
QY	541	GTTATGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA	600		
Db	608	GTTATG-TTATGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA	666		
QY	601	ACTAAGCAAGCTTAGTTATATGAGCACTTTAGAGTGCTTTATGGGCTGCTCTATGT	660		
Db	667	ACTAAGCAAGCTTAGTTATATGAGCACTTTAGAGTGCTTTATGGGCTGCTCTATGT	726		
QY	661	TTTGTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT	717		



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727 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAAGATCATGTTTGT 783

RESULT 7
AY581853
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 842)
Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.Z.
Isolation of peanut genes encoding arachins and conglutins by
expressed sequence tags
2 (bases 1 to 842)
Plant Sci. 169 (2), 439-445 (2005)
cDNA clone of peanut seed storage protein gene
Yan, Y., Wang, L. and Huang, S.
Unpublished
3 (bases 1 to 842)
Yan, Y., Wang, L., Liao, B., Li, H., Lin, X. and Huang, S.
Direct Submission
Submitted (01-MAR-2004) Department of Biology and Biotechnology,
School of Life Science, Sun Yat-sen University, Guangzhou,
Guangdong 510275, China
Location/Qualifiers
1..842
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/mol_type="mRNA"
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/db_xref="taxon:3818"
<1..564
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/protein_id="AA00598.1"
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RNLPQCGLRAPQRCDLVESGGDRY"

CDS
Query Match 89.98; Score 644.6; DB 4; Length 842;
Best Local Similarity 93.98; Pred. No. 3.3e-180;
Matches 707; Conservative 0; Mismatches 9; Indels 37; Gaps 2;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGTCGCCACGCACTCTCGAGGCA 60
|||||
DB 54 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGTCGCCACGCACTCTCGAGGCA 113
|||||
QY 61 GCAGTGGGAACCTCAAGGACAGAAAGATCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120
|||||
DB 114 GCAGTGGGAACCTCAAGGACAGAAAGATCCAGAGCCAGCTCGAGAGGCGCAACCTTAG 173
|||||
QY 121 GCCTCGGAGCACATCTCATGAGAGATCCACGCTGAGGAGATTCATATCAACGGGA 180
|||||
DB 174 GCCTCGGAGCACATCTCATGAGAGAAATCCACGCTGAGGAGATTCATATGACGGGA 233
|||||
QY 181 CCGGTACAGCCCTAGTCAG-----GATCC 204
|||||
DB 234 CCGGTACAGCCCTAGTCAGGATCGGTACAGCCCTAGTCAGAGCCCGGACAGCGTGATCC 293
|||||
QY 205 GTACAGCCCTAGTCATATGATCGGAGAGCGGTGGATCTCTCAGACCAAGAGAGGTG 264
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DB 294 GTACAGCCCTAGTCATATGATCGGAGAGCGGTGGATCTCTCAGACCAAGAGAGGTG 353
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QY 265 TTGCAATGAGCTGAACGAGTTTGAGAAACAACCAAGGTGCATGTCGAGGCAATTCGAACA 324
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DB 354 TTGCAATGAGCTGAACGAGTTTGAGAAACAACCAAGGTGCATGTCGAGGCAATTCGAACA 413
|||||
QY 325 GATCATGGAGAAACAGAGCGCATAGTTGCAGGGGAGGCAACAGGAGCAACAGTTCAAGAG 384
|||||
DB 414 GATAATGGAGAAACAGAGCGCATAGTTGCAGGGGAGGCAACAGGAGCAACAGTTCAAGAG 473
|||||
QY 385 GGAGCTCAGGAACCTTCCTCAACAGTGCCTTTAGGGACACACAGCGTTTGCAGCTTGA 444
|||||
DB 474 GGAGCTCAGGAACCTTCCTCAACAGTGCCTTCAGGGCACCACAGCGTTTGCAGCTTGA 533
|||||
QY 445 CGTCGAAAGTGGCGGAGACAGATACATAACACACCTATCTCAAAAAAGAAAAAGAAAG 504
|||||
DB 534 AGTCGAAAGTGGCGGAGACAGATACATAACACACCTATCTCAAAAAAGAAAAAGAAAG 593
|||||
QY 505 AAAAGAAAATAGCTTATATATATAAGCTATTATCTATGGTTATGTTTGTAGTTTGTGTAAT 564
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DB 594 AAAAGAAAATAGCTTATATATAAGCTATTATCTATGGTTATGTTTGTAGTTTGTGTAAT 652
|||||
QY 565 AAAGATCATCATATATGAATGTTGATCGTCTTAACGCAAGCTTAGGTTATATG 624
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DB 653 AAAGATCATCATATATGAATGTTGATCGTCTTAACGCAAGCTTAGGTTATATG 712
|||||
QY 625 AGCACCTTTAGAGTGTCTTTATGGCGTTGTCTATGTTTGTCTGCAGAGTTGTAACCA 684
|||||
DB 713 AGCACCTTTAGAGTGTCTTTATGGCGTTGTCTATGTTTGTCTGCAGAGTTGTAACCA 772
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QY 685 TCTTGAATAATAATAAAAAAGATCATGTTTGT 717
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DB 773 TCTTGAATAATAATAAAAAAGATCATGTTTGT 805
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RESULT 8
AY581854
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 678)
Yan, Y., Wang, L., Liao, B., Li, H., Lin, X. and Huang, S.
cDNA cloning of peanut seed storage protein
Unpublished
2 (bases 1 to 678)
Yan, Y., Wang, L., Liao, B., Li, H., Lin, X. and Huang, S.
Direct Submission
Submitted (01-MAR-2004) Department of Biology and Biotechnology,
School of Life Science, Sun Yat-sen University, Guangzhou,
Guangdong 510275, China
Location/Qualifiers
1..678
/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="SanYou523"
/db_xref="taxon:3818"
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/codon_start=1
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/protein_id="AA00599.1"
/db_xref="GI:46560482"
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CDS
FEATURES
source
ORIGIN
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Best Local Similarity 99.8%; Pred. No. 5.5e-129;
Matches 473; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2  CTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACGCAATCTGGAGGCAG 61
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DB  1  CTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACGCAATCTGGAGGCAG 60

QY  62  CAGTGGGAATCCCAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCCTGAGG 121
    |||
DB  61  CAGTGGGAATCCCAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCCTGAGG 120

QY  122  CCCTGCCAGCAACATCTCATGCAGAAATCCAACTGACGAGGATTCATATGAACGGGAC 181
    |||
DB  121  CCCTGCCAGCAACATCTCATGCAGAAATCCAACTGACGAGGATTCATATGAACGGGAC 180

QY  182  CCGTACAGCCCTAGTCAGATCCGTA CAGCCCTAGTCCATATGATCGAGAGGCGCTTGA 241
    |||
DB  181  CCGTACAGCCCTAGTCAGATCCGTA CAGCCCTAGTCCATATGATCGAGAGGCGCTTGA 240

QY  242  TCCTCTCAGCACCAGAGAGGTGTGCAATGAGCTGAACGATTTGAGAACCAACCAAGG 301
    |||
DB  241  TCCTCTCAGCACCAGAGAGGTGTGCAATGAGCTGAACGATTTGAGAACCAACCAAGG 300

QY  302  TGCATGTGCGAGGATTCAGAGGAGCTCAGGAAC CAGAGCGATAGTTGCGAGGGGAGG 361
    |||
DB  301  TGCATGTGCGAGGATTCAGAGGAGCTCAGGAAC CAGAGCGATAGTTGCGAGGGGAGG 360

QY  362  CAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAAC TTGCTCAACAGTCCGCGCTTAGG 421
    |||
DB  361  CAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAAC TTGCTCAACAGTCCGCGCTTAGG 420

QY  422  GCACCAGCGTTGCGACTTGGAGCTGAAAGTGGCGGCGAGACAGACAGATACTAA 475
    |||
DB  421  GCACCAGCGTTGCGACTTGGAGCTGAAAGTGGCGGCGAGACAGACAGATACTAA 474

RESULT 11
BD172108
LOCUS             BD172108             474 bp      DNA      linear      PAT 18-FEB-2003
DEFINITION       Peanut allergen and method.
ACCESSION        BD172108
VERSION          BD172108.1 GI:28413406
KEYWORDS         JP 200223783-A/1.
SOURCE           Arachis hypogaea (peanut)
ORGANISM         Arachis hypogaea
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
                 Aeschynomeneae; Arachis.
                 1 (bases 1 to 474)
REFERENCE        1
AUTHORS          Jt,W.A.B., Helm,R.M., Cockrell,G., Steven, Stanley,J. and
                 Bannon,G.A.
TITLE            Peanut allergen and method
JOURNAL          UNIVERSITY OF ARKANSAS
COMMENT          OS Arachis hypogaea (peanut)
                 PN JP 200223783-A/1
                 PD 13-AUG-2002
                 PF 21-NOV-2001 JP 2001356754
                 PR 29-DEC-1995 US 60/009 455, 04-MAR-1996 US 08/610.424 PI
                 WESLEY A BURKS JR,RICKI M HELM,GARL COCKRELL,STEVEN PI J
                 STANLEY,GARY A BANNON
                 PC C12N15/09,A61K38/00,A61P37/04,C07K14/415,C12N15/00,A61K37/02
                 CC Strandedness: Double;
                 Topology: Linear;
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CC seed storage protein and allergen
FH Key Location/Qualifiers
FT source 1..474
FT /organism="Arachis hypogaea (peanut)".

FEATURES             source          Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:3818"

ORIGIN
Query Match      65.7%; Score 470.8; DB 2; Length 474;
Best Local Similarity 99.6%; Pred. No. 1.7e-128;
Matches 472; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2  CTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACGCAATCTGGAGGCAG 61
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DB  1  CTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACGCAATCTGGAGGCAG 60

QY  62  CAGTGGGAATCCCAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCCTGAGG 121
    |||
DB  61  CAGTGGGAATCCCAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCCTGAGG 120

QY  122  CCCTGCCAGCAACATCTCATGCAGAAATCCAACTGACGAGGATTCATATGAACGGGAC 181
    |||
DB  121  CCCTGCCAGCAACATCTCATGCAGAAATCCAACTGACGAGGATTCATATGAACGGGAC 180

QY  182  CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTTGA 241
    |||
DB  181  CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTTGA 240

QY  242  TCCTCTCAGCACCAGAGAGGTGTGCAATGAGCTGAACGATTTGAGAACCAACCAAGG 301
    |||
DB  241  TCCTCTCAGCACCAGAGAGGTGTGCAATGAGCTGAACGATTTGAGAACCAACCAAGG 300

QY  302  TGCATGTGCGAGGATTCGCAACAGATCATGAGAAC CAGAGCGATAGTTGCGAGGGGAGG 361
    |||
DB  301  TGCATGTGCGAGGATTCGCAACAGATCATGAGAAC CAGAGCGATAGTTGCGAGGGGAGG 360

QY  362  CAACAGGAGCAACAGTTCAAGAGGAGCTCAGAGGAGCTCAGGAAC TTGCTCAACAGTCCGCGCTTAGG 421
    |||
DB  361  CAACAGGAGCAACAGTTCAAGAGGAGCTCAGAGGAGCTCAGGAAC TTGCTCAACAGTCCGCGCTTAGG 420

QY  422  GCACCAGCGTTGCGACTTGGAGCTGAAAGTGGCGGCGAGACAGACAGATACTAA 475
    |||
DB  421  GCACCAGCGTTGCGACTTGGAGCTGAAAGTGGCGGCGAGACAGACAGATACTAA 474

RESULT 12
AY007229
LOCUS             AY007229             472 bp      DNA      linear      PLN 23-OCT-2002
DEFINITION       Arachis hypogaea allergen II gene, partial cds.
ACCESSION        AY007229
VERSION          AY007229.1 GI:15418704
KEYWORDS         .
SOURCE           Arachis hypogaea (peanut)
ORGANISM         Arachis hypogaea
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
                 Aeschynomeneae; Arachis.
                 1 (bases 1 to 472)
REFERENCE        1
AUTHORS          Viquez,O.M., Summer,C.G. and Dodo,H.W.
TITLE            Isolation and molecular characterization of the first genomic clone
                 of a major peanut allergen, Ara h 2
JOURNAL          J. Allergy Clin. Immunol. 107 (4), 713-717 (2001)
COMMENT          PUBMED 11295663
                 2 (bases 1 to 472)
                 Viquez,O.M., Dodo,H.W. and Summer,C.G.
                 Direct Submission
                 Submitted (16-AUG-2000) Food and Animal Sciences, Alabama A&M
                 University, Meridian Street, 4900, Normal, AL 35762, USA
                 Location/Qualifiers
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            /db_xref="taxon:3818"
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CDS         3..>.472
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ORIGIN
Query Match      64.4%; Score 462; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 6.9e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 60
DB      11 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 70
QY      61 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGCGGAACCTGAG 120
DB      71 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGCGGAACCTGAG 130
QY      121 GCCTCGGAGCAACATCTCATGCAGAGATGCCAAGCTGAGAGGATTCATATGAACGGGA 180
DB      131 GCCTCGGAGCAACATCTCATGCAGAGATGCCAAGCTGAGAGGATTCATATGAACGGGA 190
QY      181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
DB      191 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 250
QY      241 ATCCTCTCAGCACACAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACACCAAG 300
DB      251 ATCCTCTCAGCACACAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACACCAAG 310
QY      301 GTGCATGTGCGAGGCAATTCGAACAGATCATGGAGAACCGAGCGATAGTTTGCAGGGGAG 360
DB      311 GTGCATGTGCGAGGCAATTCGAACAGATCATGGAGAACCGAGCGATAGTTTGCAGGGGAG 370
QY      361 GCAACAGGAGCAACAGTTCGAAGAGGAGCTCAGAACTTCCTCTCAACAGTGCAGGCTTAG 420
DB      371 GCAACAGGAGCAACAGTTCGAAGAGGAGCTCAGAACTTCCTCTCAACAGTGCAGGCTTAG 430
QY      421 GGCACACAGCGTTGGAGCTTGACGTCGAAAGTGGCGGCGAG 462
DB      431 GGCACACAGCGTTGGAGCTTGACGTCGAAAGTGGCGGCGAG 472

RESULT 13
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DEFINITION Sequence 3 from patent US 6943010.
ACCESSION AR716327
VERSION AR716327.1 GI:77364702
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 682)
AUTHORS Dodo,H.W., Arntzen,C.J., Viquez,O.M. and Konan,K.N.
TITLE Down-regulation and silencing of allergen genes in transgenic
peanut seeds
JOURNAL Patent: US 6943010-A 3 13-SEP-2005;
FEATURES Location/Qualifiers
source 1. .682
/mol_type="genomic DNA"

ORIGIN
Query Match      64.4%; Score 462; DB 2; Length 682;
Best Local Similarity 100.0%; Pred. No. 7.3e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 60
DB      67 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 126
QY      61 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGCGGAACCTGAG 120
DB      127 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGCGGAACCTGAG 186
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DB      187 GCCTCGGAGCAACATCTCATGCAGAGATGCCAAGCTGAGAGGATTCATATGAACGGGA 246
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RESULT 14
AX148740 LOCUS      682 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION Sequence 3 from Patent WO0136621.
ACCESSION AX148740
VERSION AX148740.1 GI:14347294
KEYWORDS
SOURCE
ORGANISM Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1
AUTHORS Dodo,H.W., Arntzen,C.J., Konan,K.N. and Viquez,O.M.
TITLE Down-regulation and silencing of allergen genes in transgenic
peanut seeds
JOURNAL Patent: WO 0136621-A 3 25-MAY-2001;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.3e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 60
DB      67 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 126
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ORIGIN
Query Match      64.4%; Score 462; DB 2; Length 682;
Best Local Similarity 100.0%; Pred. No. 7.3e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 60
DB      67 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 126
QY      61 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGCGGAACCTGAG 120
DB      127 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGCGGAACCTGAG 186
QY      121 GCCTCGGAGCAACATCTCATGCAGAGATGCCAAGCTGAGAGGATTCATATGAACGGGA 180
DB      187 GCCTCGGAGCAACATCTCATGCAGAGATGCCAAGCTGAGAGGATTCATATGAACGGGA 246
QY      181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
DB      247 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 306
QY      241 ATCCTCTCAGCACACAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACACCAAG 300
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QY      361 GCAACAGGAGCAACAGTTCGAAGAGGAGCTCAGAACTTCCTCTCAACAGTGCAGGCTTAG 420
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DB      487 GGCACACAGCGTTGGAGCTTGACGTCGAAAGTGGCGGCGAG 528

RESULT 14
AX148740 LOCUS      682 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION Sequence 3 from Patent WO0136621.
ACCESSION AX148740
VERSION AX148740.1 GI:14347294
KEYWORDS
SOURCE
ORGANISM Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1
AUTHORS Dodo,H.W., Arntzen,C.J., Konan,K.N. and Viquez,O.M.
TITLE Down-regulation and silencing of allergen genes in transgenic
peanut seeds
JOURNAL Patent: WO 0136621-A 3 25-MAY-2001;
FEATURES Location/Qualifiers
source 1. .682
/organism="Arachis hypogaea"
/mol_type="unassigned DNA"
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ORIGIN
Query Match      64.4%; Score 462; DB 2; Length 682;
Best Local Similarity 100.0%; Pred. No. 7.3e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 60
DB      67 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGAGGCA 126
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Db 187 GCCCTGGGAGCAACATCTCATGCGAGAGATCCACGCTGACGAGATTTCATATGAACGGGA 246
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RESULT 15
AR716326
LOCUS AR716326 1162 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 1 from patent US 6943010.
ACCESSION AR716326
VERSION AR716326.1 GI:77364701
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1162)
Dodo,H.W., Arntzen,C.J., Viquez O.M. and Konan,K.N.
Down-regulation and silencing of allergen genes in transgenic
peanut seeds
JOURNAL Patent: US 6943010-A 1 13-SEP-2005;
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/organism="unknown"
/mol_type="genomic DNA"
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Query Match 64.4%; Score 462; DB 2; Length 1162;
Best Local Similarity 100.0%; Pred. No. 7.9e-126; Mismatches 0; Indels 0; Gaps 0;
Matches 462; Conservative 0;
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Qy 361 GCAACAGGAGCAACAGTTTCAAGAGGGAGCTCAGGAACTTGCCCTCAACAGTGCGGCCCTTAG 420
Db 478 GCAACAGGAGCAACAGTTTCAAGAGGGAGCTCAGGAACTTGCCCTCAACAGTGCGGCCCTTAG 537
Qy 421 GGCACCAACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCAG 462
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2006, 09:14:45 ; Search time 319.487 Seconds  
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15647.278 Million cell updates/sec

Title: US-10-728-051-2

Perfect score: 717

Sequence: 1 gctcaccatactagtagcc.....taaaagatcatgtttgtt 717

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	717	100.0	717	2 AAT76615	Aat76615 Peanut al
2	717	100.0	717	2 AAT76614	Aat76614 Peanut al
3	717	100.0	717	14 ADV97538	Adv97538 Peanut Ar
4	717	100.0	717	14 ADV97541	Adv97541 Peanut Ar
5	475	66.2	480	14 ADV97602	Adv97602 Peanut Ar
6	474	66.1	474	2 AAZ06383	Aaz06383 Peanut al
7	474	66.1	474	4 AAS08538	Aas08538 DNA encod
8	474	66.1	474	8 ABX70606	Abx70606 Peanut Ar
9	474	66.1	474	10 ADG27517	Adg27517 Peanutur CD
10	462	64.4	682	4 AAF90337	Aaf90337 Peanut al
11	462	64.4	1162	4 AAF90336	Aaf90336 Peanut al
12	80	11.2	80	4 AAF90342	Aaf90342 Peanut al
13	65.6	9.1	777	2 AAT86282	Aat86282 Soybean a
14	64	8.9	777	2 AAT86283	Aat86283 Chimeric
15	63.4	8.8	770	2 AAX25346	Aax25346 Soybean G
16	62	8.6	62	4 AAF90343	Aaf90343 Peanut al
17	59.2	8.3	477	10 ADH89268	Adh89268 G. max 2S
18	59.2	8.3	477	12 ADG44003	Adg44003 G. max 2S

19	54.4	7.6	468	10	ADH89266	Adh89266 G. max na
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21	54.4	7.6	723	2	AAT86281	Aat86281 Soybean a
22	51.4	7.2	5392	2	AAZ08720	Aaz08720 Chimeric
C 23	49.8	6.9	62658	13	ABD33339	Abd33339 Human can
C 24	49.6	6.9	52216	4	AAH28355	Aah28355 Nucleotid
C 25	49.6	6.9	52216	6	ABL50307	AbL50307 Human mus
C 26	49.6	6.9	169739	6	ABQ88186	Abq88186 Human ost
27	49	6.8	129	4	AAF87134	Aaf87134 Soybean c
28	49	6.8	129	4	AAF83653	Aaf83653 Lunsan c
29	49	6.8	9407	4	AAF83654	Aaf83654 pPIC9K-lu
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33	47.4	6.6	97835	6	ABK84796	Abk84796 Human cDN
34	45.6	6.4	2000	8	ADA71938	Ada71938 Rice gene
35	45.6	6.4	6063	6	ABK28393	Abk28393 DNA trans
C 36	45.4	6.3	5823	6	ABK28382	Abk28382 DNA trans
37	45.2	6.3	121724	6	ABQ88143	Abq88143 Human ost
38	44.8	6.2	20001	13	ADT77147	Adt77147 Type II d
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C 40	44.4	6.2	6385	4	AAS45353	Aas45353 Chemicall
C 41	44.4	6.2	6385	6	ABK28186	Abk28186 DNA trans
42	44.4	6.2	110000	2	AAV21209_04	Continuation (5 of
43	44	6.1	608	6	ABN62524	Abn62524 Human can
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45	43.8	6.1	7566	4	AAI07322	Aai07322 Human rep

ALIGNMENTS

RESULT 1

AAT76615

ID AAT76615 standard; cDNA to mRNA; 717 BP.

XX AC AAT76615;

XX 17-OCT-2003 (revised)

DT 29-DEC-1997 (first entry)

XX Peanut allergen Ara hII cDNA clone.

XX Peanut; seed storage protein; allergen; allergy; hypersensitivity;

KW vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody;

KW ELISA; analysis; Ara hII; ds.

XX Arachis hypogaea; strain Florunner.

XX Key Location/Qualifiers

FT CDS 2..475

FT polyA\_signal 562..567

FT /\*tag= a

FT /\*tag= b

XX WO9724139-A1.

XX PD 10-JUL-1997.

XX PF 23-SEP-1996; 96WO-US015222.

XX PR 29-DEC-1995; 95US-0009455P.

XX PR 04-MAR-1996; 96US-00610424.

XX (UYAR-) UNIV ARKANSAS.

XX Burks AW, Helm RM, Cockrell G, Stanley JS, Bannon GA;

XX WPI; 1997-363453/33.

XX P-PSDB; AAW24153.

XX Peanut allergens Ara hI and Ara hII - used for vaccination and in two-

PT site monoclonal antibody based ELISA.

XX Claim 31; Page 196; 354pp; English.

XX This cDNA clone codes for the major peanut allergen Ara hII (AAW22153), which contains multiple IgE-binding epitopes. It was amplified from a peanut seed cDNA library using a primer (see AAT58683) based on an isolated Ara hII peptide (see AAW24151). The sequence shows significant homology with the conglutin family of seed storage proteins of other legumes. The gene is capable of producing a protein product in prokaryotic cells that is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hII and Ara hI (see AAW24149-50) can be used to raise monoclonal antibodies which are used in a specific two-site Mab ELISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara hII antigen epitopes (see AAW24188- 93) may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;

Query Match 100.0%; Score 717; DB 2; Length 717;  
Best Local Similarity 100.0%; Pred. No. 7e-178;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGGGCGAACCTTGAG 120  
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QY 121 GCCCTCGGAGCAACATCTCATGAGAGATGCCAGCTGACGAGATTCATATGAACGGGA 180  
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QY 241 ATCCTCTCAGCACCAAGAGAGTGTGCAATGAGCTGAACGAGTTTGAGAACCAACAAAG 300  
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QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAATAATAATAATAATAATAATA 717  
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RESULT 2

AAW76614

ID AAT76614 standard; cDNA to mRNA; 717 BP.

XX AAT76614;

XX 17-OCT-2003 (revised)

DT 29-DEC-1997 (first entry)

XX Peanut allergen Ara hII cDNA clone P38.

DE Peanut; seed storage protein; allergen; allergy; hypersensitivity;

XX Peanut; anaphylactic shock; immunotherapy; therapy; monoclonal antibody;

KW ELISA; analysis; Ara hII; ds.

XX Arachis hypogaea; strain Florunner.

OS Key Location/Qualifiers

XX CDS 2..475

FT polyA\_signal /\*tag= a

FT /\*tag= b

XX WO9724139-A1.

XX 10-JUL-1997.

XX 23-SEP-1996; 96WO-US015222.

XX 29-DEC-1995; 95US-0009455P.

PR 04-MAR-1996; 96US-00610424.

XX (UYAR-) UNIV ARKANSAS.

XX Burks AW, Helm RM, Cockrell G, Stanley JS, Bannon GA;

XX WPI; 1997-363453/33.

XX Peanut allergens Ara hI and Ara hII - used for vaccination and in two-site monoclonal antibody based ELISA.

XX Claim 31; Page 183-185; 354pp; English.

XX This cDNA clone, designated p38, codes for the major peanut allergen Ara hII (AAW22153), which contains multiple IgE-binding epitopes. It was amplified from a peanut seed cDNA library using a primer (see AAT58683) based on an isolated Ara hII peptide (see AAW24151). The sequence shows significant homology with the conglutin family of seed storage proteins of other legumes. The gene is capable of producing a protein product in prokaryotic cells that is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hII and Ara hI (see AAW24149-50) can be used to raise monoclonal antibodies which are used in a specific two-site Mab ELISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara hII antigen epitopes (see AAW24188- 93) may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;

Query Match 100.0%; Score 717; DB 2; Length 717;  
Best Local Similarity 100.0%; Pred. No. 7e-178;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCATCTCGGAGGCA 60  
DB |||||

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCATCTCGGAGGCA 60  
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QY 121 GCCCTCGGAGCAACATCTCATGAGAGATGCCAGCTGACGAGATTCATATGAACGGGA 180  
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RESULT 3
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ID ADV97538 standard; cDNA; 717 BP.
XX
AC ADV97538;
XX
DT 10-MAR-2005 (first entry)
XX
DE Peanut Ara h II allergen clone P38 cDNA encoding a seed storage protein.
XX
KW allergen; atopic dermatitis; diagnostic; immunotherapy;
KW immediate type hypersensitivity; Ara h II; dermatological; antiallergic;
KW immunosuppressive; antibody engineering; ss; gene.
XX
OS Arachis hypogaea.
XX
FH Key Location/Qualifiers
FT CDS 2..475
FT /*tag= a
FT /partial
FT /product= "Ara h II protein"
FT /note= "Start codon is absent"
XX
US6835824-B1.
XX
PD 28-DEC-2004.
XX
XX 13-NOV-1998; 98US-00191593.
XX
XX 29-DEC-1995; 95US-0009455P.
XX
XX 23-SEP-1996; 96US-00717933.
XX
PA (UYAR-) UNIV ARKANSAS.
```

```
XX Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;
XX WPI: 2005-045982/05.
XX P-PSDB; ADV97542.
XX
PT New isolated nucleic acid encoding peanut allergen Ara h 1, useful for
PT obtaining diagnostics with optimal concentrations of each allergen, for
PT developing panels of mixtures of recombinant allergens, and in
PT immunotherapy.
XX
PS Disclosure; SEQ ID NO 6; 141pp; English.
XX
CC This invention relates to a novel isolated nucleic acid molecule encoding
CC the peanut allergen Ara h I that has been identified in patients with
CC atopic dermatitis. Specifically, it refers to a monoclonal antibody
CC enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the
CC peanut allergens, where the monoclonal antibodies have specificity for a
CC selected peanut allergen antigen. The present invention also describes
CC hybridomas that produce two-site monoclonal antibodies specific for a
CC peanut allergen that can be used in an ELISA to detect and determine the
CC concentration of a specific peanut allergen in a food product or in food
CC processing. Furthermore, it provides an expression vector and the
CC isolated nucleic acid or its fraction can include a diagnostic label.
CC Accordingly, these nucleic acids are useful for obtaining diagnostics
CC with optimal concentrations of each allergen or for developing panels of
CC mixtures of large numbers of recombinant allergens such that it can be
CC used in immunotherapy for the treatment of food hypersensitivity
CC reactions. This polynucleotide sequence is the peanut Ara h II allergen
CC cDNA (P38 clone) of the invention. NB. This sequence is identical to that
CC identified as SeqID 9.
XX
SQ Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;
Query Match 100.0%; Score 717; DB 14; Length 717;
Best Local Similarity 100.0%; Pred. No. 7e-178;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTGCTGCCACGATCTGCGAGGCA 60
Db 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTGCTGCCACGATCTGCGAGGCA 60
QY 61 GCAGTGGGAACTCCAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGCGAACCTTGAG 120
Db 61 GCAGTGGGAACTCCAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGCGAACCTTGAG 120
QY 121 GCCCTGCGAGCAACATCTCATGCGAAGATCCAACTGACGAGATTCATATGAACGGGA 180
Db 121 GCCCTGCGAGCAACATCTCATGCGAAGATCCAACTGACGAGATTCATATGAACGGGA 180
QY 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 240
Db 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 240
QY 241 ATCCTCTCAGCACCAAGAGAGGTTGTCATAGAGTGAACGAGTTTGAGAACACCAAG 300
Db 241 ATCCTCTCAGCACCAAGAGAGGTTGTCATAGAGTGAACGAGTTTGAGAACACCAAG 300
QY 301 GTGCATGTGCGAGGATTCGCAACAGATCATGGAGAACGAGCGATAGTTGCGAGGGAG 360
Db 301 GTGCATGTGCGAGGATTCGCAACAGATCATGGAGAACGAGCGATAGTTGCGAGGGAG 360
QY 361 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCTCAACAGTGGCGCTTAG 420
Db 361 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCTCAACAGTGGCGCTTAG 420
QY 421 GGCAACAGAGGTTGCGAGCTTGGACGTCGAAAGTGGCGGAGACAGATCTAAACACC 480
Db 421 GGCAACAGAGGTTGCGAGCTTGGACGTCGAAAGTGGCGGAGACAGATCTAAACACC 480
QY 481 TATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
Db 481 TATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
```

QY 541 GTTATGTTAGTTTGGTAATAATAAAGATCATCATATATGAATGTGTGATCGTGTTA 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
541 GTTATGTTAGTTTGGTAATAATAAAGATCATCATATATGAATGTGTGATCGTGTTA 600  
QY 601 ACTAAGCGAGCTTAGTTATATAGCACCTTTTAGAGTGTCTTTATGGCGTTGCTATGT 660  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
601 ACTAAGCGAGCTTAGTTATATAGCACCTTTTAGAGTGTCTTTATGGCGTTGCTATGT 660  
QY TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATCATGTTTGT 717  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATCATGTTTGT 717

RESULT 4  
ADV97541  
ID ADV97541 standard; cDNA; 717 BP.  
XX  
AC ADV97541;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE Peanut Ara h II allergen clone P38 cDNA encoding a seed storage protein.  
XX  
KW allergen; atopic dermatitis; diagnostic; immunotherapy;  
KW immediate type hypersensitivity; Ara h II; dermatological; antiallergic;  
KW immunosuppressive; antibody engineering; ss.  
XX  
OS Arachis hypogaea.  
XX  
FH Key Location/Qualifiers  
FT CDS 2..475  
FT FT /\*tag= a  
FT FT /partial  
FT FT /product= "Ara h II protein"  
FT FT /note= "Start codon is absent"  
XX  
PN US6835824-B1.  
XX  
PD 28-DEC-2004.  
XX  
PF 13-NOV-1998; 98US-00191593.  
XX  
PR 29-DEC-1995; 95US-0009455P.  
PR 23-SEP-1996; 96US-00717933.  
XX  
PA (UVAR-) UNIV ARKANSAS.  
XX  
PI Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;  
XX  
DR WPI; 2005-045982/05.  
DR P-PSDB; ADV97542.  
XX  
PT New isolated nucleic acid encoding peanut allergen Ara h 1, useful for  
PT obtaining diagnostics with optimal concentrations of each allergen, for  
PT developing panels of mixtures of recombinant allergens, and in  
PT immunotherapy.  
XX  
PS Disclosure; SEQ ID NO 9; 141pp; English.

XX This invention relates to a novel isolated nucleic acid molecule encoding  
XX the peanut allergen Ara h I that has been identified in patients with  
XX atopic dermatitis. Specifically, it refers to a monoclonal antibody  
XX enzyme-linked immunosorbant assay (ELISA) used to detect and quantify the  
XX peanut allergens, where the monoclonal antibodies have specificity for a  
XX selected peanut allergen antigen. The present invention also describes  
XX hybridomas that produce two-site monoclonal antibodies specific for a  
XX peanut allergen that can be used in an ELISA to detect and determine the  
XX concentration of a specific peanut allergen in a food product or in food  
XX processing. Furthermore, it provides an expression vector and the  
XX isolated nucleic acid or its fraction can include a diagnostic label.  
XX Accordingly, these nucleic acids are useful for obtaining diagnostics  
XX with optimal concentrations of each allergen or for developing panels of

CC mixtures of large numbers of recombinant allergens such that it can be  
CC used in immunotherapy for the treatment of food hypersensitivity  
CC reactions. This polynucleotide sequence is the peanut Ara h II allergen  
CC cDNA (P38 clone) of the invention. NB. This sequence is identical to that  
CC identified as SeqID 6.  
XX  
SQ Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 717; DB 14; Length 717;  
Best Local Similarity 100.0%; Pred. No. 7e-178;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GCTCACCATACTAGTAGCCCTGCGCCCTTTTCTCTCGCTGCCCGCATCTCGAGGCA 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 GCTCACCATACTAGTAGCCCTGCGCCCTTTTCTCTCGCTGCCCGCATCTCGAGGCA 60  
QY 61 GCAGTGGGAACCTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 GCAGTGGGAACCTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120  
QY 121 GCCCTGCGAGCAACATCTCATGCAGAAAGATCCAACTGACGAGGATTCATATGAACGGGA 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 GCCCTGCGAGCAACATCTCATGCAGAAAGATCCAACTGACGAGGATTCATATGAACGGGA 180  
QY 181 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 240  
QY 241 ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAAGAGTTTGAGAACCAACAAAG 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAAGAGTTTGAGAACCAACAAAG 300  
QY 301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAACACGAGCGATAGTTGCGAGGGAG 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAACACGAGCGATAGTTGCGAGGGAG 360  
QY 361 GCAACAGGAGCAACAGTTCAAGAGGAGGCTCAGGAACTTGCCTCAACAGTGGCGCTTAG 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
361 GCAACAGGAGCAACAGTTCAAGAGGAGGCTCAGGAACTTGCCTCAACAGTGGCGCTTAG 420  
QY 421 GGCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGACAGACAGATATAAACACC 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
421 GGCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGACAGACAGATATAAACACC 480  
QY 481 TATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
481 TATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540  
QY 541 GTTATGTTTGTGTTTGTGTAATAATAAAGATCATCATATATGAATGTGTGATCGTGTTA 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
541 GTTATGTTTGTGTTTGTGTAATAATAAAGATCATCATATATGAATGTGTGATCGTGTTA 600  
QY 601 ACTAAGCGAGCTTAGTTATATGAGCACTTTTAGAGTGTCTTTATGGCGTTGCTATGT 660  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
601 ACTAAGCGAGCTTAGTTATATGAGCACTTTTAGAGTGTCTTTATGGCGTTGCTATGT 660  
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATCATGTTTGT 717  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATCATGTTTGT 717  
  
RESULT 5  
ADV97602  
ID ADV97602 standard; cDNA; 480 BP.  
XX  
AC ADV97602;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE Peanut Ara h II allergen clone P38 cDNA encoding a seed storage protein.  
XX allergen; atopic dermatitis; diagnostic; immunotherapy;  
KW immediate type hypersensitivity; Ara h II; dermatological; antiallergic;  
KW immediate type hypersensitivity; Ara h II; dermatological; antiallergic;

immunosuppressive; antibody engineering; sg; gene.

```

KW  Arachis hypogaea.
OS
FH  Key
FT  CDS      Location/Qualifiers
FT  1..480
FT  /*tag= a
FT  /partial
FT  /product= "Ara h II protein"
FT  /note= "Start codon is absent"
XX
XX  US6835824-B1.
XX
XX  28-DEC-2004.
XX
XX  13-NOV-1998; 98US-00191593.
XX
XX  29-DEC-1995; 95US-0009455P.
XX  23-SEP-1996; 96US-00717933.
XX
XX  (UYAR-) UNIV ARKANSAS.
XX
XX  Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;
XX
XX  WPI; 2005-045982/05.
XX  P-PSDB; ADV97603.
XX
XX  New isolated nucleic acid encoding peanut allergen Ara h 1, useful for
XX  obtaining diagnostics with optimal concentrations of each allergen, for
XX  developing panels of mixtures of recombinant allergens, and in
XX  immunotherapy.
XX
XX  Disclosure; Fig 27; 141pp; English.
XX
XX  This invention relates to a novel isolated nucleic acid molecule encoding
XX  the peanut allergen Ara h I that has been identified in patients with
XX  atopic dermatitis. Specifically, it refers to a monoclonal antibody
XX  enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the
XX  peanut allergens, where the monoclonal antibodies have specificity for a
XX  selected peanut allergen antigen. The present invention also describes
XX  hybridomas that produce two-site monoclonal antibodies specific for a
XX  peanut allergen that can be used in an ELISA to detect and determine the
XX  concentration of a specific peanut allergen in a food product or in food
XX  processing. Furthermore, it provides an expression vector and the
XX  isolated nucleic acid or its fraction can include a diagnostic label.
XX  Accordingly, these nucleic acids are useful for obtaining diagnostics
XX  with optimal concentrations of each allergen or for developing panels of
XX  mixtures of large numbers of recombinant allergens such that it can be
XX  used in immunotherapy for the treatment of food hypersensitivity
XX  reactions. This polynucleotide sequence is the peanut Ara h II allergen
XX  cDNA (P38 clone) of the invention.
XX
XX  Sequence 480 BP; 134 A; 126 C; 142 G; 78 T; 0 U; 0 Other;

Query Match      66.2%; Score 475; DB 14; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.1e-114;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  GCTCACCATACTAGTAGCCCTTCGCCCTTTCCCTCCCTCGCTGCCACCGCATCTCGGAGCA 60
DB  6  GCTCACCATACTAGTAGCCCTTCGCCCTTTCCCTCCCTCGCTGCCACCGCATCTCGGAGCA 65
QY  61  GCAGTGGGAACCTCAAGGAGACAGAAGATGCCAGGCGAGCTCGAGAGGCGGAACCTGAG 120
DB  66  GCAGTGGGAACCTCAAGGAGACAGAAGATGCCAGGCGAGCTCGAGAGGCGGAACCTGAG 125
QY  121  GCCCTGCGAGCAACATCTCATGCAAGAGATCCAAACGTGACGAGATTCATATGAACGGGA 180
DB  126  GCCCTGCGAGCAACATCTCATGCAAGAGATCCAAACGTGACGAGATTCATATGAACGGGA 185
QY  181  CCGGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
DB  186  CCGGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 245

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# RESULT 6

```

AAZ06383
ID  AAZ06383 standard; DNA; 474 BP.
XX
XX  AC  AAZ06383;
XX
XX  17-OCT-2003 (revised)
DT  09-NOV-1999 (first entry)
XX
XX  Peanut allergen, Ara h 2.
XX
XX  allergy; immune response; transgenic; allergen; epitope;
XX  immunoglobulin E; Ig E; binding site; peanut; ds.
XX
XX  Arachis hypogaea.
XX
XX  W09939978-A1.
XX
XX  05-AUG-1999.
XX
XX  29-JAN-1999; 99WO-US002031.
XX
XX  31-JAN-1998; 98US-0073283P.
XX  13-FEB-1998; 98US-0074590P.
XX  13-FEB-1998; 98US-0074624P.
XX  13-FEB-1998; 98US-0074633P.
XX  27-AUG-1998; 98US-00141220.
XX
XX  (UYAR-) UNIV ARKANSAS.
XX  (UNY ) UNIV NEW YORK MT SINAI SCHOOL MEDICINE.
XX  (SOSI) SOSIN H.
XX
XX  Sosin H, Bannon GA, Burks AW, Sampson HA;
XX
XX  WPI; 1999-479189/40.
XX  P-PSDB; AAY15245.
XX
XX  Modified allergen with reduced IgE binding, useful for treating e.g.
XX  allergies.
XX
XX  Disclosure; Page 37; 46pp; English.
XX
XX  This is the nucleotide sequence of the Ara h 2 protein from Arachis
XX  hypogaea. The Ara h 2 protein has 10 IGE (Immunoglobulin E) binding
XX  epitopes, three of which are immunodominant (AAY15272, AAY15275, and
XX  AAY15276). By modifying the IGE binding sites the ability of the allergen
XX  to provoke an immune response is downregulated. The epitopes of the IGE
XX  binding sites can therefore be modified in genetically engineered plants
XX  and animals to elicit less of an allergic response. (Updated on 17-OCT-
XX  2003 to standardise OS field)
XX
XX  Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;

Query Match      66.1%; Score 474; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.8e-114;

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Matches	474;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	CTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCATCTGCGAGCGAG	61						
Db	1	CTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCATCTGCGAGCGAG	60						
Qy	62	CAGTGGGAACCTCCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCGAGG	121						
Db	61	CAGTGGGAACCTCCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCGAGG	120						
Qy	122	CCCTGCGAGCAACATCTCATGCGAAGAATCCAAGGTGACGAGGATTTCATATGAACGGGAC	181						
Db	121	CCCTGCGAGCAACATCTCATGCGAAGAATCCAAGGTGACGAGGATTTCATATGAACGGGAC	180						
Qy	182	CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGGCGCTGGA	241						
Db	181	CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGGCGCTGGA	240						
Qy	242	TCCTCTCAGCACCAAGAGAGGTGTTCGCAATGAGCTGAACTGAGTTTGAGAACCAACAAAGG	301						
Db	241	TCCTCTCAGCACCAAGAGAGGTGTTCGCAATGAGCTGAACTGAGTTTGAGAACCAACAAAGG	300						
Qy	302	TGCATGTGCGAGGCAATTCGAACAGATCATGAGAACCCAGACCGATAGGTTGCGAGGGAGG	361						
Db	301	TGCATGTGCGAGGCAATTCGAACAGATCATGAGAACCCAGACCGATAGGTTGCGAGGGAGG	360						
Qy	362	CAACAGAGCAACAGTTTCAAGAGGGAGCTCAGGAACTTGGCTCAACAGTCGGCGCTTAGG	421						
Db	361	CAACAGAGCAACAGTTTCAAGAGGGAGCTCAGGAACTTGGCTCAACAGTCGGCGCTTAGG	420						
Qy	422	GCACCAGCGTTGCGACTTGGACGTCGAAAGTCGGCGCAGACAGATACTAA	475						
Db	421	GCACCAGCGTTGCGACTTGGACGTCGAAAGTCGGCGCAGACAGATACTAA	474						

RESULT 7  
AAS08538  
ID AAS08538 standard; cDNA; 474 BP.  
XX  
XX AAS08538;  
XX  
XX  
XX  
DT 23-OCT-2001 (first entry)  
XX  
XX DNA encoding anaphylactic antigen Ara h 2.  
DE  
XX  
XX Ara h 2; anaphylactic antigen; immunoglobulin E; IgE; immunogenic;  
KW allergen; mast cell; basophil; mouse; ss.

Key	Location/Qualifiers
XX	
PH	
FT	1. .474
FT	
FT	/*tag= a
FT	/product= "peptide antigen Ara h 2"
XX	
XX	
PN	WO200140264-A2.
XX	
XX	
PD	07-JUN-2001.
XX	
PF	06-DEC-2000; 2000WO-US033124.
XX	
XX	
PR	06-DEC-1999; 99US-00455294.
PR	23-JUN-2000; 2000US-0213765P.
PR	27-SEP-2000; 2000US-0235797P.
PR	

XX Antigenic fragments useful for reducing anaphylactic risk and reducing  
PT the severity and/or number of allergic symptoms in individuals sensitive  
PT to antigens, have reduced ability to bind Immunoglobulin E.  
XX Disclosure; Fig 10; 100pp; English.  
XX  
XX The sequence represents the coding sequence of anaphylactic antigen Ara h  
CC 2. Ara h 2 is an anaphylactic antigen (A), which was used to design  
CC antigenic peptides having a reduced ability to bind immunoglobulin E  
CC (IgE) as compared with the intact (A), or having a sequence substantially  
CC identical to a portion of sequence of an antigen that includes at least  
CC one IgE binding site, where at least one IgE binding site of the peptide  
CC is altered. The antigenic peptides are used in a composition which is  
CC useful for reducing risk or severity of allergic reaction to an antigen.  
CC This is done by identifying an individual at risk of allergic reaction to  
CC an antigen by identifying prior display of allergic symptoms when exposed  
CC to the antigen, or a familial relationship with an individual who  
CC previously displayed allergic symptoms when exposed to the antigen.  
CC Following this an antigen-specific IgE present on one or more mast cells  
CC or basophils in the individual's serum is identified. The individual is  
CC then contacted with a peptide corresponding to a portion of the antigen,  
CC which is selected, formulated, and delivered so that binding of the  
CC peptide to antigen-specific IgE is reduced as compared with IgE binding  
CC of intact antigen. The composition is also useful for treating and  
CC preventing allergic reactions  
XX Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;  
SQ

Query Match 66.1%; Score 474; DB 4; Length 474;  
Best Local Similarity 100.0%; Pred. No. 3.8e-114;  
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
ABX70606  
ID ABX70606 standard; cDNA; 474 BP.  
XX  
AC ABX70606;  
XX  
DT 26-MAR-2003 (first entry)



```
PA (SHIN/) SHIN D. S.
PA (STAN/) STANLEY J. S.
XX
XX Caplan MJ, Sosin HB, Sampson H, Bannon GA, Burks AW, Cockrell G;
PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;
PI Rabjohn PA, Shin DS, Stanley JS;
XX
XX WPI; 2003-075632/81.
DR P-PSDB; ADG27518.
XX
XX New modified anaphylactic food allergen comprising a cysteine residue
PT which has been modified so that it cannot participate in the disulfide
PT bond, useful for treating allergic reactions or wounds.
XX
XX Example 10; SEQ ID NO 62; 194pp; English.
XX
XX The invention relates to a modified anaphylactic food allergen whose
CC amino acid sequence is substantially identical to that of a natural
CC anaphylactic food allergen. The natural anaphylactic food allergen
CC includes at least one cysteine residue that participates in a disulphide
CC bond when the natural anaphylactic food allergen is in its native
CC conformation, except that the cysteine residue has been modified so that
CC it cannot participate in the disulphide bond. Also included are a method
CC of making a modified anaphylactic food allergen, a nucleotide molecule
CC encoding a modified anaphylactic food allergen defined above, a
CC nucleotide molecule for causing a site specific mutation in a gene
CC encoding a natural anaphylactic food allergen, a transgenic plant or
CC animal expressing a modified anaphylactic food allergen defined above, a
CC method of treating an individual by reducing the clinical response to a
CC natural anaphylactic food allergen by administering a modified
CC anaphylactic food allergen and an isolated fragment of peanut allergen
CC Arh 1, comprising at least 10 consecutive amino acids of ADG27464 or
CC ADG27465. About 10-17% of the amino acids have been modified in at least
CC one IGE epitope or all the IGE epitopes recognised when the natural
CC anaphylactic food allergen is contacted with serum IgE from individual(s)
CC allergic to the natural anaphylactic food allergen. The invention
CC discloses Peanut allergens Ara h1, Ara h2, Ara h3 (and their encoding
CC cDNAs), Soybean Glycinin A2Bia and IGE-binding epitopes of the English
CC walnut allergen Jug n1. The modified anaphylactic food allergen can be
CC used for treating allergic reactions or wounds. The present sequence
CC encodes a Peanut allergen of the invention.
XX
XX Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;
SQ
Query Match 66.1%; Score 474; DB 10; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.8e-114;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTCACCATCTAGTAGCCCTCGCCCTTTTCTCTCTGCTGCCACGCATCTGCGAGGCGAG 61
DB 1 CTCACCATCTAGTAGCCCTCGCCCTTTTCTCTCTGCTGCCACGCATCTGCGAGGCGAG 60
QY 62 CAGTGGGAATCCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGCAACCTGAGG 121
DB 61 CAGTGGGAATCCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGCAACCTGAGG 120
QY 122 CCCTGCGAGCAACATCTATGTCAGAAATCAACGTCACAGAGATTCATATGAACGGGAC 181
DB 121 CCCTGCGAGCAACATCTCATGCAAGATCAACGTCACAGGAGTTCATATGAACGGGAC 180
QY 182 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGGCGCTTGA 241
DB 181 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGGCGCTTGA 240
QY 242 TCCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTGAACGAGTTTGAACAACCAAGAAG 301
DB 241 TCCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTGAACGAGTTTGAACAACCAAGAAG 300
QY 302 TGCATGTGCGAGGCGATTTCACACAGATCATGAGAAACACAGACCGATAGTTGCGAGGGGAGG 361
DB 301 TGCATGTGCGAGGCGATTTCACACAGATCATGAGAAACACAGACCGATAGTTGCGAGGGGAGG 360
QY 362 CAACAGGAGCAACAGTTTCAAGAGGGGAGGCTCAGGAACTTGCTCAACAGTGGCGCTTAGG 421
DB 421
```

```
Db 361 CAACAGGAGCAACAGTTTCAAGAGGGGAGGCTCAGGAACTTGCTCAACAGTGGCGCTTAGG 420
QY 422 GCACACACACGTTGGCAGCTTGGACGTCGAAAGTGGCGGAGAGACAGATACTAA 475
Db 421 GCACACACACGTTGGCAGCTTGGACGTCGAAAGTGGCGGAGAGACAGATACTAA 474

RESULT 10
AAF90337
ID AAF90337 standard; DNA; 682 BP.
XX
XX AAF90337;
AC
XX
XX 11-SEP-2003 (revised)
DT 23-JUL-2001 (first entry)
DT
XX
XX Peanut allergen Ara h2 gene.
DE
XX
XX Peanut; allergen; Ara h2; Ara h6; Ara h7; transgenic plant; allergy; ds.
KW
XX
XX Arachis hypogaea.
XX
XX Key Location/Qualifiers
FT CDS 59..682 /tags= a
FT sig_peptide 59..121 /tag= b
FT mat_peptide 122..679 /tag= c
FT misc_feature 321..528 /tag= d
FT /note= "PCR amplified fragment"
FT
XX
XX WO200136621-A2.
XX
XX 25-MAY-2001.
PD
XX
XX 20-NOV-2000; 2000WO-US031657.
PF
XX
XX 19-NOV-1999; 99US-0167255P.
PR
XX
XX (UYAL-) UNIV ALABAMA A & M.
PA
XX
XX Dodo HW, Arntzen CJ, Konan KN, Viquez OM;
PI
XX
XX WPI; 2001-355630/37.
DR
XX
XX P-PSDB; AAB82383.
DR
XX
XX Producing transgenic peanut plants that produce allergen-free seeds,
PT useful in non-allergenic foods, by antisense or sense co-suppression of
PT allergen-encoding genes.
XX
XX Claim 6; Fig 3; 72pp; English.
PS
XX
XX The present sequence is that of the peanut allergen Ara h2 gene coding
XX region. A portion of the Ara h2 gene is homologous to corresponding
XX regions of the peanut allergen Ara h6 and Ara h7 genes. This region has
XX been PCR amplified, cloned in transformation vectors (pUC18 and pBI4434)
XX in sense and antisense orientations and used to down-regulate Ara h2, Ara
XX h6 and Ara h7 allergens in peanut. This is an example of the method of
XX the invention, which relates to the production of a peanut plant having
XX reduced, or undetectable, allergenic protein (AP) content in its seed. A
XX peanut plant cell is transformed with a DNA construct containing an
XX antisense AP gene and/or sense AP gene, or their fragments, regenerated
XX to plants, and fertile transgenic plants that produce seeds with reduced
XX AP content are identified. The AP sense or antisense gene may comprise at
XX least a portion of the Ara h2 gene. The seeds are useful for preparation
XX of allergen-free foods. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 682 BP; 170 A; 189 C; 202 G; 121 T; 0 U; 0 Other;
SQ
Query Match 64.4%; Score 462; DB 4; Length 682;
```

Best Local Similarity 100.0%; Pred. No. 6.3e-111;  
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCATCTCGAGGCA 60  
DB 67 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCATCTCGAGGCA 126  
QY 61 GCAGTGGGAACCTCAAGGAGACAGAAGATGCCAGGCCAGCTCGAGAGGGCGAACCTTGAG 120  
DB 127 GCAGTGGGAACCTCAAGGAGACAGAAGATGCCAGGCCAGCTCGAGAGGGCGAACCTTGAG 186  
QY 121 GCCCTGGCAGCAATCTCATGCAGAAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 180  
DB 187 GCCCTGGCAGCAATCTCATGCAGAAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 246  
QY 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG 240  
DB 247 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG 306  
QY 241 ATCTCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300  
DB 307 ATCTCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 366  
QY 301 GTGCATGTGCGAGCATTTGCAACAGATCATGGAACCCAGAGCGATAGGTTGCGAGGGAG 360  
DB 367 GTGCATGTGCGAGCATTTGCAACAGATCATGGAACCCAGAGCGATAGGTTGCGAGGGAG 426  
QY 361 GCAACAGGACCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCCTCAACAGTGCAGCTTAG 420  
DB 427 GCAACAGGACCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCCTCAACAGTGCAGCTTAG 486  
QY 421 GGCAACCAACAGCTTGGACCTTGACAGCTCGAAAGTGGCGGAG 462  
DB 487 GGCAACCAACAGCTTGGACCTTGACAGCTCGAAAGTGGCGGAG 528

## RESULT 11

AAF90336  
ID AAF90336 standard; DNA; 1162 BP.

XX AAF90336;

XX 11-SEP-2003 (revised)

DT 23-JUL-2001 (first entry)

XX Peanut allergen Ara h2 gene.

XX Peanut; allergen; Ara h2; transgenic plant; allergy; ds.

XX Arachis hypogaea.

XX Key Location/Qualifiers

FT TATA\_signal 39..46

FT /\*tag= a

FT CDS 110..733

FT /\*tag= b

FT sig\_peptide 110..172

FT /\*tag= c

FT mat\_peptide 172..730

FT /\*tag= d

FT polyA\_signal 1060..1065

FT /\*tag= e

XX WO200136621-A2.

XX 25-MAY-2001.

XX 20-NOV-2000; 2000WO-US031657.

XX 19-NOV-1999; 99US-0167255P.

XX (UYAL-) UNIV ALABAMA A &amp; M.

XX

PI Dodo HW, Arntzen CJ, Konan KN, Viquez OM;

XX WPI; 2001-355630/37.

DR P-PSDB; AAB82383.

XX Producing transgenic peanut plants that produce allergen-free seeds,

PT useful in non-allergenic foods, by antisense or sense co-suppression of

PT allergen-encoding genes.

XX Claim 5; Fig 2; 72pp; English.

PS The present sequence is that of the peanut allergen Ara h2 gene. The gene

XX was identified following screening of genomic DNA using a probe (see

CC AAF90342) based on the known Ara h2 cDNA sequence, subcloning of positive

CC clones into a phagemid vector, restriction enzyme digestion, ligation

CC with vector DNA, Southern hybridisation and sequencing. The gene encodes

CC a 207-amino acid allergenic protein (see AAB82383). The invention relates

CC to a method for producing a peanut plant having reduced, or undetectable,

CC allergenic protein (AP) content in its seed. A peanut plant cell is

CC transformed with a DNA construct containing an antisense AP gene and/or

CC sense AP gene, or their fragments, regenerated to plants, and fertile

CC transgenic plants that produce seeds with reduced AP content are

CC identified. The AP sense or antisense gene may comprise at least a

CC portion of the present sequence. The seeds are useful for preparation of

CC allergen-free foods. Recombinant AP may be produced and used to produce

CC antibodies useful for detecting AP in foods, and for treatment or

CC prevention of peanut allergy. (Updated on 11-SEP-2003 to standardise OS

CC field)

XX Sequence 1162 BP; 272 A; 325 C; 329 G; 236 T; 0 U; 0 Other;

SQ Query Match 64.4%; Score 462; DB 4; Length 1162;

Best Local Similarity 100.0%; Pred. No. 7.8e-111;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCATCTCGAGGCA 60

DB 118 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCATCTCGAGGCA 177

QY 61 GCAGTGGGAACCTCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTTGAG 120

DB 178 GCAGTGGGAACCTCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTTGAG 237

QY 121 GCCCTGCGAGCAACATCTCATGCAGAAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 180

DB 238 GCCCTGCGAGCAACATCTCATGCAGAAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 297

QY 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG 240

DB 298 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG 357

QY 241 ATCTCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300

DB 358 ATCTCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 417

QY 301 GTGCATGTGCGAGGCAATTCACACAGATCATGGAACCCAGAGCGATAGGTTGCGAGGGAG 360

DB 418 GTGCATGTGCGAGGCAATTCACACAGATCATGGAACCCAGAGCGATAGGTTGCGAGGGAG 477

QY 361 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGCAGCTTAG 420

DB 478 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGCAGCTTAG 537

QY 421 GGCAACCAACAGCTTGGACCTTGACAGCTCGAAAGTGGCGGAG 462

DB 538 GGCAACCAACAGCTTGGACCTTGACAGCTCGAAAGTGGCGGAG 579

## RESULT 12

AAF90342

ID AAF90342 standard; DNA; 80 BP.

XX

AC AAF90342;





```
QY 283 GTTTGAGAACCAACCAAGGTGCATGTGCGAGGCATTCACACAGATCATGTGAGAACCCAGAG 342
DB 336 GCT--GAGAAAGCCCAATGCCAGTCAAAGCGCTCCAGAGATATGAGAGAACCCAGAG 392
QY 343 CGATAGTTGTCAGGGAGGCAACGAGGACACAGTTCAAGAGGGAGCTCAGGAACCTTGCC 402
DB 393 CGAGGAACCTGGAGGAGGAGCAGAGAGAAA---ATGGAGAAGGAGCTCATTAACTTTGC 449
QY 403 TCAACAGTGGCGCTTAGGCGCACACACAGCGTTGCGACTTGGAGCTCGAAGAGTGGCGGCGAG 462
DB 450 TACTATGTGAGGTTTGGAGCCCATGATCCAGTGGAGCTTGTCTCCGA-----TGACTA 503
QY 463 AGACAGATACATAACACCTATCTCAAAAAAGAAAAGAAAAGAAAAGAAAATAGCTTATA 522
DB 504 AGAAGTTAAAAGCAATGTTGCTACCTGCTACTAACAACATGATGTGATAGTTATGCT 563
QY 523 TATAAGCTATTATCTATGTTATGTTAGTTTGGTAAATTAATAAGATCATCATATATG 582
DB 564 AGCTAGCTATAACATAAGCTGTCTGTGAGTGTGTGTATATTAATAAAGATCATCACTGG 623
QY 583 AATGTGTTGATCGTTTAACTAAGGCAAGCTTAGGTTATATGACCACTTTAGAGTGCTT 642
DB 624 TGAATGTTGATCGTTGATACCTTACTTAGTAGGCAATGGAAGCACTTAGAGTGTGCTT 683
QY 643 T---TATGGCGTTGCTCTATGTTTGTGTCGACAGTTGTAAACCATCTTGAAT 693
DB 684 TGTGCATGGCTTGCCTCTGTTTGAGACCTTTTGTAAATGTTTCGAGTTTAAAT 737

RESULT 14
AAT86283
ID AAT86283 standard; cDNA; 777 BP.
AC AAT86283;
XX
XX
XX 08-APR-1998 (first entry)
XX Chimeric Soybean albumin 1/3 coding sequence.
XX
XX Soybean albumin 1; seed storage protein; SSP; transgenic seed;
KW transgenic soybean plant; animal feed production; chimeric protein; ss.
XX
XX Synthetic.
OS Glycine max.
XX
XX Key Location/Qualifiers
FH 28..504
FT CDS /*tag= a
XX
XX WO9735023-A2.
XX
XX 25-SEP-1997.
XX
XX 19-MAR-1997; 97WO-US004409.
XX
XX 20-MAR-1996; 96US-00618911.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Jung R, Hastings C, Coughlan S, Hu D;
XX
XX WPI; 1997-480228/44.
DR P-PSDB; AAW23420.
XX
XX Increasing the nutritional quality of soybean - by genetically increasing
PT the amount of lysine, methionine and/or cysteine in albumin proteins.
XX
XX Disclosure; Page 48-49; 62pp; English.
XX
XX This sequence represents the coding sequence for a chimeric soybean
CC albumin protein. This sequence was created from the albumin 1 and albumin
CC 3 sequences (see AAT86281 and AAT86282). This sequence represents a DNA
```

```
CC molecule of the invention. The DNA molecules of the invention comprise a
CC preselected DNA segment encoding a seed storage protein (SSP). (I) is
CC used to produce transgenic seeds and plants, especially soybean plants
CC that have increased levels of lysine and also increased levels of
CC methionine and/or cysteine in albumin protein type 1 and/or 3. Increasing
CC the levels of these amino acids increases the nutritional value of
CC soybean produced. This is especially useful for producing animal feeds.
CC The amount of lysine in the seed is increased by 5-10 %, the amount of
CC methionine and cysteine is increased by 10-30%
XX
SQ Sequence 777 BP; 253 A; 157 C; 197 G; 170 T; 0 U; 0 Other;

Query Match 8.9%; Score 64; DB 2; Length 777;
Best Local Similarity 50.7%; Pred. No. 2.2e-06;
Matches 362; Conservative 0; Mismatches 310; Indels 42; Gaps 7;

QY 7 CATACTAGTAGCCCTCGCCCTTTTCTCTCTCGCTGCCAGCCATCTCGAGGAGCAGAGTG 66
DB 39 CACAATCCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 98
QY 67 GGAACTCCAAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGCGGCAACCTGAGGCCCTG 126
DB 99 GCAGCACACAGCAAGA---TAGCTGCCGCAAGCAGCTTTAAGGGGTGAACCTCAGCCCTG 155
QY 127 CGAGCAACATCTCATGACAGAAGATCCAAACGTGACGAGGATTCATATGAACGGACCCGTA 186
DB 156 CGAGAAGCACATCATGGAGAAGATCCAAAGCCGCGCGATGACGATGATGATGACGA 215
QY 187 CAGC-----CCTAGTCAGGATCCGTACAGCCCTTAGTCCATATGATCGGAGAGG----- 234
DB 216 CGACAATCATCTTCTCAGGACCATGCGGGAAGAATCACTACATACGTAAAGAGGAAG 275
QY 235 -----CGCTGGATCTCTCTCAGCAACCAAGAGAGGTGTTGCAATCAGCTGAACGA 282
DB 276 AAAAGACGAAGACGAAGAGAGAGAGACAGATGCGAAGAGTGTGCGACAGAATATGCGA 335
QY 283 GTTTGAGAACAAACAAAGGTGCATGTGCGAGGCATTTGCAACAGATCATTGAGAACCCAGAG 342
DB 336 GCTTAAAGAGCCCCAAA---TGCCAGTGCAAAGCGCTGCAGAAGATATGCGAAGAACCA 392
QY 343 CGATAGTTGTCAGGGAGGCAACAGAGACACAGTTCAAGAGGGAGCTCAGGAACCTTGCC 402
DB 393 CGAGGAACCTGGAGGAGAGGAGAACAAAGAAA---ATGGAGAAGGAGCTTATGAACCTTGC 449
QY 403 TCAACAGTGGCGCTTAGGCGCACACAGCGTTGCGACTTGGAGCTCGAAGAGTGGCGGCGAG 462
DB 450 TACTATGTGAGGTTTGGGCCCATGATCGGATCGGACTTGTCTCCGA-----TGACTA 503
QY 463 AGACAGATATAACACACCTATCTCAAAAAAGAAAAGAAAAGAAAAGAAAATAGCTTATA 522
DB 504 AGAAGTTAAAAGCAATGTTGTCACCTTGTACGTACTAACACATGATGTGATGTTATGCT 563
QY 523 TATAAGCTATTATCTATGTTATGTTAGTTTGGTAAATTAATAAGATCATCATATATG 582
DB 564 AGCTAGCTATAACATAAGCTGTCTCTGAGTGTGTGTATATTAATAAAGATCATCACTGG 623
QY 583 AATGTGTTGATCGTTTAACTAAGGCAAGCTTAGGTTATATGACCACTTTAGAGTGCTT 642
DB 624 TGAATGTTGATCGTTGATACCTTACTTAGTAGGCAATGGAAGCACTTAGAGTGTGCTT 683
QY 643 T---TATGGCGTTGCTCTATGTTTGTGTCGACAGTTGTAAACCATCTTGAAT 693
DB 684 TGTGCATGGCTTGCCTCTGTTTGAGACCTTTTGTAAATGTTTCGAGTTTAAAT 737

RESULT 15
AAX25346
ID AAX25346 standard; cDNA; 770 BP.
XX
XX AAX25346;
AC AAX25346;
XX
XX 19-JUL-1999 (first entry)
DT
XX
```



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 3685.01 Seconds  
(without alignments)  
10880.347 Million cell updates/sec

Title: US-10-728-051-2

Perfect score: 717

Sequence: 1 gtcaccatactagtagcccc.....taaaagatcatgttttgg 717

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_est7:\*
- 7: gb\_est8:\*
- 8: gb\_est9:\*
- 9: gb\_est10:\*
- 10: gb\_est11:\*
- 11: gb\_est12:\*
- 12: gb\_est13:\*
- 13: gb\_est14:\*
- 14: gb\_est15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	686.4	95.7	788	4	CD038434	CD038434 UTPPI007
2	666	92.9	689	4	CD038213	CD038213 UTPPI004
3	555.2	77.4	732	4	CD038384	CD038384 UTPPI006
4	524	73.1	524	8	CO897505	CO897505 EST000010
5	487.8	68.0	634	4	CD038323	CD038323 UTPPI005
6	315	43.9	405	4	CD038306	CD038306 UTPPI005
7	289	40.3	308	4	CD038459	CD038459 UTPPI007
8	283.4	39.5	375	8	CO897504	CO897504 EST000009
9	223.8	31.2	696	4	CD038415	CD038415 UTPPI006
10	215.2	30.0	732	4	CD038394	CD038394 UTPPI006
11	208.8	29.1	661	4	CD038326	CD038326 UTPPI005
12	147.8	20.6	255	13	C2550856	C2550856 02S0166-0
13	143.4	20.0	211	8	CO897508	CO897508 EST000013
14	137.6	19.2	286	8	CO897506	CO897506 EST000011
15	133.2	18.6	680	4	CD038092	CD038092 UTPPI002
16	131.8	18.4	351	8	CO897507	CO897507 EST000012
17	129.6	18.1	714	4	CD038841	CD038841 UTPPI012
18	86	12.0	638	10	DT454366	DT454366 UWA065 cd
19	86	12.0	638	10	DT454367	DT454367 UWA066 cd

20	81	11.3	290	8	CO897509	CO897509 EST000014
21	71.6	10.0	659	8	CN825259	CN825259 LjPEST4f3
22	67.6	9.4	305	4	CD038103	CD038103 UTPPI002
23	65.8	9.2	445	7	BF594963	BF594963 su74h01.y
24	63	8.8	719	7	BE661358	BE661358 442 GnaXS
25	62.6	8.7	707	7	BE658140	BE658140 GM700005A
26	62.4	8.7	479	2	BG237204	BG237204 saa98a03.y
27	60.6	8.5	504	1	AJ498204	AJ498204 AJ498204
28	59.8	8.3	468	1	AI960869	AI960869 sc91g03.y
29	59.2	8.3	469	7	AW279501	AW279501 ef50d06.y
30	59.2	8.3	469	7	AW318110	AW318110 sg60e10.y
31	59.2	8.3	471	7	AW318155	AW318155 sg61b03.y
32	59.2	8.3	474	7	AW318193	AW318193 sg62c02.y
33	59.2	8.3	475	7	AW395515	AW395515 sg72b07.y
34	59.2	8.3	475	7	AW395679	AW395679 sg73h12.y
35	59.2	8.3	475	7	AW398039	AW398039 sg71d12.y
36	59.2	8.3	477	1	AI759696	AI759696 sb62h10.y
37	59.2	8.3	479	7	BF595027	BF595027 su74e01.y
38	59.2	8.3	479	7	AW395742	AW395742 sg74g08.y
39	59.2	8.3	481	7	AW396869	AW396869 sg64c10.y
40	59.2	8.3	482	7	AW397141	AW397141 sg67d07.y
41	59.2	8.3	486	1	AI941225	AI941225 sb66b06.y
42	59.2	8.3	487	7	AW397497	AW397497 sg79f01.y
43	59.2	8.3	489	7	BF596512	BF596512 su72c09.y
44	59.2	8.3	490	1	AI748087	AI748087 sb48a09.y
45	59.2	8.3	490	7	AW397370	AW397370 sg78a09.y

ALIGNMENTS

RESULT 1  
LOCUS CD038434 788 bp mRNA linear EST 07-MAY-2003  
DEFINITION UTPPI007 C04 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
ACCESSION CD038434  
VERSION CD038434.1 GI:30420272  
KEYWORDS EST.  
SOURCE Arachis hypogaea (peanut)  
ORGANISM Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.  
REFERENCE 1 (bases 1 to 788)  
AUTHORS Luo M., Dang P., Guo B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.  
and Lynch, R.E.  
TITLE Generation and Analyses of ESTs for Arachis hypogaea  
JOURNAL Unpublished (2003)  
COMMENT Contact: Baozhu Guo  
Molecular Genetics  
USDA/ARS, Crop Protection and Management Research Unit  
2747 Davis Rd., Tifton, GA 31794, USA  
Tel: 229-387-2334  
Fax: 229-387-2321  
Email: bguo@tifton.usda.gov  
Seq primer: T3.  
FEATURES  
source Location/Qualifiers  
1..788  
/organism="Arachis hypogaea"  
/mol\_type="mRNA"  
/cultivar="A13"  
/db\_xref="taxon:3818"  
/clone="UTPP1007\_C04"  
/tissue\_type="Immature pods"  
/dev\_stage="R6"  
/lab\_host="XL1-blue"  
/clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"  
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;  
cDNA library was constructed from peanut cultivar A13;  
(NCV11XAR4). A13 has resistance to Aspergillus infection

and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 95.7%; Score 686.4; DB 4; Length 788;  
Best Local Similarity 99.7%; Pred. No. 6.7e-160;  
Matches 698; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 GCTCACCATACTAGTAGCCCTCCCTTTCTCTCGCTGCCACGCGCATCTGCCGAGGCA 60  
DB 90 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACGCGCATCTGCCGAGGCA 149  
QY 61 GCAGTGGGAACCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGTAG 120  
DB 150 GCAGTGGGAACCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGTAG 209  
QY 121 GCCTCGGAGCACATCTCATGCAGAGATCCAACTGACGAGGATTCATATGAACGGGA 180  
DB 210 GCCTCGGAGCACATCTCATGCAGAGATCCAACTGACGAGGATTCATATGAACGGGA 269  
QY 181 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGGCGCTGG 240  
DB 270 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGGCGCTGG 329  
QY 241 ATCCTCTCAGCACCAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300  
DB 330 ATCCTCTCAGCACCAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 389  
QY 301 GTGCATGTCGAGGCACTTCAACAGATCATGGAGAACCGAGCGATAGTTGCAGGGGAG 360  
DB 390 GTGCATGTCGAGGCACTTCAACAGATCATGGAGAACCGAGCGATAGTTGCAGGGGAG 449  
QY 361 GCAACAGGAGCAACAGTTTCAAGAGGGAGCTCAGGAACCTTGCCCTCAACAGTGGCGCTTAG 420  
DB 450 GCAACAGGAGCAACAGTTTCAAGAGGGAGCTCAGGAACCTTGCCCTCAACAGTGGCGCTTAG 509  
QY 421 GGCACACAGCGTTGCGACTTGACGCTGAAAGTGGCGGAGAGACAGATATAACACC 480  
DB 510 GGCACACAGCGTTGCGACTTGACGCTGAAAGTGGCGGAGAGACAGATATAACACC 569  
QY 481 TATCTCAAAAAAGAAAGAAAGAAAGAAATAGCTTATATATAGCTATTATCTATG 540  
DB 570 TATCTCAAAAAAGAAAGAAAGAAAGAAATAGCTTATATATAGCTATTATCTATG 629  
QY 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGATGTTGATCGTGTAA 600  
DB 630 GTTATG-TTAGTTTGGTAAATAAAGATCATCACTATATGATGTTGATCGTGTAA 688  
QY 601 ACTAAGCGAAGCTTAGGTTATATGAGCAGCTTTAGAGTGCTTTATGGCGTGTCTATGT 660  
DB 689 ACTAAGCGAAGCTTAGGTTATATGAGCAGCTTTAGAGTGCTTTATGGCGTGTCTATGT 748  
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATATAA 700  
DB 749 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATATAA 788

RESULT 2  
CD038213

LOCUS CD038213 689 bp mRNA linear EST 07-MAY-2003  
DEFINITION UTPI004 A09 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
Arachis hypogaea cDNA clone UTPI004\_A09 5', mRNA sequence.  
ACCESSION CD038213  
VERSION CD038213.1 GI:30420051  
KEYWORDS EST.  
SOURCE Arachis hypogaea (peanut)  
ORGANISM Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschomeneae; Arachis.  
1 (bases 1 to 689)  
REFERENCE Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.  
and Lynch,R.E.  
Generation and Analyses of ESTs for Arachis hypogaea  
Unpublished (2003)  
CONTACT: Baozhu Guo  
Molecular Genetics  
USDA/ARS, Crop Protection and Management Research Unit  
2747 Davis Rd., Tifton, GA 31794, USA  
Tel: 229-387-2334  
Fax: 229-387-2321  
Email: bguo@tifton.usda.gov  
Seq primer: T3.  
Location/Qualifiers  
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/cultivar="A13"  
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/clone="UTPI004\_A09"  
/tissue\_type="Immature pods"  
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/lab\_host="XL1-blue"  
/clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"  
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;  
cDNA library was constructed from peanut cultivar A13;  
(NCV1XAR4). A13 has resistance to Aspergillus infection  
and drought tolerance. The immature pods that developed to  
R6 stage were collected from different plants, and placed  
into liquid N2 immediately and stored in -80oC freezer.  
Total RNA was isolated with TRIzol-Reagent  
ultrapure(GIBCOBRL). mRNA was extracted and purified from  
total RNA (Promega). cDNA synthesis and library  
construction followed the protocol of by ZAP-cDNA Gigapack  
III Gold cloning kit (Stratagene). The cDNA above 500bp  
were collected after size-fraction. The inserts were  
directionally cloned into Uni-ZAP XR vector using XhoI  
EcoRI sites adapters. The lambda library was packed into  
phages using Gigapack III Gold (Stratagene). The  
un-amplified library was used to excise pBluescript  
phagemids from the Uni-ZAP XR vector, and the phagemids  
was used to transform the host bacteria SOLR. The library  
was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 92.9%; Score 666; DB 4; Length 689;  
Best Local Similarity 99.6%; Pred. No. 8e-155;  
Matches 677; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 38 GCTGCCCGCCGATCTCGAGGCGAGCTGGGAATCCAAAGGAGACAGAAGATGCCGAGC 97  
DB 1 GCTGCCCGCCGATCTCGAGGCGAGCTGGGAATCCAAAGGAGACAGAAGATGCCGAGC 60  
QY 98 CAGCTCGAGAGGGCGAACCTGAGGGCCCTCGAGCAACATCTCATGAGAAGATCCAAAGCT 157  
DB 61 CAGCTCGAGAGGGCGAACCTGAGGGCCCTCGAGCAACATCTCATGAGAAGATCCAAAGCT 120  
QY 158 GACGAGGATTTCATATGAACGGGACCCGCTACAGCCCTAGTCAGGATCCGTCAGCCCTACT 217  
DB 121 GACGAGGATTTCATATGAACGGGACCCGCTACAGCCCTAGTCAGGATCCGTCAGCCCTACT 180

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Qy 218 CCATATGATCGAGAGCGCTGGATCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTG 277
Db 181 CCATATGATCGAGAGCGCTGGATCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTG 240
Qy 278 AACGAGTTTGAGAACACCAACCAAGGTGATGTCGAGGAGGTGCAACAGATCATGGAAAC 337
Db 241 AACGAGTTTGAGAACACCAACCAAGGTGATGTCGAGGAGGTGCAACAGATCATGGAAAC 300
Qy 338 CAGAGCGATAGTTGTCAGGGGAGGCAACAGAGCAACAGATGTTCAAGAGGGAGCTCAGGAAC 397
Db 301 CAGAGCGATAGTTGTCAGGGGAGGCAACAGAGCAACAGATGTTCAAGAGGGAGCTCAGGAAC 360
Qy 398 TTGCTCTCAACAGTCGCGCTTAGGGCACCAACAGCGTTTGCAGCTTGGAGCTGGAAGTGGC 457
Db 361 TTGCTCTCAACAGTCGCGCTTAGGGCACCAACAGCGTTTGCAGCTTGGAGCTGGAAGTGGC 420
Qy 458 GGCAGACAGACATTAACACCTATCTCAAAAAAGAAAGAAAGAAAGAAAGAAATAGC 517
Db 421 GGCAGACAGACATTAACACCTATCTCAAAAAAGAAAGAAAGAAAGAAAGAAATAGC 480
Qy 518 TTATATTAAGCTATTATCTATGCTTATGTTTATGTTTGGTAAATAAAGATCATCACT 577
Db 481 TTATATTAAGCTATTATCTATGCTTATGTTTATGTTTGGTAAATAAAGATCATCACT 539
Qy 578 ATATGAATGTGTTGATCGTGTAACTAAGCAAGCTTAGGTTATATGAGCACCTTTTAGAG 637
Db 540 ATATGAATGTGTTGATCGTGTAACTAAGCAAGCTTAGGTTATATGAGCACCTTTTAGAG 599
Qy 638 TGCTTTTATGCGTGTCTATGTTTGTGCTGAGAGTGTGAACCATCTTGAATAATA 697
Db 600 TGCTTTTATGCGTGTCTATGTTTGTGCTGAGAGTGTGAACCATCTTGAATAATA 659
Qy 698 TAAAGATCATGTTTTGTT 717
Db 660 TAAAGATCATGTTTTGTT 679
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RESULT 3
LOCUS CD038384
DEFINITION 732 bp mRNA linear EST 07-MAY-2003
UTPPI006_E02 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPPI006_E02 5', mRNA sequence.
CD038384
CD038384.1 GI:30420222
EST.
Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 732)
Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.
and Lynch, R. E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3
Location/Qualifiers
1..732
/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPPI006_E02"
/tissue_type="Immature pods"
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/lab_host="XL1-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
/notes="vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI;
cDNA library was constructed from peanut cultivar A13
(NCv1XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adaptors. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
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## ORIGIN

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Query Match 77.4%; Score 555.2; DB 4; Length 732;
Best Local Similarity 93.1%; Pred. No. 3.3e-127;
Matches 617; Conservative 0; Mismatches 9; Indels 37; Gaps 2;
Qy 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACCGATCTGCGAGCA 60
Db 70 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACCGATCTGCGAGCA 129
Qy 61 GCAGTGGAACTCCAAGGACAGAGATCCAGAGCCAGCTCGAGAGGGCGAACCTGAG 120
Db 130 GCAGTGGAACTCCAAGGACAGAGATCCAGAGCCAGCTCGAGAGGGCGAACCTGAG 189
Qy 121 GCCCTGCGAGCAACATCTCATGCGAAGATCCAAAGTGCAGGAGGATTCATATGAACGGA 180
Db 190 GCCCTGCGAGCAACATCTCATGCGAAGATCCAAAGTGCAGGAGGATTCATATGAACGGA 249
Qy 181 CCGGTACAGCCCTAGTCAG-----GATCC 204
Db 250 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCAGGAGCCCGGACAGAGCTGATCC 309
Qy 205 GTACAGCCCTAGTCATATGATCGAGAGCGCTGGATCTCTCAGCACCAAGAGAGGTG 264
Db 310 GTACAGCCCTAGTCATATGATCGAGAGCGCTGGATCTCTCAGCACCAAGAGAGGTG 369
Qy 265 TTGCAATGAGCTGAACGAGTTTGAGAACCAACAAAGTGCATGTGCGAGGCATTTGCAACA 324
Db 370 TTGCAATGAGCTGAACGAGTTTGAGAACCAACAAAGTGCATGTGCGAGGCATTTGCAACA 429
Qy 325 GATCATGGAGAACCAAGCGATAGTTGCGAGGAGGCAACAGAGCAACAGTTCAAGAG 384
Db 430 GATAATGGAGAACCAAGCGATAGTTGCGAGGAGGCAACAGAGCAACAGTTCAAGAG 489
Qy 385 GGAGCTCAGGAACCTGCTCAACAGTCGCGCTTAGGGACCAACAGAGCTTGGACTTGA 444
Db 490 GGAGCTCAGGAACCTGCTCAACAGTCGCGCTTAGGGACCAACAGAGCTTGGACTTGA 549
Qy 445 CGTCTGAAAGTGGCGGAGACAGATACATAAACACCTATCTCAAAAAAGAAAGAAAG 504
Db 550 AGTCGAAAGTGGCGGAGACAGATACATAAACACCTATCTCAAAAAAGAAAGAAAG 609
Qy 505 AAAAGAAATAGCTTATATATAAGCTATTATCTATGTTATGTTTGGTAAATAT 564
Db 610 AAAAGAAATAGCTTATATATAAGCTATTATCTATGTTATGTTTGGTAAATAT 668
Qy 565 AAAGATCATCACTATATGAATGTTGATCGTGTAACTAAGCAAGCTTAGGTTATATG 624
Db 669 AAAGATCATCACTATATGAATGTTGATCGTGTAACTAAGCAAGCTTAGGTTATATG 728
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[illegible]

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.

REFERENCE  
AUTHORS  
1 (bases 1 to 308)  
Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G. and Lynch, R. E.

TITLE  
JOURNAL  
COMMENT  
Generation and Analyses of ESTs for Arachis hypogaea  
Unpublished (2003)  
Contact: Baozhu Guo

Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd. Tifton, GA 31794, USA

Tel: 229-387-2334

Fax: 229-387-2321

Email: bguo@tifton.usda.gov

Seq primer: T3.

FEATURES

source

1..308

/organism="Arachis hypogaea"

/mol\_type="mRNA"

/cultivar="A13"

/db\_xref="taxon:3818"

/clone="UTPPI007\_F09"

/tissue\_type="Immature pods"

/dev\_stage="R6"

/lab\_host="XLI-blue"

/clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"

/notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapur (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

# ORIGIN

Query Match 40.3%; Score 289; DB 4; Length 308;  
Best Local Similarity 99.7%; Pred. No. 6e-61;  
Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 417 TTAGGCGCACACGCTTGCGACTTGGACCTCGAAAGTGGCGGACAGACAGATCTAAA 476

DB 1 TTAGGCGCACACGCTTGCGACTTGGACCTCGAAAGTGGCGGACAGACAGATCTAAA 60

QY 477 CACCTATCTCAAAAAGAAAAGAAAAGAAAATAGCTTTATATATAGCTATTATC 536

DB 61 CACCTATCTCAAAAAGAAAAGAAAAGAAAATAGCTTTATATATAGCTATTATC 120

QY 537 TATGGTTATGTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTGTCGT 596

DB 121 TATGGTTATG-TTATGTTTGGTAAATAAAGATCATCACTATATGAATGTGTGTCGT 179

QY 597 GTTAACTAAGCAAGCTTAGCTTATATAGCACCTTTAGAGTGCCTTTATGGCGTGTCT 656

DB 180 GTTAACTAAGCAAGCTTAGCTTATATAGCACCTTTAGAGTGCCTTTATGGCGTGTCT 239

QY 657 ATGTTTTGTTGCTGCAGAGTTGTAAACCATCTTGAATAATATAAAGATCATGTTTGT 716

DB 240 ATGTTTTGTTGCTGCAGAGTTGTAAACCATCTTGAATAATATAAAGATCATGTTTGT 299

QY 717 T 717

DB 300 T 300

## RESULT 8

CO897504

LOCUS

DEFINITION

EST00009 Peanut Lambda Express Library Arachis hypogaea cDNA 5',

mRNA sequence.

ACCESSION

CO897504

VERSION

CO897504.1 GI:51237294

KEYWORDS

EST.

SOURCE

Arachis hypogaea (peanut)

ORGANISM

Arachis hypogaea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.

REFERENCE

1 (bases 1 to 375)

Yan, Y.S., Wang, L., Zhong, Y.J. and Huang, S.Z.

Expressed sequence tags of mid-matured cotyledons of peanut

Unpublished (2004)

JOURNAL

COMMENT

Contact: Shangzhi Huang

Plant Development and Molecular Biology

Sun Yat-sen University, Department of Biology and Biotechnology

Guangzhou, 510275, China

Tel: (860)02084036592

Email: YYS9803@yahoo.com.cn

Seq primer: pTriplex2 Forward.

FEATURES

source

1..375

/organism="Arachis hypogaea"

/mol\_type="mRNA"

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/db\_xref="taxon:3818"

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/lab\_host="E.coli SM25.8"

/clone\_lib="Peanut Lambda Express library"

/notes="Organ: Seed; Vector: lambdaTriplex2"

ORIGIN

Query Match 39.5%; Score 283.4; DB 8; Length 375;

Best Local Similarity 88.8%; Pred. No. 1.5e-59;

Matches 333; Conservative 0; Mismatches 6; Indels 36; Gaps 1;

QY 103 CGAGAGGGCGAACCTGAGGCCCTGCCAGCAACATCTCATGAGAAGATCCAACTGACGA 162

DB 1 CGAGAGGGCGAACCTTAGGCCCTGCCAGCAACATCTCATGAGAAGATCCAACTGACGA 60

QY 163 GGATTCAATGAACGGGACCCGTACAGCCCTAGTCAG----- 199

DB 61 GGATTCAATGAACGGGACCCGTACAGCCCTAGTCAGCCCTAGTCAGGA 120

QY 200 -----GATCCGTACAGCCCTAGTCAGCCCTAGTCAGCCCTAGTCAGGA 246

DB 121 CCAGGACAGACGTGATCCGTACAGCCCTAGTCAGCCCTAGTCAGCCCTAGTCAGGA 180

QY 247 TCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACAAAGGTGCAT 306

DB 181 TCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACAAAGGTGCAT 240

QY 307 GTCGAGGCATTCGAAACAGATCATGGAGAACCGAGCGATAGTTGCAGGGGGGCAACA 366

DB 241 GTCGAGGCATTCGAAACAGATCATGGAGAACCGAGCGATAGTTGCAGGGGGGCAACA 300

QY 367 GGAGCAACAGTTCAAGAGGGAGCTCAGGAATCTTGCCTCAACAGTGCAGCCCTTAGGGCACC 426

DB 301 GGAGCAACAGTTCAAGAGGGAGCTCAGGAATCTTGCCTCAACAGTGCAGCCCTTAGGGCACC 360

QY 427 ACAGCGTTGCGACTT 441



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Db      361  ACAGCGTTGGCACTT 375
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RESULT 9
CD038415 696 bp mRNA linear EST 07-MAY-2003
LOCUS
DEFINITION
  Arachis hypogaea cDNA clone UTPPI006_H11 5', mRNA sequence.
ACCESSION
CD038415
VERSION
CD038415.1 GI:30420253
KEYWORDS
SOURCE
  Arachis hypogaea (peanut)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
  Aeschynomeneae; Arachis.
REFERENCE
  1 (bases 1 to 696)
  Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
  and Lynch,R.E.
  Generation and Analyses of ESTs for Arachis hypogaea
  Unpublished (2003)
  Contact: Baozhu Guo
  Molecular Genetics
  USDA/ARS, Crop Protection and Management Research Unit
  2747 Davis Rd., Tifton, GA 31794, USA
  Tel: 229-387-2334
  Fax: 229-387-2321
  Email: bguo@tifton.usda.gov
  Seq primer: T3.
  Location/Qualifiers
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    (UTPP)"
  /notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
  cDNA library was constructed from peanut cultivar A13
  (NCV11X94). A13 has resistance to Aspergillus infection
  and drought tolerance. The immature pods that developed to
  R6 stage were collected from different plants, and placed
  into liquid N2 immediately and stored in -80oC freezer.
  Total RNA was isolated with TRIzol-Reagent
  ultrapur (GIBCOBRL). mRNA was extracted and purified from
  total RNA (Promega). cDNA synthesis and library
  construction followed the protocol of By ZAP-cDNA Gigapack
  III Gold cloning kit (Stratagene). The cDNA above 500bp
  were collected after size-fraction. The inserts were
  directionally cloned into Uni-ZAP XR vector using XhoI
  EcoRI sites adapters. The lambda library was packed into
  phages using Gigapack III Gold (Stratagene). The
  un-amplified library was used to excise pBluescript
  phagemids from the Uni-ZAP XR vector, and the phagemids
  was used to transform the host bacteria SOLR. The library
  was constructed by Dr. Meng Luo and Dr. Phat Dang."

FEATURES
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ORIGIN
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Query Match 31.2%; Score 223.8; DB 4; Length 696;
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Matches 346; Conservative 0; Mismatches 107; Indels 28; Gaps 3;

Qy      219  CATATGTCGAGAGCGGTGGATCTCTCAGCAACCAAGAGAGGTGTTCGATGAGCTGA 278
Db      234  CCTACGATATTAGGAGTACTCGATCTCCGACCACCAAGAGAGGTGTTCGATGAGCTGA 293
Qy      279  ACGAGTTTGAGAACCAACCAAGGTGCATGTGCGAGGCATTTGCAACAGATCATGGGAACC 338
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Db      294  ACAGATGGAGAACACACAGAGATGCATGTGCGAGGCATTTGCAGCAGATAATGGGAACC 353
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Qy      399  TGCCTCAACAGTGGCGCTTTAGGGCCACACAGCGTTTCGCGACTTTGGACGTGCAAAAGTGGCG 458
Db      414  TGCCCCAACAGTGAACCTTTAGGGCCACACAGCGTTTCGCGATTTGGACGT-----GA 464
Qy      459  GCAGAGACAGATACATAACACCTATCTCAAAAAAAGAAAAAGAAAAAGAAAAAATAGCT 518
Db      465  GTGGCGCAGATGCTAGACTCAAAAAATAATACTGTGCCCCAACAACTAGTAGGAAGT 524
Qy      519  TATATATAGCTATTATCTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTT 578
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Qy      579  TATGAATGTGTTGATCGTGTAACTAAGCAAGCTTAGGTTATATGAGCACCTTTAGAGT 638
Db      578  TATGAATGTGTTGAT-----AGTAGTAAGTTATATGAGCCCCCTTCGGTGT 625
Qy      639  GCTTTTATGCGTTGTCTATGTTTGTGCTGCAGAGTTGTAACCATCTTTGAAATAATAT 698
Db      626  GCTCTTATGCGTTTACCTGTGTTTGTCTACTGCAAAAGTTTAAACCACCATGAAATAAAAG 685
Qy      699  A 699
Db      686  A 686

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283	Qy	GAGATGCATGTGCGAGGCATTGCGACAGATTAATGAGGAACAGTCGCTAGTGTTCGAGCA	342
358	Qy	GAGGCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTTGCCCTCAACAGTCGGCGCT	417
343	Db	CAGGCAAAATGTTGCAGCAGTTTCAAGAGAGAGCTCATGAACTTTGCTTCAACAGTGTAACTT	402
418	Qy	TAGGGCACCAAGCGTTTCGCACTTGGACGTTCGAAAGTGGCGGCAGAGACAGATACCTAAAC	477
403	Db	CAGGGCACCAAGCGTTTCGCACTTGGACGT-----GAGTGGCGGCAGATGCTAGAC	453
478	Qy	ACCTATCTCAAAAAAGAAAAGAAAAGAAAAGAAATAGCTTATATATAAGCTATTATCT	537
454	Db	TCAAAAATAATAATCTGTGTCAAAAGAAACCTAGTAGGAAGTAGCTTTATGAGCTATTATGT	513
538	Qy	ATGGTTATGTTTGGTTTTGGTAAATAATAAAGATCATCACTATATGAATGTGTGATCGTG	597
514	Db	ATGCTT-----GTTTCGTTAATAATAATAATCATCACTGTATGAAATGTGGTGAAT	562
598	Qy	TTAACTAAGGCAAGCTTAGGTTATATAGCACCTTTTAGAGTGCCTTTATGCGGTTGTCTTA	657
563	Db	-----AGGTAAGTTATATAGCA-C TTCGGTGTCTCTTATGGCTTTACCTA	609
658	Qy	TGTTTTGTGTGCAGAGTTGTAACCATCTTCTGAAATAATATA	699
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[illegible]

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Class: transposon insertion site.
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                    /clone_lib="UniformMu MutAIL Library"
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                    the Mu terminal inverted repeat and a set of 16 arbitrary
                    primers. Amplicons were size enriched using Sepharose 400
                    spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
    Query Match      20.6%; Score 147.8; DB 13; Length 255;
    Best Local Similarity 83.9%; Pred. No. 1.1e-24;
    Matches 162; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

ORIGIN
    QY      267  GCAATGAGCTGAACGAGTTTGAGAACCAACCAAGGTGCATGTGCGAGGCATTGCAACAGA 326
    Db      11  GCGATGAGCTGAACGAGATGGAGAACACACAGAGATGCATGTGCGAGGCATTGCGAGCAGA 70
    QY      327  TCATGAGAAACACAGAGCGATAGTTGTCAGGGGAGGCAACAGGTCAGTTCGAAGAGG 386
    Db      71  TAATGGAGNACAGTGCATAGTTGTCAGGACAGGCAATGTCGACGAGTCGTCGAAGAG 130
    QY      387  AGCTCAGGAACCTTGCTCTCAACAGTCCGGCCCTTAGGGCACACAGCGTTGCGACTTGGACG 446
    Db      131  AGCTCATGAACCTTGCCCAACAGTGAACCTTTAGGGCACACAGCGTTGCGACTTGGACG 190

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## ORIGIN

### Query Match

20.6%; Score 147.8; DB 13; Length 255;

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QY      447 TCGAAAGTGGCGG 459
Db      191 TGAGTGGCGGCG 203

RESULT 14
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LOCUS   EST000011 Peanut Lambda Express library Arachis hypogaea cDNA 5',
DEFINITION
ACCESSION CO897506
VERSION   CO897506.1 GI:51237296
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SOURCE    Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
          Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 286)
AUTHORS  Yan,Y.S., Wang,L., Zhong,Y.J. and Huang,S.Z.
TITLE    Expressed sequence tags of mid-matured cotyledons of peanut
JOURNAL  Unpublished (2004)
COMMENT  Contact: Shanghai Huang
          Plant Development and Molecular Biology
          Sun Yat-sen University, Department of Biology and Biotechnology
          Guangzhou, 510275, China
          Tel: (860)02084036592
          Email: yys9803@yahoo.com.cn
          Seq primer: pTriplex2 Forward.
FEATURES             Location/Qualifiers
     source           1..286
                     /organism="Arachis hypogaea"
                     /mol_type="mRNA"
                     /cultivar="Yueyou 523"
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Best Local Similarity 80.5%; Pred. No. 3.1e-23;
Matches 161; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY      219 CATATGATCGGAGGCGCTGGATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGA 278
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QY      399 TGCCTCAACAGTGGGCTT 418
Db      267 TGCCCCAACAGTGTAACTTT 286

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DEFINITION
ACCESSION CD038092
VERSION   CD038092.1 GI:30419930
KEYWORDS EST.

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ORGANISM Arachis hypogaea
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
          Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 286)
AUTHORS  Yan,Y.S., Wang,L., Zhong,Y.J. and Huang,S.Z.
TITLE    Expressed sequence tags of mid-matured cotyledons of peanut
JOURNAL  Unpublished (2004)
COMMENT  Contact: Shanghai Huang
          Plant Development and Molecular Biology
          Sun Yat-sen University, Department of Biology and Biotechnology
          Guangzhou, 510275, China
          Tel: (860)02084036592
          Email: yys9803@yahoo.com.cn
          Seq primer: pTriplex2 Forward.
FEATURES             Location/Qualifiers
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                     /note="Organ: Seed; Vector: lambdaTriplex2"

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Best Local Similarity 80.5%; Pred. No. 3.1e-23;
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QY      219 CATATGATCGGAGGCGCTGGATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGA 278
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Db      207 AGTGCATAGTTGCGAGGAGGCAATGTTGCGAGCAGTTCAAGAGAGAGCTCATGAAC 266

QY      399 TGCCTCAACAGTGGGCTT 418
Db      267 TGCCCCAACAGTGTAACTTT 286

SOURCE
ORGANISM Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 680)
AUTHORS  Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
          and Lynch,R.E.
TITLE    Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL  Unpublished (2003)
COMMENT  Contact: Baozhu Guo
          Molecular Genetics
          USDA/ARS, Crop Protection and Management Research Unit
          2747 Davis Rd., Tifton, GA 31794, USA
          Tel: 229-387-2334
          Fax: 229-387-2321
          Email: bguo@tifton.usda.gov
          Seq primer: T3
          Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="A13"
                     /db_xref="taxon:3818"
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                     /tissue_type="Immature pods"
                     /dev_stage="R6"
                     /lab_host="XL1-blue"
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                     (UTPP)"
                     /note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
                     cDNA library was constructed from peanut cultivar A13
                     (NCVILX44). A13 has resistance to Aspergillus infection
                     and drought tolerance. The immature pods that developed to
                     R6 stage were collected from different plants, and placed
                     into liquid N2 immediately and stored in -80oC freezer.
                     Total RNA was isolated with TRIzol-Reagent
                     ultrapure(GIBCOBRL). mRNA was extracted and purified from
                     total RNA (Promega). cDNA synthesis and library
                     construction followed the protocol of by ZAP-cDNA Gigapack
                     III Gold cloning kit (Stratagene). The cDNA above 500bp
                     were collected after size-fraction. The inserts were
                     directionally cloned into Uni-ZAP XR vector using XhoI
                     EcoRI sites adapters. The lambda library was packed into
                     phages using Gigapack III Gold (Stratagene). The
                     un-amplified library was used to excise pBluescript
                     phagemids from the Uni-ZAP XR vector, and the phagemids
                     was used to transform the host bacteria SOLR. The library
                     was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN
Query Match      18.6%; Score 133.2; DB 4; Length 680;
Best Local Similarity 58.3%; Pred. No. 4.4e-22;
Matches 344; Conservative 0; Mismatches 213; Indels 33; Gaps 5;

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QY      196 TCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGGATCTCTCAGCACCA 255
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QY      316 ATTGCAACAGATCATGAGAACCAAGAGCGATAGTT---GCAGGGGAGGCAACAGGAGCA 372

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:43:18 ; Search time 111.753 Seconds  
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	717	100.0	717	3	US-09-191-593-6
3	717	100.0	717	3	US-09-191-593-9
4	713.8	99.6	743	3	US-09-106-872A-1
5	462	64.4	682	3	US-09-715-036-3
6	462	64.4	1162	3	US-09-715-036-1
7	80	11.2	80	3	US-09-715-036-7
8	65.6	9.1	777	2	US-08-618-911-3
9	64	8.9	777	2	US-08-618-911-5
10	63.4	8.8	770	3	US-08-938-675A-1
11	63.4	8.8	770	3	US-09-531-727-1
12	62	8.6	62	3	US-09-715-036-8
13	58.8	8.2	7218	2	US-08-232-463-14
14	54.4	7.6	723	2	US-08-618-911-1
15	48.4	6.8	25590	3	US-09-949-002-777
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17	44.4	6.2	168105	3	US-09-949-016-16554
18	44.4	6.2	1664976	3	US-08-916-421B-1
19	44.4	6.2	1664976	3	US-09-692-570-1
20	44.2	6.2	56655	3	US-09-949-016-14026
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22	43.6	6.1	601	3	US-09-949-016-44480
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ALIGNMENTS

RESULT 1  
US-09-106-872A-20  
; Sequence 20, Application US/09106872A  
; Patent No. 6486311  
; GENERAL INFORMATION:  
; APPLICANT: Burks Jr., A. Wesley  
; APPLICANT: Stanley, J. Steven  
; APPLICANT: Cockrell, Gael  
; APPLICANT: King, Nina E.  
; APPLICANT: Sampson, Hugh A.  
; APPLICANT: Helm, Ricki M.  
; APPLICANT: Bannan, Gary A.  
; TITLE OF INVENTION: Peanut Allergens and Methods  
; FILE REFERENCE: HS 103 CIP  
; CURRENT APPLICATION NUMBER: US/09/106, 872A  
; CURRENT FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: PCT/US96/15222  
; PRIOR FILING DATE: 1996-09-23  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 717  
; TYPE: DNA  
; ORGANISM: Atachis hypogaea  
US-09-106-872A-20  
  
Query Match 100.0%; Score 717; DB 3; Length 717;  
Best Local Similarity 100.0%; Pred. No. 1.1e-185;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GCTCACCATACTAGTAGCCCTCTTCCTCTCGCTGCCACGCATCTCGAGGCA 60  
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Db 181 CCGGTACGCCCTAGTCCAGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 240

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Qy	421	GGCACCACAGCGTTCGCACTTGGACGTCGAAAGTGGCGG	CAGACAGACAGATACTAAACACC	480	
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## RESULT 2

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; US-09-191-593-6  
; Sequence 6, Application US/09191593  
; Patent No. 6835824  
; GENERAL INFORMATION:  
; APPLICANT: BURKS, A Wesley, HELM, Ricki M,  
; APPLICANT: COCKRELL, Gael, STANLEY, J Steven,  
; APPLICANT: BANNON, Gary A.  
; TITLE OF INVENTION: PEANUT ALLERGENS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Head, Johnson & Kachigian  
; STREET: 112 W. Center St., Suite 230  
; CITY: Fayetteville  
; STATE: Arkansas AR  
; COUNTRY: United States of America  
; ZIP: 72701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 6.2  
; SOFTWARE: Wordperfect 6.0C  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/191,593  
; FILING DATE: 13 NOVEMBER 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/717,933  
; FILING DATE: 23 SEPTEMBER 1996  
; APPLICATION NUMBER: US 07/998,377  
; FILING DATE: 30 DECEMBER 1992  
; APPLICATION NUMBER: US 08/158,704  
; FILING DATE: 29 NOVEMBER 1993  
; APPLICATION NUMBER: US 60/009,455  
; FILING DATE: 29 DECEMBER 1995  
; APPLICATION NUMBER: US 08/610,424  
; FILING DATE: 04 MARCH 1996  
; ATTORNEY/AGENT INFORMATION:
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UNITS: No. 6835824 applicable  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..475  
IDENTIFICATION METHOD: By agreement with  
IDENTIFICATION METHOD: protein information and established  
IDENTIFICATION METHOD: consensus sequence  
OTHER INFORMATION: Seed storage protein and  
OTHER INFORMATION: allergen  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-09-191-593-6
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RESULT 3

US-09-191-593-9  
Sequence 9, Application US/09191593  
Patent No. 6835824  
GENERAL INFORMATION:  
APPLICANT: BURKS, A Wesley, HELM, Ricki M,  
APPLICANT: COCKRELL, Gael, STANLEY, J Steven,  
APPLICANT: BANNON, Gary A  
TITLE OF INVENTION: PEANUT ALLERGENS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Head, Johnson & Kachigian  
STREET: 112 W. Center St., Suite 230  
CITY: Fayetteville  
STATE: Arkansas AR  
COUNTRY: United States of America  
ZIP: 72701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS 6.2  
SOFTWARE: Wordperfect 6.0C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/191,593  
FILING DATE: 13 NOVEMBER 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/717,933  
FILING DATE: 23 SEPTEMBER 1996  
APPLICATION NUMBER: US 07/998,377  
FILING DATE: 30 DECEMBER 1992  
APPLICATION NUMBER: US 08/158,704  
FILING DATE: 29 NOVEMBER 1993

Query Match 100.0%; Score 717; DB 3; Length 717;  
Best Local Similarity 100.0%; Pred No. 1,1e-185;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGTGGCCACCGCATCTCGGAGGCA 60  
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APPLICATION NUMBER: US 60/009,455  
FILING DATE: 29 DECEMBER 1995  
APPLICATION NUMBER: US 08/610,424  
FILING DATE: 04 MARCH 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: ALEXANDER, DANIEL R  
REGISTRATION NUMBER: 32,604  
REFERENCE/DOCKET NUMBER: ARK00895601B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (501) 582-9111  
TELEFAX: (501) 521-4931  
TELEX: No. 6835824 applicable  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 717 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
DESCRIPTION: identified as Ara h II cDNA clone  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE: No. 6835824 applicable  
ORIGINAL SOURCE: Arachis hypogaea  
STRAIN: Florunner  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE: seed  
HAPLOTYPE: No. 6835824 applicable  
TISSUE TYPE: seed cDNA  
CELL TYPE: No. 6835824 applicable  
CELL LINE: No. 6835824 applicable  
ORGANELLE: No. 6835824 applicable  
IMMEDIATE SOURCE:  
LIBRARY: florunner seed cDNA expression  
LIBRARY: library in Uni-ZAP XR vector  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: No. 6835824 applicable  
MAP POSITION: No. 6835824 applicable  
UNITS: No. 6835824 applicable  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD: By agreement with  
IDENTIFICATION METHOD: protein information and established  
IDENTIFICATION METHOD: consensus sequence  
OTHER INFORMATION: Seed storage protein and  
OTHER INFORMATION: allergen  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-09-191-593-9



Query Match 64.4%; Score 462; DB 3; Length 682;  
Best Local Similarity 100.0%; Pred. No. 4.2e-116;  
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACCGCATCTGGAGGCA 60  
DB 67 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACCGCATCTGGAGGCA 126  
QY 61 GCAGTGGGAACTCCAAAGGAGACAGAAGATGCGAGAGCCAGCTCGAGAGGGCGAACTTGAG 120  
DB 127 GCAGTGGGAACTCCAAAGGAGACAGAAGATGCGAGAGCCAGCTCGAGAGGGCGAACTTGAG 186  
QY 121 GCCTGCGAGCAACATCTCATGCAAGAGATCCAAAGTGAAGAGATTCATATGAACGGGA 180  
DB 187 GCCTGCGAGCAACATCTCATGCAAGAGATCCAAAGTGAAGAGATTCATATGAACGGGA 246  
QY 181 CCGGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGAGCCGCTGG 240  
DB 247 CCGGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGAGCCGCTGG 306  
QY 241 ATCTCTCAGCACCACAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACAAACAAAG 300  
DB 307 ATCTCTCAGCACCACAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACAAACAAAG 366  
QY 301 GTGCATGTGCGAGGCAATTCGAACAGATCATGGAGAACAGAGCGATAGTTGCAGGGGAG 360  
DB 367 GTGCATGTGCGAGGCAATTCGAACAGATCATGGAGAACAGAGCGATAGTTGCAGGGGAG 426  
QY 361 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
DB 427 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 486  
QY 421 GGCAACACAGCGTTGCGACTTGGACGTGCAAAAGTGGCGGCGAG 462  
DB 487 GGCAACACAGCGTTGCGACTTGGACGTGCAAAAGTGGCGGCGAG 528

RESULT 6  
US-09-715-036-1  
; Sequence 1, Application US/09715036  
; Patent No. 6943010  
; GENERAL INFORMATION:  
; APPLICANT: DODO, HORTENSE W.  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: KONAN, KOFFI N'DA  
; APPLICANT: VIQUEZ, OLGA  
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN  
; FILE REFERENCE: 072121/0104  
; CURRENT APPLICATION NUMBER: US/09/715,036  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/167,255  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1162  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (110)..(730)  
US-09-715-036-1

Query Match 64.4%; Score 462; DB 3; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 5.3e-116;  
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACCGCATCTGGAGGCA 60  
DB 118 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACCGCATCTGGAGGCA 177  
QY 61 GCAGTGGGAACTCCAAAGGAGACAGAAGATGCGAGAGCCAGCTCGAGAGGGCGAACTTGAG 120

DB 178 GCAGTGGGAACTCCAAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAG 237  
QY 121 GCCTGCGAGCAACATCTCATGCAAGAGATCCAAAGTGAAGAGATTCATATGAACGGGA 180  
DB 238 GCCTGCGAGCAACATCTCATGCAAGAGATCCAAAGTGAAGAGATTCATATGAACGGGA 297  
QY 181 CCGGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGAGCCGCTGG 240  
DB 298 CCGGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGAGCCGCTGG 357  
QY 241 ATCTCTCAGCACCACAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACAAACAAAG 300  
DB 358 ATCTCTCAGCACCACAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACAAACAAAG 417  
QY 301 GTGCATGTGCGAGGCAATTCGAACAGATCATGGAGAACAGAGCGATAGTTGCAGGGGAG 360  
DB 418 GTGCATGTGCGAGGCAATTCGAACAGATCATGGAGAACAGAGCGATAGTTGCAGGGGAG 477  
QY 361 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
DB 478 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 537  
QY 421 GGCAACACAGCGTTGCGACTTGGACGTGCAAAAGTGGCGGCGAG 462  
DB 538 GGCAACACAGCGTTGCGACTTGGACGTGCAAAAGTGGCGGCGAG 579

RESULT 7  
US-09-715-036-7  
; Sequence 7, Application US/09715036  
; Patent No. 6943010  
; GENERAL INFORMATION:  
; APPLICANT: DODO, HORTENSE W.  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: KONAN, KOFFI N'DA  
; APPLICANT: VIQUEZ, OLGA  
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN  
; FILE REFERENCE: 072121/0104  
; CURRENT APPLICATION NUMBER: US/09/715,036  
; CURRENT FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: 60/167,255  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 80  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Probe  
US-09-715-036-7

Query Match 11.2%; Score 80; DB 3; Length 80;  
Best Local Similarity 100.0%; Pred. No. 2.9e-12;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACCGCATCTCGGAGGAGCAGTAGTGGA 70  
DB 1 CTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACCGCATCTCGGAGGAGCAGTAGTGGA 60  
QY 71 CTCCAAGGAGACAGAAGATG 90  
DB 61 CTCCAAGGAGACAGAAGATG 80

RESULT 8  
US-08-618-911-3  
; Sequence 3, Application US/08618911  
; Patent No. 5850016  
; GENERAL INFORMATION:  
; APPLICANT: Jung, Rudolf





Galvez, Alfredo F.  
TITLE OF INVENTION: Lunasin Peptides  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/531,727  
FILING DATE: 21-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/938,675  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: B98-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 770 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-531-727-1

Query Match	8.8%;	Score 63.4;	DB 3;	Length 770;
Best Local Similarity	51.6%;	Pred. No. 2.7e-07;		
Matches 369;	Conservative 0;	Mismatches 301;	Indels 45;	Gaps 8;
Qy	7	CATACTAGTAGCCCTCGCGCCCTTTTCCCTCCTCGCTGCCACGCACTCTGCGAGGACGACGTG	66	
Db	28	CACAACTCTCTCATCTCTCTTCTCTCTCTGCAATCGCCACACTTGCAGCGCCTCCAATG	87	
Qy	67	GGAACTCCAAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGCGCAACTCTGAGGCCCTG	125	
Db	88	GCAGCACCCAGCAAGA--TAGCTGCCGAAGCAGCTCCAGGGGTGAACCTCAGCGCCCTG	144	
Qy	127	CGAGCAACATCTCATGACAGAAGATCCACGTGACGAGGATTCATATGAAACGGGACCCGTA	186	
Db	145	CGAAGACACATCATGGAGAAGATCCAAGGCCGCGGAGATGACGATGATGATGACGA	204	
Qy	187	CAGC-----CCTAGTTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAG-----	231	
Db	205	CGACAATCACATTTCTAGGACCATCGGGGAAGAAATCAAATTACATAGGAGGAACGAAGG	264	
Qy	232	-----AGCGCTGGATCCTCTCAGCACCAAGAGAGGTGTTGCAATATGACTGTAACGA	282	
Db	265	AAAGACGAACGACGAAGAAGAAGGACACATGCAGAAAGTGTCTCACAGAAATGAGCGA	324	
Qy	283	GTTTGTGAGNACAACCAAGGTGCATGTGCGAGGCATTGCCAACAGATCATGGAGAACCGAG	342	
Db	325	GCT---GAGAAGCCCCCAATGCCAGTGCAAAGCGCTGCAGAAAGATAATGGAGAACCAGAG	381	
Qy	343	CGATAGGTTGCAGGGGAGGCAACAGGACCAACAGTTCAAGAGGGAGCTCAGAGAACTTCCC	402	
Db	382	CGGGAATCGAGGAGACGAGAGAGAGAAA---ATGAGAGAGAGAGCTCATTTACTTGGC	438	
Qy	403	TCAAACAGTGCAGCCCTTAGGGGCCCAACAGCGTTTGGCACTTGGACGTCGA-AGTGCGCGCA	461	

439	Db	TACTATGTGCAGGTTTGGACCCATGATCCAGTCGCACTTGTGCTCCGATCAAGAGT	498
462	Qy	GAGACAGATACTAAACACCTATCTCAAAAAAGAAAAAGAAAAAGAAATAGCTTAT	521
499	Db	TAAAGCAATGTTGTCACTTGTGCTACTAACACATGATGTGATAGTTATATGCTAGCT---	555
522	Qy	ATATAAGCTATTATCTATAGGTTATGTTTGTGTTTGGTTAAATAAAGATCATCACTATAT	581
556	Db	-----AGCTATAACATAAGCTGTCTCTGAGTGTGTTGTATATTAATAAAGATCATCACTG	610
582	Qy	GAATGTGTTGATCGTGTTAACTAAGGCAAGCTTAGGTTATATGAGCAACCTTTAGAGTGCT	641
611	Db	GTGAATGGTGATCGTGATAGTACCCTACTTAGTAGGCAATGGAAGCACTTTAGAGTGTGCT	670
642	Qy	TT---TATGGCGTTGCTATGTTTGTGCTGCAGAGTTGTTAACCATCTTCGAAAT	693
671	Db	TTGTGCATGGCTCTGCCTCTGTTTGGAGACTTTTGTGAATGTTTTCGAGTTTAAAT	725

RESULT 12

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US-09-715-036-8
; Sequence 8, Application US/09715036
; Patent No. 6943010
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIOUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN
; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/09/715,036
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-715-036-8

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Query Match      8.6%; Score 62; DB 3; Length 62;
Best Local Similarity 100.0%; Pred.No. 2.1e-07;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 301 GTGCATGTGCGAGGCATTGCAACAGATCATGCGAGAACAGAGCCATAGGTTGCAGGGGAG 360
    |||||
Db 1 GTGCATGTGCGAGGCATTGCAACAGATCATGCGAGAACAGAGCCATAGGTTGCAGGGGAG 60
Qy 361 GC 362
    ||
Db 61 GC 62

```

RESULT 13

US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA

COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-F18  
US-08-232-463-14

Query Match 8.2%; Score 58.8; DB 2; Length 7218;

Best Local Similarity 2.3%; Pred. No. 1.3e-05;  
Matches 9; Conservative 229; Mismatches 146; Indels 0; Gaps 0;

QY 129 AGCAACATCTCATGACAGATCAACGCTGACGAGGATTCATATGACGGGACCGTACA 188  
DB 1449 AGAAGATTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1390  
QY 189 GCCTAGTCAGATCCGTACAGCCCTAGTCCATATGATCGGAGCGCTGGATCTCTC 248  
DB 1389 RRR 1330  
QY 249 AGCACCAGAGAGTGTGCAATGACGTGACGAGTTTGAGAACCAACCAAGTGATGT 308  
DB 1329 RRR 1270  
QY 309 GCAGGCGATTGCAACAGATCATGAGAACCAAGAGCGATAGTTGCGAGGGGACCAAG 368  
DB 1269 RRR 1210  
QY 369 AGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCTCAACAGTGGCGCTTAGGCGACCAC 428  
DB 1209 RRR 1150  
QY 429 AGCGTTCGACTTGGAGCTGAAAGTGGCGGAGACAGACATATAACACCTATCTCAA 488  
DB 1149 RRR 1090  
QY 489 AAAAAAGAAAGAAAGAAAGAA 512  
DB 1089 RRR 1066

RESULT 14

US-08-618-911-1  
; Sequence 1, Application US/08618911  
; Patent No. 5850016  
; GENERAL INFORMATION:  
; APPLICANT: Jung, Rudolf

APPLICANT: Hastings, Craig  
APPLICANT: Coughlan, Sean  
APPLICANT: Hu, David  
TITLE OF INVENTION: ALTERATION OF AMINO ACID COMPOSITIONS IN  
TITLE OF INVENTION: SEEDS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.  
STREET: 700 Capital Square, 400 Locust Street  
CITY: Des Moines  
STATE: Iowa  
COUNTRY: USA  
ZIP: 50309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,911  
FILING DATE: Concurrently herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Simon, Soma  
REGISTRATION NUMBER: 37,444  
REFERENCE/DOCKET NUMBER: 365-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (515) 248-4800  
TELEFAX: (515) 248-4844  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 723 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 10..474  
US-08-618-911-1

Query Match 7.6%; Score 54.4; DB 2; Length 723;

Best Local Similarity 61.5%; Pred. No. 7.5e-05;  
Matches 123; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 251 CACCAAGAGAGGTGTTGCAATGAGCTGAACAGTTTGAGAACCAACCAAGCTGCATGTC 310  
DB 277 CATATCGAAGAGTGTGCGAGCGAATGAGCGAGCT---GAAAAGCCCATATGCCAGTGC 333  
QY 311 GAGGCATTGCAACAGATCATGGAGAACCAAGAGCGATAGTTGCGAGGGGAGGCAACAGGAG 370  
DB 334 AAAGCGCTACAGAAGATAATGGATAACCAAGCGGAGCAACTGGAGGGGAGGAGAAGAG 393  
QY 371 CAACAGTTCAAGAGGAGCTCAGGAACCTTCCTCAACAGTGCAGCGCTTAGGGCACCACAG 430  
DB 394 ---CAGATGGAGAGAGAGCTCATGAACCTTGGCTATTAGGTGAGGTGGGACCCATGATA 450  
QY 431 CGTTGCGACTTGGACGTCGA 450  
DB 451 GGTGCGACTTGTCTCCGA 470

RESULT 15

US-09-949-002-777/c  
; Sequence 777, Application US/09949002  
; Patent No. 6900016  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; CURRENT FILING DATE: 2000-01-28

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; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 25590
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25590)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-777

Query Match      6.8%; Score 48.4; DB 3; Length 25590;
Best Local Similarity 50.9%; Pred. No. 0.016;
Matches 115; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 488 AAAAAAGAAAGAAAGAAAGAAATAGCTTATATATATAGCTATTATCTATGCTTATGT 547
Db 4123 AATAGATATTATATATATAATAATAATAATAATAATAATAATAATAATAATAATA 4064

Qy 548 TTAGTTTGGTAAATAATAAAGATCATCACTATATGAATGTTGATCGTGTAACTAAGG 607
Db 4063 AATAATAATGTAATAATAATTGTTATTATTATTATTATAGTCTACTTTATATAATATTA 4004

Qy 608 CAAGCTTAGGTTATATGAGCACCTTTTAGAGTGCTTTTATGGCGTTGCTATGTTTGTG 667
Db 4003 TATTTATACATAATATACGTATATATAAAATTACATAATGGATTATATAGTATATATTA 3944

Qy 668 CTCGAGTTGTAACCATCTTGAATAATAATAAAGATCATGTTT 713
Db 3943 TATCAAAATACATATGCATATATAATACATTTATATTATATAGTCT 3898
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Job time : 115.753 secs



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 18:12:55 ; Search time 980.107 Seconds  
(without alignments)  
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Title: US-10-728-051-2  
Perfect score: 717  
Sequence: 1 gctcaccatactagtagcc.....taaaagatcatgtttgtt 717

Scoring table: IDENTITY NUC  
Gap 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main.\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
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- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	717	100.0	717	3	US-09-731-375A-2
2	717	100.0	717	9	US-10-728-323-2
3	717	100.0	717	9	US-10-728-051-2
4	717	100.0	717	10	US-10-899-551-3
5	474	66.1	474	6	US-10-228-806-3
6	474	66.1	474	6	US-10-100-303A-62
7	462	64.4	462	10	US-10-958-324-3
8	462	64.4	1162	10	US-10-958-324-1
9	80	11.2	80	10	US-10-958-324-7
10	65.6	9.1	1013	8	US-10-424-599-26383
11	63.4	8.8	770	7	US-10-302-633-1
12	62	8.6	62	10	US-10-958-324-8
13	59.2	8.3	477	10	US-10-508-263-43
14	54.4	7.6	468	10	US-10-508-263-41
15	54.4	7.6	883	8	US-10-424-599-121530
16	51.4	7.2	5392	16	US-11-224-807-6
17	49.8	6.9	62658	8	US-10-322-281-420

c	18	49.6	6.9	454	4	US-09-925-065A-566559	Sequence 566559,
c	19	49.6	6.9	454	4	US-09-925-065A-566560	Sequence 566560,
c	20	49.6	6.9	454	5	US-09-925-065A-566559	Sequence 566559,
c	21	49.6	6.9	454	5	US-09-925-065A-566560	Sequence 566560,
c	22	49.6	6.9	52216	3	US-09-747-810-1	Sequence 1, Appli
c	23	49.6	6.9	169739	8	US-10-450-826-93	Sequence 93, Appli
c	24	49.6	6.8	349	8	US-10-424-599-133074	Sequence 133074,
c	25	49	6.8	62001	8	US-10-316-459-13	Sequence 13, Appli
c	26	48.2	6.7	7758	7	US-10-311-455-1076	Sequence 1076, Ap
c	27	48	6.7	6509	7	US-10-311-455-199	Sequence 199, App
c	28	47.8	6.7	1237	6	US-10-027-632-122633	Sequence 122633,
c	29	47.8	6.7	1237	7	US-10-027-632-122633	Sequence 122633,
c	30	47.6	6.6	451	8	US-10-424-599-24494	Sequence 24494, A
c	31	47.4	6.6	325	8	US-10-424-599-76496	Sequence 76496, A
c	32	46.4	6.5	945	12	US-10-301-480-585566	Sequence 585566,
c	33	46.4	6.5	945	12	US-10-301-480-1198975	Sequence 1198975,
c	34	46.2	6.4	1325	4	US-09-925-065A-19652	Sequence 19652, A
c	35	46.2	6.4	1325	5	US-09-925-065A-19652	Sequence 19652, A
c	36	46.2	6.4	1325	12	US-10-301-480-120889	Sequence 120889,
c	37	46.2	6.4	1325	12	US-10-301-480-734298	Sequence 734298,
c	38	46	6.4	686	4	US-09-925-065A-940622	Sequence 940622,
c	39	46	6.4	686	5	US-09-925-065A-940622	Sequence 940622,
c	40	46	6.4	1089	10	US-10-956-157-107	Sequence 107, App
c	41	46	6.4	1089	10	US-10-956-157-5342	Sequence 5342, App
c	42	45.6	6.4	6063	7	US-10-240-453-267	Sequence 267, App
c	43	45.4	6.3	5823	7	US-10-240-453-256	Sequence 256, App
c	44	45.2	6.3	611	4	US-09-925-065A-500442	Sequence 500442,
c	45	45.2	6.3	611	5	US-09-925-065A-500442	Sequence 500442,

ALIGNMENTS

RESULT 1

US-09-731-375A-2  
; Sequence 2, Application US/09731375A  
; Publication No. US20030035810A1  
; GENERAL INFORMATION:  
; APPLICANT: Caplan, Michael  
; TITLE OF INVENTION: Microbial Delivery System  
; FILE REFERENCE: 2002834-0100  
; CURRENT APPLICATION NUMBER: US/09/731,375A  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/195,035  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 717  
; TYPE: DNA  
; ORGANISM: Atachis hypogaea  
US-09-731-375A-2

Query Match	100.0%	Score	717;	DB	3;	Length	717;
Best Local Similarity	100.0%	Pred. No.	5.4e-177;				
Matches	717;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGTCCCGCCACGCACTCGGAGGCA	60				
Db	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGTCCCGCCACGCACTCGGAGGCA	60				
Qy	61	GCAGTGGGAACCTCCAAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG	120				
Db	61	GCAGTGGGAACCTCCAAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG	120				
Qy	121	GCCTCGGAGCAACATCTCATGAGAAGATCCAACTGACGAGGATTCATATGAAACGGGA	180				
Db	121	GCCTCGGAGCAACATCTCATGAGAAGATCCAACTGACGAGGATTCATATGAAACGGGA	180				
Qy	181	CCCGTACAGCCCTAGTTCAGGATCCGCTACAGCCCTAGTTCATATGATCGGAGGCGCCTGG	240				
Db	181	CCCGTACAGCCCTAGTTCAGGATCCGCTACAGCCCTAGTTCATATGATCGGAGGCGCCTGG	240				

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QY 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300
DB 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300
QY 301 GTGCATGTGGAGGCATTCGAACAGATCATGGAGAACCCAGAGCGATAGGTTGCAGGGGAG 360
DB 301 GTGCATGTGGAGGCATTCGAACAGATCATGGAGAACCCAGAGCGATAGGTTGCAGGGGAG 360
QY 361 GCAACAGGAGCAACAGTTCGAAGAGGAGCTCAGGAACTTGCCTCAACAGTGGCGCCTTAG 420
DB 361 GCAACAGGAGCAACAGTTCGAAGAGGAGCTCAGGAACTTGCCTCAACAGTGGCGCCTTAG 420
QY 421 GGCAACACAGCGTTGGCACTTGGAAGTGCAGAGTGGCGGCGAGACAGATACATAACACCC 480
DB 421 GGCAACACAGCGTTGGCACTTGGAAGTGCAGAGTGGCGGCGAGACAGATACATAACACCC 480
QY 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 540
DB 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 540
QY 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA 600
DB 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA 600
QY 601 ACTAAGCAAGCTTAGGTTATATGAGCACCCTTTAGAGTGCCTTTATGGCGTGTCTATGT 660
DB 601 ACTAAGCAAGCTTAGGTTATATGAGCACCCTTTAGAGTGCCTTTATGGCGTGTCTATGT 660
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAAATAATATAAAAAAGATCATGTTTTGTT 717
DB 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAAATAATATAAAAAAGATCATGTTTTGTT 717

RESULT 2
US-10-728-323-2
; Sequence 2, Application US/10728323
; Publication No. US2004020894A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0232
; CURRENT FILING DATE: 2003-12-04
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-323-2

Query Match 100.0%; Score 717; DB 9; Length 717;
Best Local Similarity 100.0%; Pred. No. 5.4e-177;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGTGCACGCGATCTCGAGGCA 60
DB 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGTGCACGCGATCTCGAGGCA 60
QY 61 GCAGTGGAACTCAAGGAGACAGAAGATCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120
DB 61 GCAGTGGAACTCAAGGAGACAGAAGATCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120
QY 121 GCCTCGGACCAATCTCATGAGAGAGATCCAAAGTGCAGAGGATTCATATCAACGGGA 180
DB 121 GCCTCGGACCAATCTCATGAGAGAGATCCAAAGTGCAGAGGATTCATATCAACGGGA 180
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DB 121 GCCTCGGAGCAACATCTCATGAGAGATCCAAAGTGCAGAGGATTCATATCAACGGGA 180
QY 181 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCCCTGG 240
DB 181 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCCCTGG 240
QY 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300
DB 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300
QY 301 GTGCATGTGGAGGCATTCGAACAGATCATGGAGAACCCAGAGCGATAGGTTGCAGGGGAG 360
DB 301 GTGCATGTGGAGGCATTCGAACAGATCATGGAGAACCCAGAGCGATAGGTTGCAGGGGAG 360
QY 361 GCAACAGGAGCAACAGTTCGAAGAGGAGCTCAGGAACTTGCCTCAACAGTGGCGCCTTAG 420
DB 361 GCAACAGGAGCAACAGTTCGAAGAGGAGCTCAGGAACTTGCCTCAACAGTGGCGCCTTAG 420
QY 421 GGCAACACAGCGTTGGCACTTGGAAGTGCAGAGTGGCGGCGAGACAGATACATAACACCC 480
DB 421 GGCAACACAGCGTTGGCACTTGGAAGTGCAGAGTGGCGGCGAGACAGATACATAACACCC 480
QY 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 540
DB 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAG 540
QY 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA 600
DB 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA 600
QY 601 ACTAAGCAAGCTTAGGTTATATGAGCACCCTTTAGAGTGCCTTTATGGCGTGTCTATGT 660
DB 601 ACTAAGCAAGCTTAGGTTATATGAGCACCCTTTAGAGTGCCTTTATGGCGTGTCTATGT 660
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAAATAATATAAAAAAGATCATGTTTTGTT 717
DB 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAAATAATATAAAAAAGATCATGTTTTGTT 717

RESULT 3
US-10-728-051-2
; Sequence 2, Application US/10728051
; Publication No. US20040234548A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0222
; CURRENT APPLICATION NUMBER: US/10/728,051
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/731,375
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-051-2

Query Match 100.0%; Score 717; DB 9; Length 717;
Best Local Similarity 100.0%; Pred. No. 5.4e-177;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGTGCACGCGATCTCGAGGCA 60
DB 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGTGCACGCGATCTCGAGGCA 60
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QY 61 GCAGTGGGAACCTCAAGGAGACAGAAAGATGCGAGAGCCAGCTCGAGAGGGCGAACCTTGAG 120  
Db |||||  
QY 61 GCAGTGGGAACCTCAAGGAGACAGAAAGATGCGAGAGCCAGCTCGAGAGGGCGAACCTTGAG 120  
Db |||||  
QY 121 GCCTTCGAGCAACATCTCATGCAAGAAGATCCAAAGCTGAGAGGATTCATATGAACGGGA 180  
Db |||||  
QY 121 GCCTTCGAGCAACATCTCATGCAAGAAGATCCAAAGCTGAGAGGATTCATATGAACGGGA 180  
Db |||||  
QY 181 CCCTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGG 240  
Db |||||  
QY 181 CCCTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGG 240  
QY 241 ATCTCTCAGACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAACCAACAAAG 300  
Db |||||  
QY 241 ATCTCTCAGACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAACCAACAAAG 300  
QY 301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGTTGCGAGGGAG 360  
Db |||||  
QY 301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGTTGCGAGGGAG 360  
QY 361 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
Db |||||  
QY 361 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
QY 421 GGCAACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGAGACAGATACCTAAACACC 480  
Db |||||  
QY 421 GGCAACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGAGACAGATACCTAAACACC 480  
QY 481 TATCTCAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540  
Db |||||  
QY 481 TATCTCAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540  
QY 541 GTTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600  
Db |||||  
QY 541 GTTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600  
QY 601 ACTAAGGCAAGCTTAGGTTATATGAGCACCCTTTAGAGTGTCTTTATGCGCTTGTCTATGT 660  
Db |||||  
QY 601 ACTAAGGCAAGCTTAGGTTATATGAGCACCCTTTAGAGTGTCTTTATGCGCTTGTCTATGT 660  
QY 661 TTTGTTGCTCGAGAGTTGTAACCATCTTGAATAATAATAATAATAATAATAATAATAATAATA 717  
Db |||||  
661 TTTGTTGCTCGAGAGTTGTAACCATCTTGAATAATAATAATAATAATAATAATAATAATAATA 717

RESULT 4  
US-10-899-551-3  
; Sequence 3, Application US/10899551  
; Publication No. US20050063994A1  
; GENERAL INFORMATION:  
; APPLICANT: Caplan, Michael J.  
; APPLICANT: Burks, A. Wesley  
; APPLICANT: Sampson, Hugh A.  
; APPLICANT: Howard, Sosin B.  
; APPLICANT: Bottomly, Kim H.  
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction to Allergy  
; FILE REFERENCE: 2002834-0233  
; CURRENT APPLICATION NUMBER: US/10/899,551  
; CURRENT FILING DATE: 2004-07-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 717  
; TYPE: DNA  
; ORGANISM: species Arachis hypogaea  
US-10-899-551-3

Query Match 100.0%; Score 717; DB 10; Length 717;  
Best Local Similarity 100.0%; Pred. No. 5.4e-177;  
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGCTGCCACGCGCATCTCGAGGCA 60  
Db |||||

Db 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGCTGCCACGCGCATCTCGAGGCA 60  
QY 61 GCAGTGGGAACCTCAAGGAGACAGAAAGATGCGAGAGCCAGCTCGAGAGGGCGAACCTTGAG 120  
Db |||||  
QY 61 GCAGTGGGAACCTCAAGGAGACAGAAAGATGCGAGAGCCAGCTCGAGAGGGCGAACCTTGAG 120  
Db |||||  
QY 121 GCCTTCGAGCAACATCTCATGCAAGAAGATCCAAAGCTGAGAGGATTCATATGAACGGGA 180  
Db |||||  
QY 121 GCCTTCGAGCAACATCTCATGCAAGAAGATCCAAAGCTGAGAGGATTCATATGAACGGGA 180  
Db |||||  
QY 181 CCCTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGG 240  
Db |||||  
QY 181 CCCTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGG 240  
QY 241 ATCTCTCAGACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAACCAACAAAG 300  
Db |||||  
QY 241 ATCTCTCAGACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAACCAACAAAG 300  
QY 301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGTTGCGAGGGAG 360  
Db |||||  
QY 301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGTTGCGAGGGAG 360  
QY 361 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
Db |||||  
QY 361 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCCTTAG 420  
QY 421 GGCAACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGAGACAGATACCTAAACACC 480  
Db |||||  
QY 421 GGCAACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGAGACAGATACCTAAACACC 480  
QY 481 TATCTCAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540  
Db |||||  
QY 481 TATCTCAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540  
QY 541 GTTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600  
Db |||||  
QY 541 GTTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600  
QY 601 ACTAAGGCAAGCTTAGGTTATATGAGCACCCTTTAGAGTGTCTTTATGCGCTTGTCTATGT 660  
Db |||||  
QY 601 ACTAAGGCAAGCTTAGGTTATATGAGCACCCTTTAGAGTGTCTTTATGCGCTTGTCTATGT 660  
QY 661 TTTGTTGCTCGAGAGTTGTAACCATCTTGAATAATAATAATAATAATAATAATAATAATAATA 717  
Db |||||  
661 TTTGTTGCTCGAGAGTTGTAACCATCTTGAATAATAATAATAATAATAATAATAATAATAATA 717

RESULT 5  
US-10-228-806-3  
; Sequence 3, Application US/10228806  
; Publication No. US20030049237A1  
; GENERAL INFORMATION:  
; APPLICANT: Bannan, et al.  
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions  
; TITLE OF INVENTION: to Allergy  
; FILE REFERENCE: 2002834-0043  
; CURRENT APPLICATION NUMBER: US/10/228,806  
; CURRENT FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 474  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea  
US-10-228-806-3

Query Match 66.1%; Score 474; DB 6; Length 474;  
Best Local Similarity 100.0%; Pred. No. 2e-113;  
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGCTGCCACGCGCATCTCGAGGCA 61  
Db |||||  
1 CTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGCTGCCACGCGCATCTCGAGGCA 60

QY 62 CAGTGGAACTCCAAGGAGACAGAAAGATGCCAGAGCAGCTCCAGAGGGCGAACTTGAGG 121  
DB |||||  
61 CAGTGGAACTCCAAGGAGACAGAAAGATGCCAGAGCAGCTCCAGAGGGCGAACTTGAGG 120  
QY 122 CCTGCGAGCAACATCTCATGACAGAGATCCACGTTGACGAGATTCATATGAACGGAC 181  
DB |||||  
121 CCTGCGAGCAACATCTCATGACAGAGATCCACGTTGACGAGATTCATATGAACGGAC 180  
QY 182 CCTACAGCCCTAGTCAGGATCCGTCAGAGCCCTAGTCCATATGATCGGAGGGCGCTGGA 241  
DB |||||  
181 CCTACAGCCCTAGTCAGGATCCGTCAGAGCCCTAGTCCATATGATCGGAGGGCGCTGGA 240  
QY 242 TCCTCTCAGCAACCAAGAGAGGTGTCATGAGCTGAAACGAGTTTGAGAACCAACGAAG 301  
DB |||||  
241 TCCTCTCAGCAACCAAGAGAGGTGTCATGAGCTGAAACGAGTTTGAGAACCAACGAAG 300  
QY 302 TGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGGTTGCAAGGGGAGG 361  
DB |||||  
301 TGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGGTTGCAAGGGGAGG 360  
QY 362 CAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGCAGCCCTTAGG 421  
DB |||||  
361 CAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGCAGCCCTTAGG 420  
QY 422 GCACCACAGCGTTGCCACTTGGACGTGGAACGTGCGGAGGAGACAGATACTAA 475  
DB |||||  
421 GCACCACAGCGTTGCCACTTGGACGTGGAACGTGCGGAGGAGACAGATACTAA 474

## RESULT 6

US-10-100-303A-62  
; Sequence 62, Application US/10100303A  
; Publication No. US20030202980A1  
; GENERAL INFORMATION:  
; APPLICANT: Caplan, et al.  
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction  
; FILE REFERENCE: to Allergy  
; CURRENT APPLICATION NUMBER: US/10/100,303A  
; PRIOR FILING DATE: 2002-03-18  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 62  
; LENGTH: 474  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea, Prot/Nucleo Ara h 2  
US-10-100-303A-62

Query Match 66.1%; Score 474; DB 7; Length 474;  
Best Local Similarity 100.0%; Pred. No. 2e-113;  
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCACCATCTAGTAGCCCTCGCCCTTTCTCCTCGCTGCCACGCATCTCGAGGCG 61  
DB |||||  
1 CTCACCATCTAGTAGCCCTCGCCCTTTCTCCTCGCTGCCACGCATCTCGAGGCG 60  
QY 62 CAGTGGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAGG 121  
DB |||||  
61 CAGTGGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAGG 120  
QY 122 CCTGCGAGCAACATCTCATGACAGATCCACGTTGACGAGATTCATATGAACGGAC 181  
DB |||||  
121 CCTGCGAGCAACATCTCATGACAGATCCACGTTGACGAGATTCATATGAACGGAC 180  
QY 182 CCGTACAGCCCTAGTCAGGATCCGTCAGAGCCCTAGTCCATATGATCGGAGGGCGCTGGA 241  
DB |||||  
181 CCGTACAGCCCTAGTCAGGATCCGTCAGAGCCCTAGTCCATATGATCGGAGGGCGCTGGA 240  
QY 242 TCCTCTCAGCACCAAGAGAGGTGTCATGAGCTGAAACGAGTTTGAGAACCAACGAAG 301  
DB |||||  
241 TCCTCTCAGCACCAAGAGAGGTGTCATGAGCTGAAACGAGTTTGAGAACCAACGAAG 300

QY 302 TGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCCATAGGTTGCGGGGAGG 361  
DB |||||  
301 TGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCCATAGGTTGCGGGGAGG 360  
QY 362 CAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGCAGCCCTTAGG 421  
DB |||||  
361 CAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGCAGCCCTTAGG 420  
QY 422 GCACCACAGCGTTGCCACTTGGACGTGGAACGTGCGGAGGAGACAGATACTAA 475  
DB |||||  
421 GCACCACAGCGTTGCCACTTGGACGTGGAACGTGCGGAGGAGACAGATACTAA 474

## RESULT 7

US-10-958-324-3  
; Sequence 3, Application US/10958324  
; Publication No. US20050114924A1  
; GENERAL INFORMATION:  
; APPLICANT: DODO, HORTENSE W.  
; APPLICANT: AKNTZEN, CHARLES J.  
; APPLICANT: KONAN, KOFFI N'DA  
; APPLICANT: VIQUEZ, OLGA  
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN  
; FILE REFERENCE: 072121/0104  
; CURRENT APPLICATION NUMBER: US/10/958,324  
; PRIOR FILING DATE: 2004-10-06  
; PRIOR APPLICATION NUMBER: US/09/715,036  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/167,255  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 682  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea  
US-10-958-324-3

Query Match 64.4%; Score 462; DB 10; Length 682;  
Best Local Similarity 100.0%; Pred. No. 3.3e-110;  
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCCTCGCTGCCACGCATCTCGAGGCA 60  
DB |||||  
67 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCCTCGCTGCCACGCATCTCGAGGCA 126  
QY 61 GCAGTGGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAG 120  
DB |||||  
127 GCAGTGGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAG 186  
QY 121 GCCTCGGAGCAACATCTCATGAGAGATCCAAAGTGCAGAGATTCATATGAACGGGA 180  
DB |||||  
187 GCCTCGGAGCAACATCTCATGAGAGATCCAAAGTGCAGAGATTCATATGAACGGGA 246  
QY 181 CCGTACAGCCCTAGTCAGATCCGTCAGAGCCCTAGTCCATATGATCGGAGAGGGCGCTGG 240  
DB |||||  
247 CCGTACAGCCCTAGTCAGATCCGTCAGAGCCCTAGTCCATATGATCGGAGAGGGCGCTGG 306  
QY 241 ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACGAAG 300  
DB |||||  
307 ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACGAAG 366  
QY 301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGGTTGCGGGGAG 360  
DB |||||  
367 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGGTTGCGGGGAG 426  
QY 361 GCAACAGGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGCAGCCCTTAG 420  
DB |||||  
427 GCAACAGGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGCAGCCCTTAG 486  
QY 421 GGCAACCAACAGCGTTGCCACTTGGACGTGGAACGTGCGGGGAG 462  
DB |||||



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136 GCAGCACCGCAAGA---TAGTGCCTCCAGAGCTCCAGGGGTGAACCTCAGCCCTG 192
127 CGAGCAACATCTCATGAGAAGATCAACGTCAGAGGATTCATATGAACGGGACCCGTA 186
193 CGAGAAGCACATCATGGAAGATCCAAAGCCGCGCGATGACGATGATGATGACGA 252
187 CAGC-----CCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAG----- 231
253 CGACAATCATTCTCAGGACCATCGGGGGAAGATCACTACATGAAGGAGCAACGAAG 312
232 -----AGGCGCTGGATCTCTCAGCACCAAGAGAGGTGTGCAATGAGTGAACGA 282
313 AAAAGCAGAGACGAAGAAGAAAGACACATGCAGAGTGTCTGCACAGAAATGAGCG 372
283 GTTTGAGAAACAACAAAGGTGCATGTGCGAGGATTCGCAACAGATCATGAGAACCCAG 342
373 GCT---GAGNAGCCCCAATGCCAGTGCAGAGCGCTGCAGAGATATGGAGAACCCAG 429
343 CGATAGGTTGACGGGAGGCAACAGAGCAACAGTTCAAGAGGGAGCTCAGGAATTTGCC 402
430 CGAGGAACCTGAGGAGAAAGCAGAAGAGAAA---ATGGAGAGGAGCTCATTAACCTGGC 486
403 TCACAGTGGCGCTTAGGCGCACACAGCGTTGCGACTTGGAGCTCGAAGTGGCGCAG 462
487 TACTATGTGAGGTTTGGAGCCCATGATCCAGTGCAGCTTGTCTCCGA-----TGACTA 540
463 AGACAGATACTAAACACCTATCTCAAAAAAGAAAAAGAAAAAGAAATAGCTTATA 522
541 AGAAGTTAAAGCAATGTTGCTACTTGTAGTACTAACACATGATGTGATGTTATGCT 600
523 TATAAGCTATTATCTATGTTATGTTTGTAGTTTGGTAATTAATAAGATCATCACTATG 582
601 AGTAGCTATAACATAAGCTGTCTCTGAGTGTGTGTATATTATAAAGATCATCACTGG 660
583 AATGTTGTGATCTGTTAACTAAGGCAAGCTTAGTTTATATGAGCACTTTAGAGTGCTT 642
661 TGAATGGTATCGTGTACGTACCGCTACTTAGTAGGCAATGGAAGCACTTAGAGTGTGCTT 720
643 T---TATGGGTTGTCTATCTTTTGTGTGTCAGAGTTGTAACCATCTTTGAAT 693
721 TGTGCATGGCTTGCCTCTGTTTGAGACTTTTGTATGTTTTCGAGTTTAAAT 774

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RESULT 11

US-10-302-633-1  
Sequence 1, Application US/10302633  
Publication No. US20030229038A1

GENERAL INFORMATION:

APPLICANT: de Lumen, Benito O.  
Galvez, Alfredo F.  
TITLE OF INVENTION: Lunasin Peptides  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/302,633  
FILING DATE: 22-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/531,727  
FILING DATE: 21-Mar-2000  
APPLICATION NUMBER: 08/938,675

```

; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B98-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-302-633-1

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Query Match      8.8%; Score 63.4; DB 7; Length 770;
Best Local Similarity 51.6%; Pred. No. 9e-06;
Matches 369; Conservative 0; Mismatches 301; Indels 45; Gaps 8;

QY 7 CATACTAGTAGCCCTCGCCCTTTTCCTCCTCGTCCACGCACTCTGCGAGGCGAGCAGTG 66
Db 28 CACAATCCTCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 87
QY 67 GGAATCTCAAGAGAGCAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTGAGGCCCTG 126
Db 88 GCAGCACCAAGCAAGA---TAGCTGCCGCAAGCAGCTCCAGGGGTGAACCTCAGCCCTG 144
QY 127 CGAGCAACATCTCATGCAAGATCCAACTGACGAGGATTCATATGAACGGGACCCGTA 186
Db 145 CGAAGAGCACATCATGGAAGATCCAAAGCCGCGCGATGACGATGATGATGATGATGATG 204
QY 187 CAGC-----CCTAGTCAGGATCCGTACAGCCCTTAGTCCATATGATCGGAG----- 231
Db 205 CGACAATCACATCTCTCAGGACCATGCGGGAAGAATCAACTACATAAGGAGGAACGAAG 264
QY 232 -----AGGCGCTGGATTCCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTGAACGA 282
Db 265 AAAAGCAGAAAGCAAGAAAGAAAGAGGACACATGCAGAAAGTGTCTGCACAGAAATGAGCG 324
QY 283 GTTTGAGAACAAACAAAGGTGCATGTGCGAGGCTTGCACACATCATGAGAACCCAGAG 342
Db 325 GCT---GAGAAAGCCCAATGCCAGTGCAGAGCGCTGCAGAGATATGAGAGAACCCAGAG 381
QY 343 CGATAGGTTGCGAGGGAGGCAACAGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCC 402
Db 382 CGAGGAACCTGGAGGAGAGCAGAGAAAGAAA---ATGGAGAGGAGCTCATTAACCTGGC 438
QY 403 TCAACAGTGGGCTTTAGGGCACCAAGCGTTCCGACTTTGGAGCTGCA-AGTGGCGGCA 461
Db 439 TACTATGTGCAAGTTTGGACCCCATGATCCAGTGCAGCTTGTCTCCGATGACTAAGAAGT 498
QY 462 GAGACAGATCTAAACACACCTATCTCAAAAAAGAAAAAGAAAAAGAAATAGCTTAT 521
Db 499 TAAAGCAATGTTGTCTACTTGTCTGCTACTAACACATGATGATGATGATGATGATGATG 555
QY 522 ATATAAGCTATTATCTATGTTATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 581
Db 556 -----AGCTATAACATAAGCTGCTCTGAGTGTGTTGTATATTATAAAGATCATCACTG 610
QY 582 GAATGTTGATCGTGTTAACCTAAGCAAGCTTAGTTATATGAGCACCTTTAGAGTGCT 641
Db 611 GTGAATGGTATCGTGTACGTACCTTACTTAGTAGGCAATGGAAGCACCTTAGAGTGCT 670
QY 642 TT---TATGGCGTGTCTATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 693
Db 671 TTGTGATGCGCCTTGCTCTGTTTGTGAGACTTTTGTAAAGTTTTCGAGTTTAAAT 725

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RESULT 12  
US-10-958-324-8







GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 18:21:18 ; Search time 15.6052 Seconds  
(without alignments)  
11014.453 Million cell updates/sec

Title: US-10-728-051-2  
Perfect score: 717  
Sequence: 1 gctcaccatactagtagcc.....taaaagatcatgttttgg 717

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_New.\*  
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2: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
5: /EMC\_Celerra\_SID33/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
7: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
8: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54.4	7.6	714	6	US-10-953-349-13196
2	43.2	6.0	8172	6	US-10-517-441-717
3	43	6.0	8172	6	US-10-517-441-443
4	41.8	5.8	56580	6	US-10-553-298-1
5	41	5.7	276	6	US-10-471-571A-969
6	40.4	5.6	8391	7	US-11-217-529-166179
7	40.2	5.6	4857	6	US-10-517-441-697
8	39.4	5.5	6521	6	US-10-517-441-309
9	39.4	5.5	6521	6	US-10-517-441-583
10	39	5.4	9859	6	US-10-517-441-730
11	38.8	5.4	8900	6	US-10-517-441-428
12	38.8	5.4	8900	6	US-10-517-441-702
13	38.6	5.4	4857	6	US-10-517-441-423
14	38.6	5.4	15355	6	US-10-517-441-415
15	38.6	5.4	15355	6	US-10-517-441-689
16	38.4	5.4	8172	6	US-10-517-441-718
17	38	5.3	3107	6	US-10-517-441-401
18	38	5.3	3107	6	US-10-517-441-675
19	38	5.3	3501	6	US-10-517-441-499
20	38	5.3	3501	6	US-10-517-441-773
21	38	5.3	8172	6	US-10-517-441-99
22	36.8	5.1	4857	6	US-10-517-441-423
23	36.8	5.1	4857	6	US-10-517-441-697
24	36.8	5.1	8172	6	US-10-517-441-444
25	36.8	5.1	9353	6	US-10-517-441-735

ALIGNMENTS

RESULT 1

US-10-953-349-13196  
; Sequence 13196, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13196  
; LENGTH: 714  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-953-349-13196

Query Match 7.6%; Score 54.4; DB 6; Length 714;  
Best Local Similarity 61.5%; Pred. No. 3.5e-05;  
Matches 123; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

Qy	251	CACCAAGAGAGGTGTTGCAATGAGCTGGAACAGATTTTGAGAACCAACCAAGTGCATGTGC	310
Db	294	CACATGCAGAGGTGCTGCAGCGAAATGAGCGAGCT--GAAAAGCCCCATATGCCAGTGC	350
Qy	311	GAGGCATTGCACAGATCATGGAGACCGAGCGATAGTTGCGAGGGGAGCAACAGAG	370
Db	351	AAAGCCCTACAGAAGATAATGGATAACCGAGCGCAACTGGAGGGGAGGAGGAAG	410
Qy	371	CAACAGTTCAGAGGGAGGCTCAGCAACTTGCCTCAACAGTGCCTTAGGGCCACACAG	430
Db	411	---CAGATGGAGAGAGCTCATGAATTTAGGTGAGGTGGACCCATGATA	467
Qy	431	CGTTGCGACTTGGACCTCGA	450
Db	468	GGGTGCGACTTGTCTCCGA	487

RESULT 2

US-10-517-441-717/c  
; Sequence 717, Application US/10517441  
; Publication No. US20060121467A1  
; GENERAL INFORMATION:  
; APPLICANT: FOKKENS, John  
; APPLICANT: HARBECK, Nadia  
; APPLICANT: KOENIG, Thomas

Sequence 64, Appl  
Sequence 27048, A  
Sequence 293, App  
Sequence 567, App  
Sequence 566, App  
Sequence 59, Appl  
Sequence 1, Appl  
Sequence 318, App  
Sequence 331, App  
Sequence 605, App  
Sequence 456, App  
Sequence 575, App  
Sequence 27978, A  
Sequence 360, App  
Sequence 634, App  
Sequence 419, App  
Sequence 410, App  
Sequence 714, App  
Sequence 308, App  
Sequence 582, App

```
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 717
; LENGTH: 8172
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-717

Query Match          6.0%; Score 43.2; DB 6; Length 8172;
Best Local Similarity 52.8%; Pred. No. 0.089;
Matches 93; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 438 ACTTGACGCTCGAAGTGGCGGAGACAGACAGATACCTAAACACCTATCTCAAAAAAGAAA 497
Db 6974 AATTATACCCACACTCTAACCTAAACAAAAATAAACTCCATCTCAAAAAAGAAA 6915

Qy 498 AGAAAAAGAAAAGTAAGCTTATATATAGCTTATTATCTATGTTGTTATGTTTGG 557
Db 6914 AAAAAAATAAATCAATTAATACTTTAAACCTAAATTTATATAATTTTATCTTTTAA 6855

Qy 558 TAATAATAAGATCATCATCATATATGATGTGTTGATCGTTAACTAAGCGCAAGCT 613
Db 6854 TAAAAATAAAACATTTATTCTTATAAAATTTACTAAAAATTAATTTATAAAATAACACT 6799

RESULT 3
US-10-517-441-443/c
; Sequence 443, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FORKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
;

; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
;

; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 717
; LENGTH: 8172
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-717

Query Match          6.0%; Score 43; DB 6; Length 8172;
Best Local Similarity 55.8%; Pred. No. 0.1;
Matches 82; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 467 AGATACCTAAACACCTATCTCAAAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAG 526
Db 6945 AAAAAATAAACTCCGCTCTCAAAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAG 6886

Qy 527 AGCTATTATCTATGTTATGTTTGGTAATAATAAAGATCATCATCTATATGAATG 586
Db 6885 CTAAATTTATTATAATTTTATCTTTTAAACAATAAAAAATAAAAACATTTTCTTATAA 6826

Qy 587 TGTGTATCGTGTTAACCTAAGCGCAAGCT 613
Db 6825 TACTAAAAATTAATTATAAAAAAACGCT 6799

RESULT 4
US-10-553-298-1
; Sequence 1, Application US/10553298
; Publication No. US20060110385A1
; GENERAL INFORMATION:
; APPLICANT: NeuroNova AG
; TITLE OF INVENTION: A Method for Diagnosing and Treating Affective Disorders
; FILE REFERENCE: XXX
; CURRENT APPLICATION NUMBER: US/10/553,298
; CURRENT FILING DATE: 2005-10-14
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 56580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon1
; LOCATION: (3000)..(3124)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon2
; LOCATION: (24841)..(25009)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon3
; LOCATION: (26134)..(26202)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon4
; LOCATION: (30958)..(31030)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon5
; LOCATION: (32481)..(32577)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon6
; LOCATION: (35416)..(35496)
; OTHER INFORMATION:
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;
; FEATURE:
; NAME/KEY: exon7
; LOCATION: (36113)..(36242)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon8
; LOCATION: (37541)..(37677)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon9
; LOCATION: (45470)..(45560)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon10
; LOCATION: (47229)..(47295)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon11
; LOCATION: (47380)..(47529)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon12
; LOCATION: (50438)..(50539)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon13
; LOCATION: (54392)..(54889)
; OTHER INFORMATION:
; US-553-298-1
;
; Query Match 5.8%; Score 41.8; DB 6; Length 56580;
; Best Local Similarity 59.8%; Pred. No. 0.5;
; Matches 70; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
;
; Qy 440 TTGACGCTCGAAGTGGCGGCGAGACAGATCTAAACACTATCTCAAAAAGAAAAG 499
; Db 5986 TTGCACCACTGCACCTCAGCGCTGAGCCAGACAGACTCTCTCAAAAAGAAAAG 6045
;
; Qy 500 AAAAGAAAAGAAATAGCTTATATAGCTATTAAGCTATTATCTATGTTAGTTTG 556
; Db 6046 AAAAGAAAAGAAATATATATATATATATATATATATATATATATATAGTTT 6102
;
; RESULT 5
; US-10-471-571A-969
; Sequence 969, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 969
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-10-471-571A-969
;
; Query Match 5.7%; Score 41; DB 6; Length 276;
; Best Local Similarity 63.9%; Pred. No. 0.07;
; Matches 62; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
;
; Qy 492 AAGAAAAGAAAAGAAAAGAAATAGCTTATATAGCTTATATAGCTTATATAGTTAG 551
; Db 66 AGGAAAAGAAATGCAAGTAACAAAGTTATATATATATATATATATATATAGTTAG 125
;
; Qy 552 TTTTGGTAATAAAGATCATCTATATGAATGTG 588
; Db 552 TTTTGGTAATAAAGATCATCTATATGAATGTG 588
; Db 552 TTTTGGTAATAAAGATCATCTATATGAATGTG 588
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Db 126 TTTTGGTATTTCATAAAATTTTATGCGCGCAAGAAATATG 162
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; RESULT 6
; US-11-217-529-166179/c
; Sequence 166179, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166179
; LENGTH: 8391
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-166179
;
; Query Match 5.6%; Score 40.4; DB 7; Length 8391;
; Best Local Similarity 63.3%; Pred. No. 0.48;
; Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
;
; Qy 488 AAAAGAAAAGAAAAGAAAAGAAAAGTATAGCTTATATATAGCTTATCTATGTTATGT 547
; Db 2951 AAATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAT 2892
;
; Qy 548 TTAGTTTGGTAAATAAAGATCATCTATATGAAT 585
; Db 2891 ATTTTATATATATATATATATATATATATATATATATAGGAAAAT 2854
;
; RESULT 7
; US-10-517-441-697/c
; Sequence 697, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKEN, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
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Dd	4460 TT	4459		

RESULT 12  
US-10-517-441-702/c  
; Sequence 702, Application US/10517441  
; Publication No. US20060121467A1  
; GENERAL INFORMATION:  
; APPLICANT: FOEKENS, John  
; APPLICANT: HARBECK, Nadia  
; APPLICANT: KOENIG, Thomas  
; APPLICANT: MAIER, Sabine  
; APPLICANT: MARTENS, John  
; APPLICANT: MODEL, Fabian  
; APPLICANT: NIMMRICH, Inko  
; APPLICANT: RUJAN, Tamas  
; APPLICANT: SCHMITT, Armin  
; APPLICANT: SCHMITT, Manfred  
; APPLICANT: LOOK, Maxime P.

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Query Match          5.4%; Score 38.8; DB 6; Length 8900;
Best Local Similarity 57.4%;
Pred. No. 1.3;
Matches 70; Conservative 0; Mismatches 52; Indexes 0;
Caps 0;
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 8993.98 Seconds  
(without alignments)  
10957.506 Million cell updates/sec

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Perfect score: 1524  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1463.6	96.0	1902	4	AY848698 Atachis h
5	1391.2	91.3	1853	2	AK716328 Sequence
6	1391.2	91.3	1853	2	AX148741 Sequence
7	1391.2	91.3	1853	4	AF086821 Atachis h
8	1373.2	90.1	1590	4	AF125192 Atachis h
9	1329.4	87.2	1901	4	AY722685 Atachis h
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DEFINITION Methods and reagents for decreasing allergic reactions.  
ACCESSION BD107900  
VERSION BD107900.1 GI:23202718  
KEYWORDS JP 2002501748-A/3.  
SOURCE unidentified  
ORGANISM unidentified sequences.  
REFERENCE 1 (bases 1 to 1524)  
AUTHORS Sosin,H., Banon,G.A., Jr,W.A.B. and Samphorn,H.A.  
TITLE Methods and reagents for decreasing allergic reactions  
JOURNAL Patent: JP 2002501748-A 3 22-JAN-2002;  
UNIVERSITY OF ARKANSAS, MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY  
UNIVERSITY OF NEW YORK, HOWARD SOSIN  
COMMENT OS Arachis L. (Peanut)  
PN JP 2002501748-A/3  
PD 22-JAN-2002  
PF 29-JAN-1999 JP 2000529437  
PR 31-JAN-1998 US 60/073283,13-FEB-1998 US 60/074590 PR  
13-FEB-1998 US 60/074624,13-FEB-1998 US 60/074633 PR  
27-AUG-1998 US 09/141220  
PI HAWADO SOSIN,GARY A BANON,WESLEY A BIRX JR,HYU A SAMPHORN PC  
C12N15/09,A01H5/00,A01K67/027,A61K39/35,C07K14/37,C07K14/415, PC  
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Rabjohn,P., Helm,E.M., Stanley,J.S., West,C.M., Sampson,H.A.,			
Burks,A.W. and Bannan,G.A.			
Molecular cloning and epitope analysis of the peanut allergen Ara h			
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J. Clin. Invest. 103 (4), 535-542 (1999)			
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10021462			
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Rabjohn,P., Helm,E.M., Stanley,J.S., West,C.M., Sampson,H.A.,			
Burks,A.W. and Bannan,G.A.			
Direct Submission			
TITLE			
JOURNAL			
Submitted (21-SEP-1998) Pediatrics, University of Arkansas for			
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ORIGIN

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AX155334	ACCESSION	AX155334			
AX155334.1	VERSION	GI:14536769			
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		rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;			
		Aeschynomeneae; Arachis.			
REFERENCE		1			
AUTHORS		Bannon,G.A., Burks,W.A., Caplan,M.J., Sampson,H. and Sosin,H.			
TITLE		Peptide antigens			
JOURNAL		Patent: WO 0140264-A 7 07-JUN-2001;			
		Panacea Pharmaceuticals, LLC (US) ; The University of Arkansas (US)			
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Best Local Similarity 99.4%; Pred. NO. 0;
Matches 1515; Conservative 0; Mismatches 9; Indels 0;
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Qy	661	CAGCACAGCCGACAGAAACGAGCAGGACAAAGAAAGAAAACGAAAGTGGAAAATCTTTC	720
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Db	901	GAAGATCAATATGAATACGATGAGAGGATAGAGGGCTGCGAGGGGACGAGAGGAGG	960
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Db	961	GGGAATGGTATTGAAGAGACGATCTGCACCGCAAGCTGTAATAAAGAACATTTGGTAGAAC	1029
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Db	1021	AGATCCCTGACATCTCAACCCCTCAAGCTGGTTTCACTCAAAACTGCGCAAGCTCTCAAC	1080
Qy	1081	CTTCTAATACTTTAGTGGCTTTGGACCTTAGTGTCTGAATATGGAAATCTCTACAGGAATGCA	1140
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1 (bases 1 to 1902)				
Yan, Y. S., Lin, X. D., Zhang, Y. S., Wang, L., Wu, K. and Huang, S. Z.				
Isolation of peanut genes encoding arachins and conglutins by expressed sequence tags				
Plant Sci. 169 (2), 439-445 (2005)				
2 (bases 1 to 1902)				
Yan, Y., Wang, L. and Huang, S.				
cDNA clone of peanut seed storage protein gene				
Unpublished				
3 (bases 1 to 1902)				
Yan, Y., Wang, L. and Huang, S.				
Direct Submission				
Submitted (03-DEC-2004) Department of Biology and Biotechnology,				
Sun Yat-sen University, Guangzhou, Guangdong 510275, China				
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ORIGIN

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DEFINITION Sequence 4 from patent US 6943010.
ACCESSION AR716328
VERSION AR716328.1 GI:77364703
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1853)
AUTHORS Dodo,H.W., Arntzen,C.J., Viquez,O.M. and Konan,K.N.
TITLE Down-regulation and silencing of allergen genes in transgenic
JOURNAL peanut seeds
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RESULT 7
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DEFINITION Arachis hypogaea glycinin (Arah4) mRNA, complete cds.
ACCESSION AF086821
VERSION AF086821.1 GI:5712198
KEYWORDS
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 1853)
AUTHORS Kleber-Janke,T., Cramer,R., Appenzeller,U., Schlaak,M. and
Becker,W.M.
TITLE Selective cloning of peanut allergens, including profilin and 2S
albumins, by phage display technology
JOURNAL Int. Arch. Allergy Immunol. 119 (4), 265-274 (1999)
PUBMED 10474031
REFERENCE 2 (bases 1 to 1853)
AUTHORS Kleber-Janke,T.
DIRECT SUBMISSION
JOURNAL Submitted (25-AUG-1998) Biochemische und Molekulare Allergologie,
Forschungszentrum Borstel, Parkallee 22, Borstel 23845, Germany
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RESULT 8

AF125192 1590 bp mRNA linear PLN 22-AUG-2000  
Arachis hypogaea Gly1 (Gly1) mRNA, complete cds.

AF125192  
AF125192.2 GI:9864776

Arachis hypogaea (peanut)

ORGANISM

Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
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Aeschynomeneae; Arachis.

REFERENCE  
1 (bases 1 to 1590)

Molecular cloning of a glycinin-type peanut seed storage protein

Arachis hypogaea

Jain, A.K. and Basha, S.M.

Unpublished

REFERENCE  
2 (bases 1 to 1590)

Direct Submission

Jain, A.K. and Basha, S.M.

Submitted (02-FEB-1999)

Plant Biotechnology, Florida A&M

University, 301 South Perry Paige Building, Tallahassee, FL 32307, USA

REFERENCE  
3 (bases 1 to 1590)

Jain, A.K. and Basha, S.M.

Direct Submission

Submitted (22-AUG-2000)

Plant Biotechnology, Florida A&M

University, 301 South Perry Paige Building, Tallahassee, FL 32307, USA

REMARK

Sequence update by submitter

On Aug 22, 2000 this sequence version replaced gi:5825430.

Location/Qualifiers



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ACCESSION AY722686
VERSION AY722686.1 GI:52001220
KEYWORDS
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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Aeschynomeneae; Arachis.  
1 (bases 1 to 1901)  
Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.Z.  
Isolation of peanut genes encoding arachins and conglutins by  
expressed sequence tags  
Plant Sci. 169 (2), 439-445 (2005)  
2 (bases 1 to 1901)  
Yan, Y., Wang, L. and Huang, S.  
cDNA clone of peanut seed storage protein gene  
Unpublished  
3 (bases 1 to 1901)  
Yan, Y., Wang, L. and Huang, S.  
Direct Submission  
Submitted (30-JUL-2004) Department of Biology and Biotechnology,  
Sun Yat-sen University, Guangzhou, Guangdong 510275, China  
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LOCUS AY722685 1934 bp mRNA linear PLN 08-JUL-2005  
DEFINITION Arachis hypogaea arachin Ahy-1 mRNA, complete cds.  
ACCESSION AY722685  
VERSION AY722685.1 GI:52001218  
KEYWORDS  
SOURCE Arachis hypogaea (peanut)  
ORGANISM Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.  
1 (bases 1 to 1934)  
Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S. Z.  
Isolation of peanut genes encoding arachins and conglutins by  
expressed sequence tags  
Plant Sci. 169 (2), 439-445 (2005)  
2 (bases 1 to 1934)  
Yan, Y., Wang, L. and Huang, S.  
cDNA clone of peanut seed storage protein gene  
Unpublished  
3 (bases 1 to 1934)  
Yan, Y., Wang, L. and Huang, S.  
Direct Submission  
Submitted (30-JUL-2004) Department of Biology and Biotechnology,  
Sun Yat-sen University, Guangzhou, Guangdong 510275, China  
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QY 62 ATGCGATTGAATCAGAGGGCGGTACATTGAGACTTGGAAACCCCAACACAGGAGTTGCG 121  
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DB 309 TCTACTCCCAATGCTCCCGAGGAGATCTTATCCAGCAAGGAGGAGATCTTTGGGTGTA 368  
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AY439332  
LOCUS 1886 bp mRNA linear PLN 26-OCT-2003  
DEFINITION Arachis hypogaea storage protein mRNA, complete cds.  
ACCESSION AY439332  
VERSION AY439332.1 GI:37789211

## KEYWORDS

SOURCE

## ORGANISM

Arachis hypogaea (peanut)  
Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eustosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.

## REFERENCE

1 (bases 1 to 1886)  
Yang H.-X., Wang, F. and Bi, Y.-P.  
Cloning of Arachin complete cDNA Sequence  
Unpublished  
2 (bases 1 to 1886)  
Yang H.-X., Wang, F. and Bi, Y.-P.  
Direct Submission  
Submitted (17-OCT-2003) Jinan, Shandong 250100, China  
Location/Qualifiers

## FEATURES

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RESULT 13
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DEFINITION Arachis hypogaea allergen Arah3/Arah4 gene, complete cds.
ACCESSION AF510854
VERSION AF510854.1 GI:21314464
KEYWORDS
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
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Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 3825)
Viquez,O.M., Konan,K.N. and Dodo,H.W.
Genomic characterization of the major peanut allergen genes, Arah3
and/or Arah4
Unpublished
REFERENCE 2 (bases 1 to 3825)
Viquez,O.M., Konan,K.N. and Dodo,H.W.
Direct Submission
Submitted (09-MAY-2002) Food and Animal Sciences, Alabama A&M
University, Meridian Street, 4900, Normal, AL 35762, USA
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DEFINITION Arachis hypogaea trypsin inhibitor mRNA, partial cds.
ACCESSION AF487543
VERSION AF487543.1 GI:22135347
KEYWORDS
SOURCE
ORGANISM
Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 657)
Dodo,H.W., Viquez,O.M., Maleki,S.J. and Konan,K.N.
cDNA clone of a putative peanut (Arachis hypogaea L.) trypsin
inhibitor has homology with peanut allergens Ara h 3 and Ara h 4
J. Agric. Food Chem. 52 (5), 1404-1409 (2004)
14995153
2 (bases 1 to 657)
Dodo,H.W. and Viquez,O.M.
Direct Submission
Submitted (25-FEB-2002) Food and Animal Sciences, Alabama A&M
University, Meridian Street, 4900, Normal, AL 35762, USA
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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

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- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1391.2	91.3	1855	4	Aaf90338 Peanut al
7	517.4	34.0	1446	2	Aav17567 Coding se
8	517.4	34.0	1446	6	Abss5193 Glycine m
9	517.4	34.0	1446	10	Adh89252 G. max gl
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11	517.4	34.0	1673	13	Adx12705 Plant ful
12	517.4	34.0	1689	13	Adx13956 Plant ful
13	517.4	34.0	1694	13	Adx14017 Plant ful
14	517.4	34.0	1697	13	Adx13008 Plant ful
15	515.8	33.8	1671	13	Adx13019 Plant ful
16	513	33.7	1431	14	Adz47095 Soybean g
17	513	33.7	1434	14	Adz47109 Soybean m
18	513	33.7	1458	14	Adz47103 N-termina

19	513	33.7	1488	2	AAV17565	Aav17565 Coding se
20	513	33.7	1488	6	ABS55191	Abss55191 Glycine m
21	513	33.7	1488	10	ADH89244	Adh89244 G. max gl
22	513	33.7	1488	12	ADG43979	Adg43979 G. max gly
23	513	33.7	1694	13	ADX13099	Adx13099 Plant ful
24	513	33.7	1716	13	ADX13981	Adx13981 Plant ful
25	513	33.7	1718	13	ADX13067	Adx13067 Plant ful
26	513	33.7	1721	13	ADX13095	Adx13095 Plant ful
27	513	33.7	1724	13	ADX14012	Adx14012 Plant ful
28	513	33.7	1724	13	ADX13038	Adx13038 Plant ful
29	513	33.7	1727	13	ADX13028	Adx13028 Plant ful
30	513	33.7	1727	13	ADX13049	Adx13049 Plant ful
31	513	33.7	1729	13	ADX13589	Adx13589 Plant ful
32	513	33.7	1730	13	ADX13558	Adx13558 Plant ful
33	513	33.7	1743	3	AAZ92638	Aaz92638 cDNA enco
34	511.4	33.6	1458	14	ADZ47107	Adz47107 C-termina
35	511.4	33.6	1729	13	ADx14009	Adx14009 Plant ful
36	505.6	33.2	1458	6	ABS55192	Abss55192 Glycine m
37	505	33.1	1746	4	AAO17536	Aao17536 Soybean g
38	504	33.1	1458	2	AAV17566	Aav17566 Coding se
39	504	33.1	1458	10	ADH89246	Adh89246 G. max gl
40	504	33.1	1458	12	ADG43981	Adg43981 G. max gl
41	504	33.1	1610	13	ADX13062	Adx13062 Plant ful
42	504	33.1	1610	13	ADX13060	Adx13060 Plant ful
43	504	33.1	1678	13	ADX13588	Adx13588 Plant ful
44	504	33.1	1679	13	ADX14013	Adx14013 Plant ful
45	504	33.1	1685	13	ADX13533	Adx13533 Plant ful

ALIGNMENTS

RESULT 1	
AAZ06384	
ID	AAZ06384 standard; DNA; 1524 BP.
XX	
AC	AAZ06384;
XX	
DT	17-OCT-2003 (revised)
DT	09-NOV-1999 (first entry)
XX	
DE	Peanut allergen, Ara h 3.
XX	
KW	allergy; immune response; transgenic; allergen; epitope;
KW	immunoglobulin E; Ig E; binding site; peanut; ds.
XX	
OS	Arachis hypogaea.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1524
FT	/*tag= a
FT	/product= "Ara h 3"
FT	/note= "first three amino acids not coded for"
XX	
PN	WO9938978-A1.
XX	
PD	05-AUG-1999.
XX	
PF	29-JAN-1999; 99WO-US002031.
XX	
PR	31-JAN-1998; 98US-0073283P.
PR	13-FEB-1998; 98US-0074590P.
PR	13-FEB-1998; 98US-0074624P.
PR	13-FEB-1998; 98US-0074633P.
PR	27-AUG-1998; 98US-00141220.
XX	
XX	(UYAR-) UNIV ARKANSAS.
PA	(UYNY ) UNIV NEW YORK MT SINAI SCHOOL MEDICINE.
PA	(SOSI/) SOSIN H.
XX	
PI	Sosin H, Bannon GA, Burks AW, Sampson HA;
DR	WPI; 1999-479189/40.



/note= "there is an apparent 6 nucleotide deletion which encodes for residues Glu and Phe respectively"  
/transl\_except= (pos:1105..1107, aa:Leu)  
/product= "Ara h 3 allergen"  
/note= "does not encode the first three residues in the corresponding protein sequence"

FT TTCTGGCTCTAACACGACCACTGATGTTGCTGTTCTTCTTACTGACCAAC 480  
FT TTTCTGGCTCTAACACGACCACTGATGTTGCTGTTCTTCTTACTGACCAAC 480  
FT TTTCTGGCTCTAACACGACCACTGATGTTGCTGTTCTTCTTACTGACCAAC 480  
FT TTTCTGGCTCTAACACGACCACTGATGTTGCTGTTCTTCTTACTGACCAAC 480  
FT TTTCTGGCTCTAACACGACCACTGATGTTGCTGTTCTTCTTACTGACCAAC 480  
XX WO9945961-A1.  
XX 16-SEP-1999. 99WO-US005494.  
XX 12-MAR-1999; 98US-0077763P.  
XX 12-MAR-1998; 98US-0077763P.  
XX 11-MAR-1999; 99US-00077763.  
XX (UYAR-) UNIV ARKANSAS.  
XX Burks W, Helm RM, Cockrell G, Bannon GA, Stanley JS, Shin DS;  
PI Sampson H, Compadre CM, Huang SK, Maleki SJ, Kopper RA;  
XX WPI: 1999-551218/46.  
XX P-PSDB; AAY40912.  
XX Tertiary structure of peanut allergen Ara h 1 for protection of a host  
PT animal from allergic reaction.  
XX Disclosure; Page 185; 193pp; English.  
XX The invention provides a tertiary structure for the peanut allergen Ara H  
CC 1. The Ara H 1 allergen is found to contain 23 linear IgE-binding  
CC epitopes. The invention also provides an isolated recombinant peanut  
CC allergen designated Ara h 3 and a nucleotide molecule encoding the peanut  
CC allergen Ara h 3. Molecules of the invention are used to protect a host  
CC animal from allergic reaction, particularly using a modified allergen  
CC which is less reactive with IgE. The invention may also be used to ensure  
CC that the allergen is not introduced into genetically modified food. The  
CC present sequence represents a DNA encoding the Ara h 3 allergen. (Updated  
CC on 17-OCT-2003 to standardise OS field)  
XX  
XX Sequence 1524 BP; 455 A; 390 C; 398 G; 281 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1524; DB 2; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGCAGCAACCGAGAGAACGGTGCAGTTCAGCGCTCAATGGCGAGACCTGAC 60  
DB 1 CGGCAGCAACCGAGAGAACGGTGCAGTTCAGCGCTCAATGGCGAGACCTGAC 60  
QY 61 AATCGCATTTGAATCAGAGGCGGTATACATTGAGACTTGGAAACCCCAACACAGGAGTTC 120  
DB 61 AATCGCATTTGAATCAGAGGCGGTATACATTGAGACTTGGAAACCCCAACACAGGAGTTC 120  
QY 121 GAATCGCGCGGCTCGCCCTCTCTCGCTTAGTCTCGCGCGCAACGCCCTTCGTAGGCCT 180  
DB 121 GAATCGCGCGGCTCGCCCTCTCTCGCTTAGTCTCGCGCGCAACGCCCTTCGTAGGCCT 180  
QY 181 TTCTACTCCATGCTCCCGAGGAGTTCATCAGCAGGAGGAGGATCTTTGGGTTG 240  
DB 181 TTCTACTCCATGCTCCCGAGGAGTTCATCAGCAGGAGGAGGATCTTTGGGTTG 240  
QY 241 ATATTCCCTGTTGCTCTAGACACTATGAAGAGCTTACACACAAAGTTCGTCTCAG 300  
DB 241 ATATTCCCTGTTGCTCTAGACACTATGAAGAGCTTACACACAAAGTTCGTCTCAG 300  
QY 301 TCCCAAGACCAACAGAGCTCTCCAGGAGAGAGACAAAGCCAAACAGACGATAGT 360  
DB 301 TCCCAAGACCAACAGAGCTCTCCAGGAGAGAGACAAAGCCAAACAGACGATAGT 360  
QY 361 CACCAGAGGTGACCGTTCGATGAGGTTGATCTATTGCAAGTTCCTCCACCGTGTGCT 420  
DB 361 CACCAGAGGTGACCGTTCGATGAGGTTGATCTATTGCAAGTTCCTCCACCGTGTGCT 420

QY	1501	CAGTCTCCGAGGGCTGTGGCTTAA	1524	Db	61	AATCGCATTTGAATCAGAGGGGTTACATTTGAGACTTTGAAACCCCAACACACAGGAGTTC	120
Db	1501	CAGTCTCCGAGGGCTGTGGCTTAA	1524	QY	121	GAATGCGCGGGCTGCGCCCTCTCTCGCTTAGTCTCTCCGCGCAACCCCTTCGTAGGCCT	180
				Db	121	GAATGCGCGGGCTGCGCCCTCTCTCGCTTAGTCTCTCCGCGCAACCCCTTCGTAGGCCT	180
RESULT 3				QY	181	TTCTACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATACCTTTGGGTTG	240
ABX70612				Db	181	TTCTACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATACCTTTGGGTTG	240
ID	ABX70612	standard; cDNA; 1524 BP.		QY	241	ATATTTCCCTGGTTGTCCTAGACACTATGAAGAGCCCTCACACAAAGTTCGTCTCATCTCAG	300
XX	AC	ABX70612;		Db	241	ATATTTCCCTGGTTGTCCTAGACACTATGAAGAGCCCTCACACAAAGTTCGTCTCATCTCAG	300
XX	26-MAR-2003	(first entry)		QY	301	TCCCAAGACCACCAAGACGCTCTCCAAAGGAGAGACCAAAAGCCAAACAGCAACGAGATAGT	360
XX	Peanut Ara h3 cDNA sequence.			Db	301	TCCCAAGACCACCAAGACGCTCTCCAAAGGAGAGACCAAAAGCCAAACAGCAACGAGATAGT	360
KW	Peanut; ss; allergy; Ara h1; Ara h2; Ara h3; gene; IgE binding site; anaphylactic food allergen; antiallergenic; vaccine; wound healing.			QY	361	CACCAGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTCAGTTTCCACCGGTGTGCT	420
KW	anaphylactic food allergen; antiallergenic; vaccine; wound healing.			Db	361	CACCAGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTCAGTTTCCACCGGTGTGCT	420
OS	Arachis hypogaea.			QY	421	TTCTGGCTCTACAAACGACCAACGACACTGATGTTGTTGCTGTTTCTTCTTACTGACACCAAC	480
XX	WO200274250-A2.			Db	421	TTCTGGCTCTACAAACGACCAACGACACTGATGTTGTTGCTGTTTCTTCTTACTGACACCAAC	480
XX	26-SEP-2002.			QY	481	AACAACGACAAACGAGCTTGCATCAGTTCCCGAGGAGATTCAAATTTGGCTGGGAAACAGGAG	540
XX	18-MAR-2002; 2002WO-US009108.			Db	481	AACAACGACAAACGAGCTTGCATCAGTTCCCGAGGAGATTCAAATTTGGCTGGGAAACAGGAG	540
XX	16-MAR-2001; 2001US-0276822P.			QY	541	CAAGAGTTCTTAAGGTACCAGCAACCAAGCAGCAACCAAGCAGCAAGCAAGAGCTTACCATAT	600
PR	18-MAR-2002; 2002US-00276822.			Db	541	CAAGAGTTCTTAAGGTACCAGCAACCAAGCAGCAACCAAGCAGCAAGCAAGAGCTTACCATAT	600
XX	(PANA-) PANACEA PHARM.			QY	601	AGCCCATACAGCCCGCAAAAGTCAGCCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGA	660
XX	Caplan M, Sosin H, Sampson H, Bannon GA, Burks WA, Cockrell G; Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ; Rabjohn PA, Shin DS, Stanley JS;			Db	601	AGCCCATACAGCCCGCAAAAGTCAGCCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGA	660
DR	WPI; 2003-018765/01.			QY	661	CAGCAGCGCGCAGAGAAACGAGCAGCAAGCAAGAAAGAAACCAAGAGTGGAAACATCTTC	720
DR	P-PSDB; ABU52484.			Db	661	CAGCAGCGCGCAGAGAAACGAGCAGCAAGCAAGAAAGAAACCAAGAGTGGAAACATCTTC	720
XX	New modified anaphylactic food allergen, useful for preventing or treating allergic reactions associated with e.g. anaphylactic allergens.			QY	721	AGCGGCTTCACCGCGGAGTTCCCTGGAAACAGCCCTCCAGGTTTCACGACAGACAGATAGTG	780
XX	Example 16; Fig 68A; 300pp; English.			Db	721	AGCGGCTTCACCGCGGAGTTCCCTGGAAACAGCCCTCCAGGTTTCACGACAGACAGATAGTG	780
CC	The invention relates to a modified anaphylactic food allergen has an amino acid sequence that is substantially identical to that of natural anaphylactic food allergen, except for a cysteine residue that has been modified so that it cannot participate in the disulphide bond. The modification may also comprise mutation of the IgE binding sites to reduce allergenicity. Also included are: (1) a method of making a modified anaphylactic food allergen; (2) a nucleotide molecule encoding or for causing a site specific mutation in the modified anaphylactic food allergen; (3) a transgenic plant or animal expressing the modified anaphylactic food allergen; (4) a method of treating an individual by reducing the clinical response to a natural anaphylactic food allergen; and an isolated fragment of peanut allergen Ara h 1. The modified anaphylactic food allergen is useful for preventing or treating allergic reactions associated with any natural allergen such as food, insect, rubber or preferably anaphylactic allergens. It is also useful for treating wounds in mammals such as bovine, canine, feline, caprine, CC ovine, porcine, murine or equine species. The present sequence is a cDNA encoding a peanut allergen (e.g. Ara hi, h2 or h3)			QY	781	CAAAACCTTAAGAGCGCAGAGCCGAGAGTGAAGAGAGGAGGCCATTTGTGACAGTGAGGGGA	840
CC				Db	781	CAAAACCTTAAGAGCGCAGAGCCGAGAGTGAAGAGAGGAGGCCATTTGTGACAGTGAGGGGA	840
CC				QY	841	GGCCTCAGAAATCTTGAGCCCGAGATGAAGAAGAGAGCTGCCGACGAAGAGGAAATACGAT	900
CC				Db	841	GGCCTCAGAAATCTTGAGCCCGAGATGAAGAAGAGAGAGCTGCCGACGAAGAGGAAATACGAT	900
CC				QY	901	GAAGATGAATATGAATACGATGAAGAGGATAGAGGCGTGGCAGGGGAACAGAGGAGG	960
CC				Db	901	GAAGATGAATATGAATACGATGAAGAGGATAGAGGCGTGGCAGGGGAACAGAGGAGG	960
CC				QY	961	GGGAATGGTATTGAAGAGAGAGATCTGCACCGCAGAGTGCTAAAAAAGAACATTGGTAGAAC	1020
CC				Db	961	GGGAATGGTATTGAAGAGAGAGATCTGCACCGCAGAGTGCTAAAAAAGAACATTGGTAGAAC	1020
QY	Sequence 1524 BP; 455 A; 390 C; 398 G; 281 T; 0 U; 0 Other;			QY	1021	AGATCCCTCGACATCTACAAACCTCAAGCTGGTTCACTCAAACTGCCACGATCTCAAC	1080
QY	Query Match 100.0%; Score 1524; DB 8; Length 1524;			Db	1021	AGATCCCTCGACATCTACAAACCTCAAGCTGGTTCACTCAAACTGCCACGATCTCAAC	1080
QY	Best Local Similarity 100.0%; Pred. No. 0;			QY	1081	CTTCTAATCTTAGTGGCTTGGACCTTAGTGTGGAATATGGAATCTCTACAGGAATGCA	1140
QY	Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			Db	1081	CTTCTAATCTTAGTGGCTTGGACCTTAGTGTGGAATATGGAATCTCTACAGGAATGCA	1140
QY	1 CGGACGACACCGGAGGAGACGGGTGCGAGTTCAGCGCCTCAATGGCGAGACCTGAC	60		QY	1141	TTGTTTGTGCTCACTACAAACCAACGACATCATATATCGATTGAGGGGACGG	1200
Db	1 CGGACGACACCGGAGGAGACGGGTGCGAGTTCAGCGCCTCAATGGCGAGACCTGAC	60					
QY	61 AATCGCATTTGAATCAGAGGGGTTACATTTGAGACTTTGAAACCCCAACACAGGAGTTC	120					







CC an antigen by identifying prior display of allergic symptoms when exposed  
CC to the antigen, or a familial relationship with an individual who  
CC previously displayed allergic symptoms when exposed to the antigen.  
CC Following this an antigen-specific IgE present on one or more mast cells  
CC or basophils in the individual's serum is identified. The individual is  
CC then contacted with a peptide corresponding to a portion of the antigen,  
CC which is selected, formulated, and delivered so that binding of the  
CC peptide to antigen-specific IgE is reduced as compared with IgE binding  
CC of intact antigen. The composition is also useful for treating and  
CC preventing allergic reactions  
XX  
SQ

Sequence 1524 BP; 455 A; 392 C; 396 G; 281 T; 0 U; 0 Other.

Query Match 99.8%; Score 1520.8; DB 4; Length 1524;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	CGGCAGCAACCGGAGGAGACGGTGCAGTTCAGCGCCTCAATGGCGAGACCTGAC	60
Db	1	CGGCAGCAACCGGAGGAGACGGTGCAGTTCAGCGCCTCAATGGCGAGACCTGAC	60
Qy	61	AATCGCAATCAATCAGAGGCGGTTACATTGAGACTTGGAAACCCCAACACACAGGAGTTC	120
Db	61	AATCGCAATCAATCAGAGGCGGTTACATTGAGACTTGGAAACCCCAACACACAGGAGTTC	120
Qy	121	GAATGCGCGCGCGTTCGCTCTCTCGCTTAGTCTCCGCGCAACCGCCTTCGTAGGCCT	180
Db	121	GAATGCGCGCGCGTTCGCTCTCTCGCTTAGTCTCCGCGCAACCGCCTTCGTAGGCCT	180
Qy	181	TTCTACTCCAATGCTCCCAAGGAGATCTTCATCAGCAAGAAAGGGGATCTTTGGGTTG	240
Db	181	TTCTACTCCAATGCTCCCAAGGAGATCTTCATCAGCAAGAAAGGGGATCTTTGGGTTG	240
Qy	241	ATATTCCCTGTTGCTCTAGACACTATGAAGAGCTTCACACAAAGTCTGCTCATCTCAG	300
Db	241	ATATTCCCTGTTGCTCTAGACACTATGAAGAGCTTCACACAAAGTCTGCTCATCTCAG	300
Qy	301	TCCCAAGACCAACCAAGACGTCTCCAAGGAGAGACCAAGCCCAACAGCAGATAGT	360
Db	301	TCCCAAGACCAACCAAGACGTCTCCAAGGAGAGACCAAGCCCAACAGCAGATAGT	360
Qy	361	CACGAGAGTGACCGTTTCGATAGGAGTCTCATTCAGCAAGTTCACCGGTGTTGCT	420
Db	361	CACGAGAGTGACCGTTTCGATAGGAGTCTCATTCAGCAAGTTCACCGGTGTTGCT	420
Qy	421	TTCTGCTCTACACGACACGACACTGATGTTGCTGCTTCTTACTGACACCAAC	480
Db	421	TTCTGCTCTACACGACACGACACTGATGTTGCTGCTTCTTACTGACACCAAC	480
Qy	481	AACAACGACCAACGAGCTTGATCAGTTTCCCGGAGAGATTCAAATTTGGCTGGGAACCGGAG	540
Db	481	AACAACGACCAACGAGCTTGATCAGTTTCCCGGAGAGATTCAAATTTGGCTGGGAACCGGAG	540
Qy	541	CAAGAGTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGAGCAAGAGCTTACCATAT	600
Db	541	CAAGAGTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGAGCAAGAGCTTACCATAT	600
Qy	601	AGCCCATACAGCCGCAAGTCTAGCCTTAGACAGAGAGCGTCAATTTAGCCCTCGAGGA	660
Db	601	AGCCCATACAGCCGCAAGTCTAGCCTTAGACAGAGAGCGTCAATTTAGCCCTCGAGGA	660
Qy	661	CAGCAGACCGCGAGAACGAGCAGGACCAAGAGAGAAACCAAGGTGGAAACATCTTTC	720
Db	661	CAGCAGACCGCGAGAACGAGCAGGACCAAGAGAGAAACCAAGGTGGAAACATCTTTC	720
Qy	721	AGCGGCTTACGCGGAGTTCCTGGAAACAAAGCCTTCAGGTTGACGACAGATAGTG	780
Db	721	AGCGGCTTACGCGGAGTTCCTGGAAACAAAGCCTTCAGGTTGACGACAGATAGTG	780
Qy	781	CAAAACCTAAGAGCGGAGACCGGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAGGGA	840
Db	781	CAAAACCTAAGAGCGGAGACCGGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAGGGA	840

Qy	841	GGCTTCAGAAATCTTGAGCCAGATAGAAAGAGAGAGCTGCCGACGAAGAGGAATACGAT	900
Db	841	GGCTTCAGAAATCTTGAGCCAGATAGAAAGAGAGAGCTGCCGACGAAGAGGAATACGAT	900
Qy	901	GAAGATGAATATGAATACGATGAAGAGGATAGAAAGCGTGGCAGGGAAGCAGAGGCGG	960
Db	901	GAAGATGAATATGAATACGATGAAGAGGATAGAAAGCGTGGCAGGGAAGCAGAGGCGG	960
Qy	961	GGGAATGGTATTGAAGAGAGAGCTTCACCGCAAGTGTCTAAAAGAAACATTTGGTAGAAAC	1020
Db	961	GGGAATGGTATTGAAGAGAGAGCTTCACCGCAAGTGTCTAAAAGAAACATTTGGTAGAAAC	1020
Qy	1021	AGATCCCTGACATCTACAAACCTCAAGCTGTGTTCACTCAAACTGCCAACATCTCAAC	1080
Db	1021	AGATCCCTGACATCTACAAACCTCAAGCTGTGTTCACTCAAACTGCCAACATCTCAAC	1080
Qy	1081	CTTCTAATCTAGTGGCTTGGACCTAGTCTGGAATATGGAATCTCTACAGGAATGCA	1140
Db	1081	CTTCTAATCTAGTGGCTTGGACCTAGTCTGGAATATGGAATCTCTACAGGAATGCA	1140
Qy	1141	TTGTTTGTGCTCCTACCTACCAACCAACGACACAGCATCATATATCGATTGAGGGGACGG	1200
Db	1141	TTGTTTGTGCTCCTACCTACCAACCAACGACACAGCATCATATATCGATTGAGGGGACGG	1200
Qy	1201	GCTCAGCTGCAAGTCTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG	1260
Db	1201	GCTCAGCTGCAAGTCTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG	1260
Qy	1261	GGTCACTGCTTGTGTCGACAGAACTTGGCGCTCGCTGGAAAGTCCCGAGCGGAGAAC	1320
Db	1261	GGTCACTGCTTGTGTCGACAGAACTTGGCGCTCGCTGGAAAGTCCCGAGCGGAGAAC	1320
Qy	1321	TTGGAATACGTGGCATTCAAGACAGACTCAAGGCCCGCAGCATAGCCAACTCGCGGTGAA	1380
Db	1321	TTGGAATACGTGGCATTCAAGACAGACTCAAGGCCCGCAGCATAGCCAACTCGCGGTGAA	1380
Qy	1381	AATCTCGTATAGATAACCTCGCGGAGGAGTGTGTTGCAAAATTCATATGGCCTTCAAGG	1440
Db	1381	AATCTCGTATAGATAACCTCGCGGAGGAGTGTGTTGCAAAATTCATATGGCCTTCAAGG	1440
Qy	1441	GAGCAGGCAAGCAGCTTAAGAACACCAACCCCTTCAAGTCTCTGCTTCCACCGTCTCAG	1500
Db	1441	GAGCAGGCAAGCAGCTTAAGAACACCAACCCCTTCAAGTCTCTGCTTCCACCGTCTCAG	1500
Qy	1501	CAGTCTCCGAGGCTGTGGCTTAA 1524	
Db	1501	CAGTCTCCGAGGCTGTGGCTTAA 1524	

RESULT 6  
AAF90338  
ID AAF90338 standard; cDNA; 1855 BP.  
XX AAF90338;  
AC AAF90338;  
XX  
DT 11-SEP-2003 (revised)  
DT 23-JUL-2001 (first entry)  
XX  
DE Peanut allergen Ara h4 cDNA.  
XX Peanut; allergen; Ara h2; Ara h3; transgenic plant; allergy; ss.  
XX Arachis hypogaea.  
XX  
PH Key Location/Qualifiers  
FT CDS 1..1593  
FT /\*tag= a  
FT misc\_feature 430..1190  
FT /\*tag= b  
FT /note= "PCR amplified fragment"  
XX  
XX WO200136621-A2.  
XX





Db	1247	AGTATGTTTCATTTCAAGACAATATGATAGACCTTCGATCGGCAACCTTGAGGTGCAACT	1306
QY	1385	CGGTATAGATAACCTGCGGAGGAGGTGGTTCGAAATTCATATGCGCTCCAAAGGGAGC	1444
Db	1307	CATTGTTGAACGATTGCGGAGGAAGTGTTCAGCAAACTTTTAACCTAAGGAGCAGC	1366
QY	1445	AGCAAGGAGCTTAAGACAACAACCCCTTCAAGTTCCTGTTCCACCGTCTCAGCAGT	1504
Db	1367	AGCCAGGAGGTCAAGAAACAACCCCTTTCAGCTTCCTGGTTCCACCTAAGGAGTCTC	1426
QY	1505	CTCCGAGGCTGGGCTTA	1523
Db	1427	AGAGGAGAGTTGTGGCTTA	1445
RESULT 8			
AB55193	AB55193 standard; DNA; 1446 BP.		
XX	AC	AB55193;	
XX	DT	17-DEC-2002 (first entry)	
XX	DE	Glycine max (Soybean) var. Dare gene.	
XX	XX	Soybean; Glycinin; atomic coordinate data; processability; soya protein;	
KW	KW	Dare; protein co-ordinate data; gene; ds.	
XX	OS	Glycine max.	
XX	Key	Location/Qualifiers	
FH	FT	1. .1446	
FT	FT	/*tag= a	
FT	FT	/product= "Glycine max (Soybean) var. Dare protein"	
XX	PN	JP2002193996-A.	
XX	PD	10-JUL-2002.	
XX	XX	21-DEC-2000; 2000JP-00405097.	
PF	XX	21-DEC-2000; 2000JP-00405097.	
PR	XX	(KYOU ) UNIV KYOTO.	
XX	XX	WPI; 2002-685438/74.	
DR	DR	P-PSDB; ABG71266.	
XX	XX	Glycinin, beta-conglycinin and proglycinin, their crystal structures, three dimensional coordinates, three dimensional structured and models and their uses.	
PT	PT	Disclosure; Page 1271-1273; 1298pp; Japanese.	
XX	PS	The present invention relates to a new Glycinin characterised by the atomic coordinate data fully defined in the specification. The structure can be used for improving processability of soya protein. The present CC	
CC	CC	nucleic acid sequence encodes the Glycine max (Soybean) var. Dare protein, as described in the specification	
XX	XX	Sequence 1446 BP; 426 A; 361 C; 354 G; 305 T; 0 U; 0 Other;	
Query Match			
Best Local Similarity 34.0%; Score 517.4; DB 6; Length 1446;			
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;			
QY	5	AGCAACGGAGGAGACCGGTGCGAGTTCAGCGCCTCAATGCGCAGAGACCTGACAATC	64
Db	71	AGCAGCCACAGCAAAACGAGTGCAGATCCAAACGCTCAATGCCCTTAAACCCGGATAACC	130
QY	65	GCATTGAATCAGAGGGCGGTACATTGAGACTTTGGAAACCCCAACAACCCAGGAGTTGGAAT	124

Db	131	GTATAGATCAAGAGTGGCTTCATTGAGACATGGNAACCTTAACAACAAGCCATCCAGT	190
QY	125	GGCGGGGTCCGCTTCTCGCTTAGTCTCTCGCGCAACGCCCTTCGTAGGCTTTCT	184
Db	191	GTGCGGTGTTGCCCTCTCTCGTGCACCTCAACCGCAACGCCCTTCGACAGCTTCT	250
QY	185	ACTCCAACTGCCAGGAGATCTTCACACAGGAGGAGGATATCTTGGTTCATAT	244
Db	251	ACACCAACCTCCCGAGGAGATCTACATCAACAAGGTAGTGGTATTTTGGCATATAT	310
QY	245	TCCTGTTGTCTAGACACTATGAAGACCTCACACACAAGTCTCGATCTCAGTCC	304
Db	311	TCCGGTTGTCTAGACATTTGAAGCCT-----	342
QY	305	AAAGACCAAGACGTCTTCAAGGAGAGAACCAAGCCCAACAGCAACGAGATAGTCACC	364
Db	343	-----CAACAAGGACAAAGCAGCAGGCCCAAGACCGTCACC	382
QY	365	AGAAGTGCACGTTTCGATGAGGTGATCTCATTTGCAGTTCCTCCACCGGTGTTCTTCT	424
Db	383	AGAAGATCTATCATTTCAGAGAGGGTGAATTCATTCAGTGCACCGGTTTTGCATAT	442
QY	425	GGCTCTACAACGACCACGACACTGATGTTGTTGCTGTTTCTCTTACTGACACCAACA	484
Db	443	GGATGTACAACAATGAAGACACTCTCTGTTGTTGCGTTCCTCTATTGACACCAACAGT	502
QY	485	AGCAACACAGTTCATGATGTTCCCGAGGAGATTCAATTTGGCTGGGAACACGGAGCAAG	544
Db	503	TCAGAAACCAAGCTCGACCAAGATCCCTAGGAGATTCTATCTGCTGGGAACCAAGAGCAAG	562
QY	545	AGTTCTTAAGTACCAGCAACAAGCAGACAAAGCAGACGAGCAAGAGCTTTACCATATAGCC	604
Db	563	AGTTTCTCAGTATCAGCCACAGAACGACGAAG-----	595
QY	605	CATACAGCCGCAAGTTCAGCCTTAGACAAGAAGAGCGTGAATTTAGCCCTCGAGGACAGC	664
Db	596	-----GAGGTACTC	604
QY	665	ACAGCCGAGAGAAACGAGCAGGACAAAGAAAGAAAGAAACGAGGTGGAACATCTTCAGCG	724
Db	605	AAAGCCAGAAAGGAAAGCGTCAGCAAGAAAGAAAGAAACGAGGAGGACGATATTGAGTG	664
QY	725	GCTTCACGCGGAGTTCTTGGAAACAGCTTCCAGGTTGACGACACAGACAGATAGTCAAA	784
Db	665	GCTTCGCCCGGAATTTTGGAAACATGCGTTC---GTCGTGACACGACGAGATAGTGA	721
QY	785	ACCTAAGAGCGGAGACCGGAGAGTGAAGAAGAGGGAGCCATTGTGACAGTGAGGGAGGCC	844
Db	722	AGCTACAAGGTGAGAAACGAAAGAGGAAGAGAGGGTGCCTTTGTGACAGTGAAGGAGGTC	781
QY	845	TCAGATCTTGAGCCGAGATAGAAGAGACGTGCCGACGAGAGAGGAAATACGATGAAG	904
Db	782	TCAGCGTGATAGCCCAACCGGAGAGCAGCAACAAGACCCGAGGAGAGGAGAGC	841
QY	905	ATGAATATCAATACGATGAAGAGGATAGAAGGCGTGGCAGGGGAAAGCAGAGGAGGGGA	964
Db	842	CAGATTGTGACGAGAAAGACAACAT-----TGCCAAAGCCAAAGCAGAA	886
QY	965	ATGGTATTCAGAGAGAGCATCTGCACCGCAAGTGCTAAAAAGAACATTTGGTAGAAAACAGAT	1024
Db	887	ATGGCATTGACGAGACCAATTTGCACAATGAGACTTCGCCACAACATTTGCCAGACTTCAT	946
QY	1025	CCCTTGACATCTACACCTCAAGCTGAGTTCCTCAAACTGCCAAGATCTCAACCTTC	1084
Db	947	CACCTGACATCTTCAACCTCAAGCTGGTAGCATCAACCGCTACAGCTCGACTTC	1006
QY	1085	TAATACCTTAGTGGCTTTGGACCTTAGTGTGTAATATGGAATCTCTACAGAAATGCAATGT	1144
Db	1007	CAGCCCTCTCGCTCAAACTCAGTGCCAGTTTGGATCACTCCGCAAGAAATGCTATGT	1066
QY	1145	TTGTCGCTCACTACAAACCAACGACAGCATCATATATCGATTGAGGGAGCGGCTC	1204
Db	1067	TCGTGCCACACTACAACTTGAACGCAACAGCATATAATACGCAATTTGAATGGAGCGGCAT	1126









CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 1673 BP; 501 A; 402 C; 396 G; 374 T; 0 U; 0 Other;  
Query Match 34.0%; Score 517.4; DB 13; Length 1673;  
Best Local Similarity 62.8%; Pred. No. 1.8e-137;  
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;  
QY 5 AGCAACCGGAGGAGAACGGGTCCAGTTCAGCGCCTCAATGCGCAGAGACCTGACAATC 64  
DB 93 AGCAGCCACAGCAAAACGAGTGCAGATCCAAAGCCTCAATGCGCCTCAAAACCGGATAACC 152  
QY 65 GCATTGAATCAGAGGGGGGTACATTGAGACTTTGGAAACCCCAACACACAGGAGTTGCAAT 124  
DB 153 GTATAGAGTCAGAAGGTGGGTTCAATTGAGACATGGAAACCCCAACAAAGCCATTCCAGT 212  
QY 125 GCGCCGGGTGCGCCTCTCTCGCTTAGTCTCGCGCGCAAGCCCTTCGTAGGCGCTTCT 184  
DB 213 GTGCCGGTGTGCGCTCTCTCGCTGACCCCTCAACCGCAAGCCCTTCGCAGACCTTCCT 272  
QY 185 ACTCCAAATGTCCTCCAGGAGATCTTCATCCAGCAAGGAAGGGGATACTTTGGTTGATAT 244  
DB 273 ACACCAACGCTCCCGAGGAGATCTACATCCAAAGGTAGTGTATTTTGGCATGATAT 332  
QY 245 TCCTCGTGTCTAGACACTATGAAGAGCCTCACACAGGTCTGTCGATCTCAGTCCC 304  
DB 333 TCCCGGGTGTCTAGACATTTTGAAGGCT----- 364  
QY 305 AAAGACCAACAGACGTCTCAAGGAGAGAACCAACCAAGCCAAACAGACGAGATGTCACC 364  
DB 365 -----CAACAAAGGACAAAGCAGCAGCGCCCAAGACCGTCACC 404  
QY 365 AGAAGTGACCGCTTCGATGAGGGTGATCTATTGAGTTCCTCCACCGGTGTTGCTTCT 424  
DB 405 AGAAGATCTATCATCTTCAGAGAGGGTGATTTGATGTCAGTGCACACCGGTTTTCATACT 464  
QY 425 GGCTCTACACGACCGACGACATGATGTTGCTGCTTCTTCTTACTGACACCAACAACA 484  
DB 465 GGATGTACAAATGAAGACATCTCTGTTGTCGGGTTTCTTATTGACCAACAGCT 524  
QY 485 ACACAAACCAAGCTTGATCAGTTCCTCCAGGAGATTCAATTTGGCTGGGAAACCGGCAAG 544  
DB 525 TCCAGAACCAAGCTCGACCATGCTTAGGAGATTCTATCTTCTGGGAAACCAAGACGAG 584  
QY 545 AGTTCTTAAGGTACCGACAAACAAAGCAGACAAGAGCAGACGAAGAGCTTACCATATAGCC 604  
DB 585 AGTTCTTACAGTATCAGCCACAGAAAGCAGCAAG----- 617  
QY 605 CATACAGCCCGCAAGTCAACCTAGACAAAGAGCGTGAATTTAGCCCTCGAGGACAGC 664  
DB 618 -----GAGGTACTC 626  
QY 665 ACAGCCGACAGAACGAGCAGGACAGCAAGAAAGAAACGAAGGTGGAACATCTTCAGCG 724  
DB 627 AAAGCCAGAAAGGAAAGCGTCAGCAAGAAAGAAACGAAGGAGCGCAGCATATTGAGTG 686  
QY 725 GCTTCACGCCGGAGTTCCTCGAACAAGCCTTCAGGTGTCGACGACAGATAGTCAAA 784  
DB 687 GCTTCGCCCGGGAATTTCTTGAACATGCGTTC---GTGCTGGACAGCAGATAGTGAGAA 743  
QY 785 ACCTAAGAGCGGAGACCGGAGAGTGAAGAAAGAGGAGGCCATTGTGACAGTGGGGAGGCC 844

DB 744 AGCTCAAGGTGAGAAACGAAGGAGGAGAAAGGGTGCCATTGTGACAGTCAAAAGGAGGTC 803  
QY 845 TCAGAAATCTTGAAGCCAGATAGAAAGAGAGACGTGCCACGAAGAGAGGAATACGATCAAG 904  
DB 804 TCAGCGTGATAAGCCACCCACCGAAGAGCAGCAACAAGACCCCGAGGAAGAGAGAAGC 863  
QY 905 ATGAATATGAATACGATGAAGAGGATAGAAAGCGGTGGCAGGGAAGCAGAGGAGGGGGA 964  
DB 864 CAGATTGTGACGAGAAAGACAAACAT-----TGCCAAAGCCCAAAGCAGAA 908  
QY 965 ATGGTATTCAAGAGAGCATCTCAGCCGCAAGTGTCTAAAGAACATTTGTTAGAAAACAGAT 1024  
DB 909 ATGGCAATTCAGGAGACCATTTGCACAATGAGACTTCGCCACAACATTTGCCAGACTTCAT 968  
QY 1025 CCCTGACATCTACAAACCCCTCAAGCTGGTTCACTCAAAATCGCCAAACGATCTCAACCTTC 1084  
DB 969 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCAACACCGCTACCAGCTCGACTTCC 1028  
QY 1085 TAATACCTTAGTGGCTTGGACCTAGTGTGTAATATGGAATCTCTACAGGAATGCATTGT 1144  
DB 1029 CAGCCCTCTGCTGGCTCAAACTCAGTCCCAGTTTGGATCACTCCGCAAGAAATGCTATGT 1088  
QY 1145 TTGTGCTCACTACAAACACCAACGCAACAGCATCATATATCGATTGAGGGGACGGGCTC 1204  
DB 1089 TGTGCCACACTACAACCTGAACGCAACAGCATATATATACGATTGAATGGACGGGCAT 1148  
QY 1205 AGTGCAAGTCTGTGGACAGCAACGCGCAACAGAGTGTACGACAGGAGCTTCAAGAGGGTC 1264  
DB 1149 TGTCAAGTGTGTGAATTCGAATGGTGGAGAGTGTTCGATGGAGAGCTGCAAGAGGGAC 1208  
QY 1265 AGTGCTTGTGGTCCACAGAACTTCGCGTGTGCTGGAAGTCCAGAGGGAGAACTTCG 1324  
DB 1209 AGTGTTTAATTTGTGCCACAAACTTTTGGCTGGCTGCAAGATCACAGAGCGCAACTTCG 1268  
QY 1325 AATACGTGCACTTCAAGACAGACTCAAGGCCCAAGCATAGCAACCTCGCGGTGAAAACT 1384  
DB 1269 AGTATGTTTCAATTCAGACCAATGATAGACCTCGATCGGCAACCTTGCAGGTGCAACT 1328  
QY 1385 CGGTATAGATAAACCCTGCGGAGGAGTGGTTGCAAAATTCATATGCGCTCCAAAGGAGC 1444  
DB 1329 CATTTGTTAAACGATTTGCCGAGGAAGTGATTTCAGCAAACTTTTAACTTAAGGAGCAGC 1388  
QY 1445 AGCAAGGAGCTTAGAACAACACCCCTTCAAGTTCTTCGTTCCACCGCTCTCAGCAGT 1504  
DB 1389 AGCCAGGAGGCTCAAGAAACAACCCCTTTCAGCTTCTCTGTTCCACCTTAAGAGGTCTC 1448  
QY 1505 CTCGAGGGGCTGTGGCTTA 1523  
DB 1449 AGAGGAGAGTGTGGCTTA 1467  
RESULT 12  
ADX13956  
ID ADX13956 standard; cDNA; 1689 BP.  
XX  
AC ADX13956;  
XX  
DT 21-APR-2005 (first entry)  
XX  
XX Plant full length insert polynucleotide seqid 8531.  
XX  
XX plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
XX protein content; gene; ss.  
OS Unidentified.  
XX



PN US2004034888-A1.  
XX 19-FEB-2004.  
XX 28-APR-2003; 2003US-00425114.  
XX 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TAB/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
DR  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
XX Claim 1; SEQ ID NO 8531; 15bp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
XX Sequence 1689 BP; 504 A; 408 C; 396 G; 381 T; 0 U; 0 Other;  
SQ  
Query Match 34.0%; Score 517.4; DB 13; Length 1689;  
Best Local Similarity 62.8%; Pred. No. 1.8e-137;  
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;  
QY 5 AGCAACGGAGGAGACCGCTCCAGTTCAGCGCCTCAATGCCAGAGACCTGCAATC 64  
DB 105 AGCAGCACAGCAAAACAGTGGCAGATCCAAACGCTCAATGCCCTCAAAACCGGATAAC 164  
QY 65 GCATTGGAATCAGAGGCGGTTCATTAGACTTTGGAACCCCAACACAGAGGTTGGAAT 124  
DB 165 GTATAGATCAGAGGTGGCTTCATTAGACATGGAAACCTTAACACAGCAATCCAGT 224  
QY 125 GCAGCGGCTGCGCTCTCTCGTCTAGTTCCTCGCGCGCAACGCCCTTCGAGCGCTTCT 184  
DB 225 GTGCGGCTGTGCTCTCTCGTCTAGTTCCTCGCGCGCAACGCCCTTCGAGACCTTCT 284  
QY 185 ACTCCATGCTCCCGAGGATCTTCATCCAGCAAGGAGGATCTTGGGTGATAT 244  
DB 285 ACACCAACGCTCCCGAGGATCTTACATCCAAACAGGTAGTGTATTTTGGCATGATAT 344  
QY 245 TCCCTGTTCTCTAGACACTATGAGAGGCTCACACACAGGTCTCGTCTCAGTCCC 304  
DB 345 TCCCGGTTGCTTAGACATTTGAAGAGCTT----- 376  
QY 305 AAAGACCACCAAGACGCTCTCCAGGAGAGAGACCAAGCCAAAGCAACGAGATAGTCACC 364

377 -----CAACAAAAAGGACAAAGCAGCAGGCCCCCAAGACGCTCACC 416  
365 AGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTCAGTTCACCGGTTGCTTTCT 424  
417 AGAAGATCTATCATCTTCAGAGAGGGTGATTTGATTCAGTGGCAACCGGTTTGCATACT 476  
425 GGCTCTACAACAGCACGACACATCTGTTGCTGCTTTCTTACTGACACCAACAACA 484  
477 GGATGTACAACAATGAAGACATCTCTGTTGCTGCTTTCTTATTGACACCAACAGCT 536  
485 ACACAAACAGCTTGATTCAGTTCCTCCAGGAGATTCATTTGGCTGGGAAACAGGCAAG 544  
537 TCCAGAAACAGCTTCGACCAATGCTTAGGAGATCTTATCTTGTGGGAAACAGAGCAAG 596  
545 AGTTCTTAAGGTACCAGCAAAAGCAGACAAAGCAGACAAAGCAGGAGCTTACCATATAGCC 604  
597 AGTTCTTACAGTATCAGCCACAGACGAGCAG- 629  
605 CATACAGCCCGCAAGTCAGCCTTAGACAAGAGCGTGAAATTTAGCCCTCGAGGACAGC 664  
630 -----GAGGTACTC 638  
665 ACAGCCGAGAGAAACGAGCAGGACAAGAAAGAAACGAGGTGAAACATCTTCAGCG 724  
639 AAAGCCAGAAAGGAAAGCGTCAGCAAGAAAGAAACGAGGAGGAGCAGCATATTGAGTG 698  
725 GCTTCACGCGGAGTTCTTGGAACAGCCTTCCAGGTTCAGCAGACACAGATAGTCAAA 784  
699 GCTTCGCCCGGAAATTTCTTGGAACATGCGGTC---GTGTTGGACAGCAGATAGTGAA 755  
785 ACCTAAGAGCGCAGACGAGAGTGGAAGAGAGGAGGAGCCATTGTGACAGTGGGGAGGCC 844  
756 AGCTACAAGTGAAGACGAAGAGAGAGAGGAGGTCCTTGTGACAGTCAAAAGGAGTTC 815  
845 TCAGAAATCTTGAAGCCAGATAGAAAGAGAGAGTCCCGACGAAAGAGAGGAAATAGCATGAAG 904  
816 TCAGCGTGATAGCCCAACCGAAGAGCAGCAACAAAGACCCGAGGAGAGAGAGAGC 875  
905 ATGAATATGAATACGATGAAGAGGATAGAGGCGTGGCAGGGAAGCAGAGGAGGAGGGA 964  
876 CAGTTGTGACGAGAAAGACAACAT-----TGCCAAAGCCAAAGCAGAA 920  
965 ATGGTATTGAAGAGAGCATCTGCACCGCAAGTCTAAAAAGAACATTGTGTAGAAACAGAT 1024  
921 ATGGCATTGACGAGACCATTTGCACAATGAGACTTCGCCACAACATTTGCCAGACTTCAT 980  
1025 CCCTGACATCTACAACCCCTCAAGCTGGTTCTACTCAAAACCTGCAAGGATCTCAACCTTC 1084  
981 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCAACCCGCTACCGCTTCGACTTCC 1040  
1085 TAATACCTTAGTGGCTTGGACCTTAGTCTGAATATGGAATCTCTACAGGAATGCAATGT 1144  
1041 CAGCCCTCTGTGGCTCAAACTCAGTGGCCAGTTTGGATCCTCCGAGAAATGCTATGT 1100  
1145 TTGTGCTCACTACACACCAACGACACAGCATCATATATCGATTGAGGGGACGGGCTC 1204  
1101 TGTGCGCACACTACAACTGAAACGCAACAGCATATATACGCAATTTGAATGGACGGCAT 1160  
1205 AGTGAAGTCTGGACAGCAACCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264  
1161 TGGTACAAGTGGTGAAATTGCAATGGTGGAGAGTGTGTTGATGGAGAGCTGCAAGAGGGAC 1220  
1265 AGTGTCTTGTGGTCCACAGAACTTCGCGTCCGCTGGAAGTCCAGAGCGAGAACTTCG 1324  
1221 AGTGTTAATTTGGCCACAAACCTTTGCGGTGGCTGCAAGATCAGAGCGGCAACTTCG 1280  
1325 AATACGTGCACTTCAAGACAGACTCAAGGCCCCAGCATAGCCAACTCGCGGTGAAACT 1384  
1281 AGTATGTTTCAATTCAGACCAATGATAGACCTTCGATCGCAACCTTGCAGGTGCAACT 1340  
1385 CGGTCAATAGATAACCTTCCGCGGAGGAGGTGGTTGCAAAATTCATATGCGCTTCCAAAGGAGC 1444

Db 1341 CATTGTTGAACGATTGCCGGAGGAAGTGAATTCAGCAAACTTTTAACCTAAGGAGCAGC 1400

QY 1445 AGCAAGGCGAGCTTAAGAACAAACCCCTTCAAGTTCCTGTTCCACCGTCTTCAGCAGT 1504

Db 1401 AGCCAGGCGAGGTCAGAGAACAAACCCCTTTCAGCTTCCTGGTTCACACCTAAGGAGTCTC 1460

QY 1505 CTCGAGGCGTGGCTTA 1523

Db 1461 AGAGGAGAGTGTGGCTTA 1479

RESULT 13

ADK14017

ID ADX14017 standard; cDNA; 1694 BP.

XX

AC ADX14017;

DT 21-APR-2005 (first entry)

XX Plant full length insert polynucleotide seqid 8592.

DE

XX plant protectant; plant growth regulant; gene therapy; plant;

KW recombinant DNA construct; physical array; plant breeding marker;

KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KW extreme osmotic condition; pathogen tolerance; pest tolerance;

KW growth rate; cell cycle pathway; disease resistance;

KW galactomannan production; lignin production; plant growth regulator;

KW yield; plant growth; plant development; seed oil; protein yield;

KW protein content; gene; ss.

XX

OS Unidentified.

XX

XX US2004034888-A1.

PN

XX 19-FEB-2004.

XX

XX 28-APR-2003; 2003US-00425114.

PF

XX

XX 06-MAY-1999; 99US-00304517.

PR

PR 05-NOV-2001; 2001US-00985678.

XX

XX (LIU/) LIU J.

PA

PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TABA/) TABASKA J E.

PA (CAOV/) CAO Y.

XX

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

PI

XX WPI; 2004-180133/17.

XX

XX New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.

XX

XX Claim 1; SEQ ID NO 8592; 15pp; English.

PS

XX

XX The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at

CC ftp.seqdata.uspro.gov/sequence.html?docid:2004034888. the polynucleotide

CC of the invention are also useful in physical arrays of molecules and as

CC plant breeding markers. The recombinant DNA construct is useful for

CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,

CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or

CC content. This sequence represents a plant full length insert

CC polynucleotide that can be used in the recombinant DNA construct of the

CC invention.

XX

SQ Sequence 1694 BP; 504 A; 410 C; 397 G; 383 T; 0 U; 0 Other;

Query Match 34.0%; Score 517.4; DB 13; Length 1694;

Best Local Similarity 62.8%; Pred. No. 1.8e-137; Indels 144; Gaps 4;

Matches 954; Conservative 0; Mismatches 421;

QY 5 AGCAACCGGAGGAGAACGGTCCAGTTCAGCGCTCAATGCGCAGAGACCTTGACAATC 64

Db 103 AGCAGCCACAGCAAAACGAGTGCAGATCCAGCGCTCAATGCCCTCAACCGGATAACC 162

QY 65 GCATTGAATCAGAGGGCGGTTACATTGAGACTTGGAAACCCCAACACAGGAGTTGCAAT 124

Db 163 GTATAGAGTCAGAAAGGTGGCTTCATTGAGACATGGAACCTTAACAACAAGCCATCCAGT 222

QY 125 GCGCCGGCGTGGCCCTCTCTCGCTTAGTCTCCGCGCAACGCCCTTCGTAGGCCCTTCT 184

Db 223 GTGCGCGTGTGGCCCTCTCTCGCTGCACCTCAACGCAACGCCCTTCGACACCTTCCT 282

QY 185 ACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATACCTTTGGGTGATAT 244

Db 283 ACACCAACGCTCCCGAGGAGATCTACATCCAAAGGTAGTGGTATTTTGGCATGATAT 342

QY 245 TCCTCGTTGTCTTAGACACTATGAAAGAGCTTCACACAAAGTGTGTCATCTCAGTCCC 304

Db 343 TCCCGGGTGTCTTAGCACATTTGAAGGCCT----- 374

QY 305 AAAGACCACCAAGACGTCTCCAGGAGAGACCAAGCCCAACAGCAACAGATAGTCACC 364

Db 375 -----CAACAAAAGGACAAAGCAGCAGCGGCCCAAGACCGTCCACC 414

QY 365 AGAAGGTGACCGTTCGATGAGGGTGATCTCATTCAGTTCCACCGGTGTGCTTCT 424

Db 415 AGAAGATCTATCATTTTCAGAGAGGGTGATTGATTCAGTGCACCGGTTCGATCT 474

QY 425 GGCTCTAACAGCAGCAGCAGTGTGTTGCTGTTCTTCTTACTGACACCAACAACA 484

Db 475 GGATGTACAAACAAATGAAGACACTCTCTGTTGTTGCGCTTCTCTTATGACACCAACAGCT 534

QY 485 AGCAACACAGCTTGTATCAGTTCCTCCAGGAGATTCAATTTGGCTGGAAACACGAGCAAG 544

Db 535 TCAGAACACAGCTCGACAGATGCTTAGAGATTCTATCTTCTGCGAACCAAGAGCAAG 594

QY 545 AGTTCTTAAGGTACCAAGCAACAAAGCAGACAAAGCAGACGAAAGCTTACCATATAGCC 604

Db 595 AGTTTCTACAGTATCAGCCACAGACAGCAGCAAG----- 627

QY 605 CATACAGCCGCAAGTACGCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGACAGC 664

Db 628 -----GAGGTACTC 636

QY 665 ACAGCGCAGAGAACGAGCAGGACAAAGAAAGAAAGAGTGTGAAACATCTTCAGCG 724

Db 637 AAAGCCAGAAAGGAAGCGTCCAGCAAGAGAGAAACGAGAGGAGCAGCATATTGAGTG 696

QY 725 GCTTCACGCGGAGTTCTTGAAACAAAGCTTCCAGTTTGACGACAGACAGATAGTCAAA 784

Db 697 GCTTCGCGCGGAATTTTGGAAACATGCGTTC---GTCGTGGACAGCAGATAGTGAA 753

QY 785 ACCTAAGAGGCGAGCAGGAGTGAAGAGAGAGGAGCCATTGTGACAGTGAAGGGAGGCC 844

Db 754 AGCTACAAGGTGAGAACGAAGAGGAGAGAGGGTGCCTATTGTGACAGTGAAGAGAGGTC 813

QY 845 TCAGAACTTTAGCCCGCAGATAGAAAGAGAGCGTCCGACGAAGAGAGGAAATACGATGAAG 904

Db 814 TCAGCGTGATAGCCCAACCCACGAGAGCAGCAACAAGACCCCGAGGAGAGGAGAGC 873

QY 905 ATGAATATGAATACGATGAAGAGGATAGAAGGCGTGGCGGGGAAGCAGAGCGGAGGGA 964

Db 874 CAGATTGTGACGAGAAAGACAAACAT-----TGCACAAAGCCAAAGCAGAA 918  
QY 965 ATGGTATTGAGAGACGATCTGCACCGCAAGTGTCTAAAAAGAACATTTGGTAGAAACAGAT 1024  
Db 919 ATGGCATTGACGAGACCAATTTGACCAATGAGACTTCGCCACACATTTGGCCAGACTTCAT 978  
QY 1025 CCCTGACATCTACACCCCTCAAGCTGAGTGTTCATCTCAAACTGCGAACGATCTCAACCTTC 1084  
Db 979 CACCTGACATCTTCAACCCCTCAAGCTGAGTGTTCATCTCAAACTGCGAACGATCTCAACCTTC 1038  
QY 1085 TATATCTTAGTGTGGACCTAGTGTCTGAATATGGAATCTCTACAGGAATGCAATGT 1144  
Db 1039 CAGCCCTCTCGTGGCTCAAACTCAGTGCCTGAGTGTGATCACTCCGCAAGATGCTATGT 1098  
QY 1145 TTCTGCTCACTCAACACCAACCGCCACACAGCATCATATATGATTGAGGGGACGGGCTC 1204  
Db 1099 TCGTGCCACACTACACCTGAACGCAACAGCATATATACGCAATTAATGATGGAGGGCAT 1158  
QY 1205 ACGTGCAAGTGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264  
Db 1159 TGGTACAAGTGTGTAATTTGCAATGGTTCAGAGAGTGTGATGAGAGCTGCAAGAGGGAC 1218  
QY 1265 ACGTGTCTGTGGTGCACAGAACTTCCGCTGCTGGAAGTCCAGAGCGGAGAACTTCG 1324  
Db 1219 AGGTGTAAATTTGGCCACAAACTTTTGCCTGCTGCAAGATCACAGAGCGCAACTTCG 1278  
QY 1325 AATACGTGGCATTTCAAGACAGACTCAAGGCCAGCATAGCAACTCGCGGTGAAACT 1384  
Db 1279 AGTATGTTTCATTCAGACCAATGATAGACCTTCGATCGCACTTGCAGGTGCAACT 1338  
QY 1385 CCGTCATAGATAACCTGCGGAGGAGTGTGTTCCAAATTCATATGCGCTTCCAAAGGAGC 1444  
Db 1339 CATTTGTTAAACGATTTGCCGAGGAGTGTATTCAGCAAACTTTTAACTTAAGGAGGAGC 1398  
QY 1445 AGCAGGAGGAGCTTAAGACAAACCCCTTCAAGTCTTCGTTCCACCGTCTCAGCAGT 1504  
Db 1399 AGCCAGGAGGAGTCAAGAAACAAACCCCTTTCAGCTTCCTGTTCCACCTAAGGAGTCTC 1458  
QY 1505 CTCGAGGGGCTGTGGCTTA 1523  
Db 1459 AGAGGAGAGTGTGGCTTA 1477  
RESULT 14  
ID ADX13008  
XX ADX13008 standard; cDNA; 1697 BP.  
AC ADX13008;  
XX  
XX  
XX 21-APR-2005 (first entry)  
XX Plant full length insert polynucleotide seqid 7583.  
DE  
XX plant protectant; plant growth regulant; gene therapy; plant;  
XX recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW Galactonnanan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
XX Unidentified.  
XX  
XX US2004034888-A1.  
XX  
XX 19-FEB-2004.  
XX  
XX 28-APR-2003; 2003US-00425114.  
XX  
XX 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX

PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
XX Claim 1; SEQ ID NO 7583; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactonnanan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 1697 BP; 505 A; 410 C; 397 G; 385 T; 0 U; 0 Other;  
Query Match 34.0%; Score 517.4; DB 13; Length 1697;  
Best Local Similarity 62.8%; Pred.No.1.8e-137;  
Matches 954; Conservative 0; Mismatches 121; Indels 144; Gaps 4;  
QY 5 AGCAACCGGAGGAGAACGCGTGCAGTTCAGCGCTCAATGCGCAGACCTTGACAATC 64  
Db 106 AGCAGCCACAGCAAAACGAGTGCAGATCCAACGCTCAATGCCCTCAAAACGATAACC 165  
QY 65 GCATTGAATCAGAGGCGGTTCATTGAGACTTTGGAACCCCAACACAGGAGTTGCAAT 124  
Db 166 GTATAGAGTCAGAAAGGTGGCTTCATTGAGACATGGAACCCCTAACACAAGCCATTCCAGT 225  
QY 125 GCGCGGCGTCCCTCTCTCGCTTAGTCTCGCGCAACGCCCTTCGTAGGCCCTTCT 184  
Db 226 GTGCGCGGTGTGCGCTCTCTCGCTGACCCCTCAACGCAACGCCCTTCGACAGCTTCT 285  
QY 185 ACTCAATCTCTCCAGGAGATCTTCATCCAGCAAGGAAGGGGATATCTTTGGTTGATAT 244  
Db 286 ACACCAACGCTCCCGAGGAGATCTACATCCAAACAGGTAGTGTATTTTGGCATGATAT 345  
QY 245 TCCCTGTTGTCTTAGACACTATGAAGAGCCTCACACACAGTCTCGATCTCAGTCCC 304  
Db 346 TCCCGGGTGTCTTAGACACTTTGAAGAGCT----- 377  
QY 305 AAAGACCACCAAGAGCTCTCCAAAGGAGAGCAACCAAGCCCAACAGCAACGAGATGTCACC 364  
Db 378 -----CAACAAAAGGACAAAGAGAGCGGCCCAAGACCGTCAAC 417  
QY 365 AGAAGGTGACCGTTTTCGATGAGGGTGTATCTCATTCAGTTCCTCCACCGGTGTGTTCT 424  
Db 418 AGAAGATCTATCACTTCAGAGAGGGTGTATTTGATTGACGTGCGCAACCGGTTTGCATACT 477  
QY 425 GGCTCTACAAACGACACGACACTGTATGTTGTTGCTGTTTCTCTTACTGACACCAACA 484

Db 478 GGATGTACAACATGAAGACATCTCTGTTGTTGCTCCGTTTCTCTTATTGACACCAACAGCT 537  
QY 485 ACGACAACACAGTTGATCAAGTTCCTCCAGGAGATTCATATTTGGCTGGAAACACGAGCAAG 544  
Db 538 TCAGAAACAGCTCGACAGATGCTTAGGAGATTCTATCTTGCTGGGAACCAAGAGCAAG 597  
QY 545 AGTTCTTAGGTACACGACCAACAAGCAGACAAAGCAGACGAAGCAGATTTACCATATAGCC 604  
Db 598 AGTTCTTAGGTACACGACCAACAAGCAGACGAAGCAGCAAG- 630  
QY 605 CATACAGCCGCAAGTCCAGCTAGACAGAGAGCGTGAAATTTAGCCCTCGAGGACAGC 664  
Db 631 -----GAGGTACTC 639  
QY 665 ACAGCCGACAGAACGAGCAGGACAAAGAAAGAAACGAAGTGAACATCTTCAGCG 724  
Db 640 AAAGCAGAAAGGAAAGCGTCAGCAAGAAGAAAGAAACGAAGGAGCAGCATATTGAGTG 699  
QY 725 GCTTCAGCGCGAGTTCTCTGGACCAAGCCTTCCAGGTTGACGACACACAGATAGTCAAA 784  
Db 700 GCTTCGCCCCGAAATCTTGGAAACATGCGTTC---GTCGTGGACAGCGCATAGTAGAA 756  
QY 785 ACCTAAGAGCCGACAGACCGAGAGTGAAGAGAGGGAGCCATTGTGACAGTCAGGGGAGGCC 844  
Db 757 AGCTACAAGGTGAGACGAGAGAGAGAGAGAGGTTGCCATTGTGACAGTGAAGGAGGTC 816  
QY 845 TCAGAAATCTTGAGCCAGATAGAAAAGAGAGAGCTGCCGACGAAGAGGAATACGATGAG 904  
Db 817 TCAGCGTGATAGCCCAACCCACCGAAGAGCAGCAACAAGACCCGAGGAAGAGGAGAGC 876  
QY 905 ATGAATATGATACGATGAGAGGATAGAGGGTGGCAGGGGAACGACGAGGAGGGGA 964  
Db 877 CAGATTGTGACGAGAGAGCAAAACAT-----TGCCAAAGCCAAAGCAGAA 921  
QY 965 ATGGTATTGAAGAGACGATCTGCACCGCAAGTCTAAAGAAAGACATTTGGTAGAAACAGAT 1024  
Db 922 ATGGCATTTGACGAGACCAATTTGCACATGAGACTTCGCCACACATTTGCCAGACTTCAT 981  
QY 1025 CCCTGACATCTACAACCCCTCAAGCTGTTCACTCAAAAAGTGCACACGATCTCAACCTTC 1084  
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QY 1085 TAATACCTAGGTGCTTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCATTGT 1144  
Db 1042 CAGCCCTCTGCTGGCTCAAACTCAGTGCCCGCAGTTTGGATCACTCCGCAAGATGCTATGT 1101  
QY 1145 TTGTCGCTCACTACAACCAACGACACACAGCATCATATATCGATTGAGGGGACGGGCTC 1204  
Db 1102 TCGTGCCACACTACAACCTGAACGCAACAGCATAATATACGCAATTGAAATGGACGGCAT 1161  
QY 1205 ACGTGAAGTCGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264  
Db 1162 TGGTACAAGTGGTGAATTTGCAATGGTGAAGAGTGTGATGAGAGAGCTGCAAGAGGGAC 1221  
QY 1265 ACGTGTCTGTGGGCCACAGAACTTCGCGCTGCTGGAAGTCCAGAGGAGCAACTTCG 1324  
Db 1222 AGGTGTAAATTTGGCCACAAAATCTTTCGGTGGCTGCAAGATCACAGAGCCACACTTCG 1281  
QY 1325 AATACGTGGCATTCAGACAGACTCAAGGCCAGCATAGCAACCTCGCGGTGAAAACT 1384  
Db 1282 AGTATGTTTCAATTCAGACCAATGATAGACCCCTCGATCGGCAACCTTCGAGGTGCAAACT 1341  
QY 1385 CCCTCATAGATAACCTCGCGGAGAGGTGTTGCAATTCATATGCGCTTCAAGAGGAGC 1444  
Db 1342 CATTTGTGAACGATTCGCCGAGGAAGTGATTTCAGCAAACTTTTAACTTAAGGAGCAGC 1401  
QY 1445 AGCAGGAGGACTTAAGAACAAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAGCAGT 1504  
Db 1402 AGCCAGGAGGCTCAAGAACAAACCCCTTTCAGTTCTCGTTCCACCTTAAGAGTCTC 1461  
QY 1505 CTCGAGGGGCTGTGGCTTA 1523  
Db 1462 AGAGGAGAGTTGTGGCTTA 1480

RESULT 15  
ADX13019  
ID ADX13019 standard; cDNA; 1671 BP.

XX AC ADX13019;  
XX DT 21-APR-2005 (first entry)  
XX DE Plant full length insert polynucleotide seqid 7594.  
XX KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.

OS Unidentified.

PN US2004034888-A1.

PD 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

PF 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TAB/) TABASKA J E.

PA (CAO/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

PI WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.

XX Claim 1; SEQ ID NO 7594; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at

CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as

CC plant breeding markers. The recombinant DNA construct is useful for

CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,

CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or

CC content. This sequence represents a plant full length insert

CC polynucleotide that can be used in the recombinant DNA construct of the

XX invention.

XX Sequence 1671 BP; 498 A; 404 C; 396 G; 373 T; 0 U; 0 Other;

Query Match 33.8%; Score 515.8; DB 13; Length 1671;  
Best Local Similarity 62.7%; Pred. No. 5.2e-137;





GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 7832.57 Seconds  
(without alignments)  
10880.347 Million cell updates/sec

Title: US-10-728-051-3  
Perfect score: 1524  
Sequence: 1 cgcgcagcaaccgaggagaa.....ctccgaggcgtgtgcttaa 1524

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hcc:\*  
7: gb\_est3:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_ges1:\*  
12: gb\_ges2:\*  
13: gb\_ges3:\*  
14: gb\_ges4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651.6	42.8	770	4	CD038329
2	604.4	39.7	725	4	CD038327
3	562.2	36.9	676	4	CD038254
4	554.6	36.4	710	4	CD038107
5	548.6	36.0	718	4	CD038332
6	487	32.0	553	8	CD0897496
7	436	28.6	602	4	CD038301
8	417.6	27.4	532	4	CD038222
9	386.2	25.3	720	4	CD038043
10	373.6	24.5	452	8	CD0897497
11	372	24.4	679	4	CD038144
12	330.4	21.7	906	3	BQ123409
13	321.6	21.1	974	3	BQ123283
14	316.2	20.7	886	4	CA857975
15	314	20.6	861	4	CA858492
16	310.6	20.4	810	4	CA858379
17	310.4	20.4	862	4	CA858208
18	310.2	20.4	907	3	BQ123241
19	307.8	20.2	822	3	BQ123014

20	305	20.0	787	4	CA857935	CA857935	EST635190
21	305	20.0	812	3	BQ123297	BQ123297	EST608873
22	304.4	20.0	782	4	CA857910	CA857910	EST635165
23	304.4	20.0	879	3	BQ123329	BQ123329	EST608905
24	303.6	19.9	824	4	CA857860	CA857860	EST635115
25	302.6	19.9	881	4	CA858490	CA858490	EST635745
26	298.4	19.6	790	4	CA858419	CA858419	EST635674
27	296.4	19.4	836	4	CA858453	CA858453	EST635708
28	296.2	19.4	812	2	B1311450	B1311450	EST531320
29	294	19.3	805	4	CA857850	CA857850	EST635105
30	293.4	19.3	827	4	CA858430	CA858430	EST635685
31	292.6	19.2	879	4	CA858252	CA858252	EST635507
32	292.4	19.2	789	2	B1310542	B1310542	EST531229
33	291.6	19.1	769	3	BQ124073	BQ124073	EST609649
34	291	19.1	903	4	CA858778	CA858778	EST636033
35	290.8	19.1	879	4	CA858395	CA858395	EST635650
36	288.8	19.0	892	4	CA858816	CA858816	EST636071
37	288.6	18.9	746	2	B1311303	B1311303	EST531305
38	288.6	18.9	787	2	B1311483	B1311483	EST531323
39	288.2	18.9	793	4	CA857838	CA857838	EST635093
40	287.6	18.9	541	4	CD038610	CD038610	UTPPI009
41	287.4	18.9	752	4	CA858702	CA858702	EST635957
42	287.2	18.8	755	4	CA858724	CA858724	EST635979
43	286.4	18.8	756	4	CA857897	CA857897	EST635152
44	286.2	18.8	811	3	BQ123350	BQ123350	EST608926
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ALIGNMENTS

RESULT 1  
CD038329  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

CD038329 770 bp mRNA linear EST 07-MAY-2003  
UTPPI007 B05 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
Arachis hypogaea cDNA clone UTPPI007\_B05 5', mRNA sequence.  
CD038329  
CD038329.1 GI:30420167  
EST.  
Arachis hypogaea (peanut)  
Arachis hypogaea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
Aeschynomeneae; Arachis.  
1 (bases 1 to 770)  
Luo M., Dang P., Guo B.Z., Holbrook C.C., Lee R.D., Bausher M.G.  
and Lynch R.E.  
Generation and Analyses of ESTs for Arachis hypogaea  
Unpublished (2003)  
Contact: Baozhu Guo  
Molecular Genetics  
USDA/ARS, Crop Protection and Management Research Unit  
2747 Davis Rd., Tifton, GA 31794, USA  
Tel: 229-387-2334  
Fax: 229-387-2321  
Email: bguo@tifton.usda.gov  
Seq primer: T3.  
Location/Qualifiers  
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/db\_xref="taxon:3818"  
/clone="UTPPI007\_B05"  
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/dev\_stage="R6"  
/lab\_host="xLI-blue"  
/clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"  
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;  
cDNA library was constructed from peanut cultivar A13  
(NCV11XAR4). A13 has resistance to Aspergillus infection

and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapur(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match		42.8%;	Score 651.6;	DB 4;	Length 770;
Best Local Similarity		92.9%;	Pred. No. 2.5e-168;		
Matches 694;		Conservative 0;	Mismatches 148;	Indels 9;	Gaps 1;
QY	391	GATCTCATTTGCAGTCCACCGGTGTGCTTCTGCTCTACAAACGACACGACACTGAT	450		
DB	33	GATCTCATGNNNACCGGGCTGCAGGAATTCGGCAGGAGGCAACGACCATGACACTGAT	92		
QY	451	GTTGTTGCTGTTTCTTTACTGACCAACAAACGACCAACGAGTTGATCAGTTCCTCC	510		
DB	93	GTTGTTGCTGTTTCTTCTACTGACCAACAAACGACCAACGAGCTTGATCAGTTCCTCC	152		
QY	511	AGGAGATTCAATTTGGCTGGACACGGAGCAGAGTCTTAAAGTACGAGCAACAAAGC	570		
DB	153	AGGAGATTCAATTTGGCTGGAAACACGAGCAAGAGTCTTAAAGTACGAGCA-----	205		
QY	571	AGCAAGACAGACGAAGAAGCTTACCATATAGCCATACAGCCGCAAAAGTCAGCCTAGA	630		
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QY	691	GAAGAGAAACCAAGGTGAACATCTTCAGCGGCTTACCGCGGAGTTCCTGGAACAA	750		
DB	324	GAAGAGAAACCAAGGTGAACATCTTCAGCGGCTTACCGCGGAGTTCCTGGAACAA	383		
QY	751	GCCTTCCAGGTTACGACACAGACAGATAGTCAAAACCTTAAGAGCGCAGACCGAGAGTGAA	810		
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QY	811	GAAGAGGAGCCATTGTGACAGTGAGGGGAGGCTCAGATCTTTGAGCCCGAGATAGAAAG	870		
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DB	504	AGAGGTGCCGACCAAGAAGAGGAATACGATGAAGATGAATATCAATACGATGAAGAGGAT	563		
QY	931	AGAAGCGTGGCAGGGGAAGCAGAGGAGGGGAATGGTATTGAAGAGACGATCTGCACC	990		
DB	564	AGAAGCGTGGCAGGGGAAGCAGAGGAGGGGAATGGTATTGAAGAGACGATCTGCACA	623		
QY	991	GCAAGTGTAAAAAGAACATTGTTAGAACACAGATCCCTGACATCTTACAACCCCTCAAGCT	1050		
DB	624	GCAAGTGTAAAAAGAACATTGTTAGAACACAGATCCCTGACATCTTACAATCTCTCAAGCT	683		
QY	1051	GGTTCTACTCAAACTGCCAACGATCTCAACCTTCTTAATCTTAGTGGCTTGGACCTAGT	1110		
DB	684	GGTTCTACTCAAACTGCCAACGATCTCCACCTTCTTAATCTTAGTGGCTTGGACCTAGT	743		
QY	1111	GCTGAATATGAAATCTCTACAGGAAT	1137		
DB	744	GCTGAATATGAAATCTCTACAGGNAT	770		

RESULT 2  
CD038327

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

Location/Qualifiers

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/mol\_type="mRNA"

/cultivar="A13"

/db\_xref="taxon:3818"

/clone="UTPPI008\_F09"

/tissue\_type="Immature pods"

/dev\_stage="R6"

/lab\_host="Xl1-blue"

/clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"

/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapur(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

CD038327 725 bp mRNA linear EST 07-MAY-2003  
UTPPI008\_F09 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
Arachis hypogaea cDNA clone UTPPI008\_F09 5', mRNA sequence.

CD038327

CD038327.1 GI:30420165

EST.

Arachis hypogaea (peanut)

Arachis hypogaea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;

Aeschynomeneae; Arachis.

1 (bases 1 to 725)

Luo, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.

and Lynch, R.E.

Generation and Analyses of ESTs for Arachis hypogaea

Unpublished (2003)

Contact: Baozhu Guo

Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd, Tifton, GA 31794, USA

Tel: 229-387-2334

Fax: 229-387-2321

Email: bguo@tifton.usda.gov

Seq primer: T3.

Location/Qualifiers

1..725

/organism="Arachis hypogaea"

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/cultivar="A13"

/db\_xref="taxon:3818"

/clone="UTPPI008\_F09"

/tissue\_type="Immature pods"

/dev\_stage="R6"

/lab\_host="Xl1-blue"

/clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"

/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapur(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match		39.7%;	Score 604.4;	DB 4;	Length 725;
Best Local Similarity		92.8%;	Pred. No. 2.7e-155;		
Matches 648;		Conservative 0;	Mismatches 41;	Indels 9;	Gaps 1;
QY	2	GGCAGCAACCGGAGGAGAACGGCTGCCAGTTCACAGCGCTCAATGCCGACAGACCTGACA	61		
DB	37	GGCAGCAGCGGAGGAAATGCGTCCAGTTCACAGCGCTCAATGCCAAAGGCTGACA	96		
QY	62	ATCGCATTTGAATCAGAGGGCGGTTACATTGAGACTTTGGAACCCCAACACAGAGTTGC	121		
DB	97	ACCGCATTTGAATCGGAGGCGGTTACATTGAGACTTTGGAACCCCAACACAGAGTTGC	156		



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122 AATCGCGCGCGCGCGCTCTCTCGCTTAGTCTCCGCCGCAACGCCCTTCGTAGGCGCTT 181
157 AATGCGCGCGCGCTCTCGCGCTTAGTCTCCGCCGCAACGCCCTTCGTAGGCGCTT 216
182 TCTACTCCAATGCTCCCGAGAGATCTTCATCCAGCAAGGAAGGGGATCTTTGGGTTGA 241
217 TCTACTCCAATGCTCCCGAGAGATCTTCATCCAGCAAGGAAGGGGATCTTTGGTTTGA 276
242 TATTTCCTGCTGTCTTAGACACTATGAAGAGCTCACACAAAGTCTCGATCTCAGT 301
277 TATTTCCTGCTGTCTTAGACACTATGAAGAGCTTCACAAAGAGCGCGCATCAGT 336
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337 CCCAAGAGACCACCAAGAGCTTTTCAAGGACAAGACCAAGCCCAACAGCAAGATAGTC 396
362 ACCAAGAGTGCACCGCTTCGATGAGGCTGATCTCATTCAGTCCACCGGTGGCTT 421
397 ACCAAGAGTGCACCGCTTCGATGAGGCTGATCTCATTCAGTCCACCGGTGGCTT 456
422 TCTGGCTCTCAACAGCAGCAGCACTGATGCTGTGCTGTTCTTCTTACTGACACCAACA 481
457 TCTGGATGTACAAGACCATGACACTGATGTTGTTGCTGTTCTTCTTACTGACACCAACA 516
482 ACAACGACACCAAGCTTGATGATCTCCCAAGAGATTTCAATTTGGCTGGGAACACGAGC 541
517 ACAACGACACCAAGCTTGATGATCTCCCAAGAGATTTCAATTTGGCTGGGAACACGAGC 576
542 AGAGATTTTAAAGGTACCAAGCAACAAGCAGACAAGAGCAGCAAGAGCTTACCATATA 601
577 AAGAGTTCTTAAAGATACCAACA-----ACAAAGCAGCAGCAAGAGCTTACCATATA 627
602 GCCCATACAGCCCGCAAGTTCAGCTAGACAAGAGAGCTGATTTAGCCCTCGAGGAC 661
628 GCCCATACAGCCCGCAAGTTCAGCTTAAACAAGAGACCGTGATTTAGCCCTCGAGGAC 687
662 AGCAGCGCGCAGAGAACGACGAGGACCAAGAAAGAA 699
688 AGCAGCGCGCAGAGAACGACGAGGACCAAGAAAGAA 725

RESULT 3
CD038254
LOCUS
DEFINITION
UTPPI004_F06 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPPI004_F06 5', mRNA sequence.
ACCESSION
CD038254
VERSION
CD038254.1 GI:30420092
SOURCE
Arachis hypogaea (peanut)
ORGANISM
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE
1 (bases 1 to 676)
Luo M., Dang P., Guo B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.
and Lynch, R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3.
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/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
/notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
cDNA library was constructed from peanut cultivar A13
(NC11XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure(GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
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## ORIGIN

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Query Match      36.9%; Score 562.2; DB 4; Length 676;
Best Local Similarity 92.2%; Pred. No. 1.2e-143;
Matches 630; Conservative 0; Mismatches 38; Indels 15; Gaps 3;

QY 538 GAGCAGAGGTTCTTAAGGTACCAGCAACAAGCAGACAGCAAGAGCGTGAATTTAGCCCTCGA 657
Db 3 GAGCAAGAGTTCTTAAGTATACCAGCAACAAGCAGACAGCAAGAGCGTGAATTTAGCCCTCAA 62

QY 598 TATAGCCCATACAGCCCGCAAGTCTAGCTAGACAAGAGAGCGTGAATTTAGCCCTCGA 657
Db 63 TTAAGCCCATACAGCCC-----TCAGCTGGACAAGAGAGCGTGAATTTAGCCCTCAA 116

QY 658 GGACAGCAGCGGCGAGAGAACGAGCAGACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717
Db 117 GGACAGCAGCGGCGAGAGAACGAGCAGACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 176

QY 718 TTCAGCGGCTTCACGCCGAGTTCCTGGAAACAGCCCTCCAGGTTTCACGACACACAGAGATA 777
Db 177 TTCAGCGGCTTCACGTCGGAGTTCCTGGCACAAGCCCTTCAGGTTTCACGACACACAGAGATA 236

QY 778 GTGCAAAACCTTAAGAGGCGAGACCCGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
Db 237 GTGCAAAATCTTAAGAGGCGAGAACGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 296

QY 838 GGAGGCTCAGAAATCTTGAGCCAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 897
Db 297 GGAGGCTCAGAAATCTTGAGCCAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 353

QY 898 GATGAAGATGAATATGAATACGATG-----AAGAGGATAGAGAGGCGTGCAGGGGAAGC 951
Db 354 GATGAAGACGAATATGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413

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QY 1012 GGTAGAAACAGATCCCTGACATCTTACACCCCTCAAGCTGGTTCACTCAAAACTGCGAAC 1071
Db 474 GGTAGAAACAGATCCCTGACATCTTACACCCCTCAAGCTGGTTCACTCAAAACTGCGAAC 533

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QY 1192 AGGGACGGGCTCACGTGCAAGT 1214  
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 Db 654 AGGGACGGGCTCATGTGCAAGT 676  
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RESULT 4  
 CD038107 710 bp mRNA linear EST 07-MAY-2003  
 LOCUS UTPPI002\_E08 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
 DEFINITION Arachis hypogaea cDNA clone UTPPI002\_E08 5', mRNA sequence.

CD038107  
 ACCESSION CD038107.1 GI:30419945  
 VERSION EST.  
 KEYWORDS Arachis hypogaea (peanut)  
 SOURCE Arachis hypogaea  
 ORGANISM Arachis hypogaea

REFERENCE 1 (bases 1 to 710)  
 AUTHORS Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.  
 and Lynch,R.E.  
 TITLE Generation and Analyses of ESTs for Arachis hypogaea  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Baozhu Guo  
 Molecular Genetics  
 USDA/ARS, Crop Protection and Management Research Unit  
 2747 Davis Rd., Tifton, GA 31794, USA  
 Tel: 229-387-2334  
 Fax: 229-387-2321  
 Email: bguo@tifton.usda.gov  
 Seq primer: T3

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 /db\_xref="taxon:3818"  
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 /clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"

/note="Vector: Uni-ZAP XR; Site.1: EcoRI; Site.2: XhoI;  
 cDNA library was constructed from peanut cultivar A13;  
 (NCV11X4). A13 has resistance to Aspergillus infection  
 and drought tolerance. The immature pods that developed to  
 R6 stage were collected from different plants, and placed  
 into liquid N2 immediately and stored in -80oC freezer.  
 Total RNA was isolated with TRIzol-Reagent  
 ultrapure (GIBCOBRL). mRNA was extracted and purified from  
 total RNA (Promega). cDNA synthesis and library  
 construction followed the protocol of by ZAP-cDNA Gigapack  
 III Gold cloning kit (Stratagene). The cDNA above 500bp  
 were collected after size-fraction. The inserts were  
 directionally cloned into Uni-ZAP XR vector using XhoI  
 EcoRI sites adapters. The lambda library was packed into  
 phages using Gigapack III Gold (Stratagene). The  
 un-amplified library was used to excise pBluescript  
 phagemids from the Uni-ZAP XR vector, and the phagemids  
 was used to transform the host bacteria SOLR. The library  
 was constructed by Dr. Meng Luo and Dr. Phat Dang."

## ORIGIN

Query Match 36.4%; Score 554.6; DB 4; Length 710;  
 Best Local Similarity 98.3%; Pred. No. 1.6e-141;  
 Matches 571; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 945 GGGACGAGCAGCGGGGAATGGTATTGAAGAGAGCATCTGCACCGCAAGTGTCTAAAAA 1004  
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 Db 1 GGGACGAGCAGCGGGGAATGGTATTGAAGAGAGCATCTGCACCGCAAGTGTCTAAAAA 60  
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QY 1005 GAACATTGGTAGAAGACAGATCCCTTGCATCTACAAACCTTCAAGCTGGTTCACTCAAAAC 1064  
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 Db 61 GAACATTGGTAGAAGACAGATCCCTTGCATCTACAAACCTTCAAGCTGGTTCACTCAAAAC 120  
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QY 1065 TGCCAACGATCTCAACCTTCTAATTAAGTGGCTTGGACCTAGTGTGTAATATGGA 1124  
 |||||  
 Db 121 TGCCAACGATCTCAACCTTCTAATTAAGTGGCTTGGACCTAGTGTGTAATATGGA 180  
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QY 1125 TCTCTACAGGAATGCAATGTTTGTGCTCACTACAAACCAACGACACAGCATCATATA 1184  
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 Db 181 TCTCTACAGGAATGCAATGTTTGTGCTCACTACAAACCAACGACACAGCATCATATA 240  
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 Db 241 TCGATTGAGGGGACGGGCTCACGTGCAAGTCTGTGACAGCAACGGCCACAGAGTGACGA 300  
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QY 1245 CGAGGAGCTTCAAGAGGGTCAGTGTGTTGGTGCCACAG-ACTTCGGCGCTGGCTGGAA 1303  
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 Db 301 CGAGGAGCTTCAAGAGGGTCAGTGTGTTGGTGCCACAGNAACCTTCGCCCTGGCTGGAA 360  
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 Db 421 CCAACCTCGCCGGTGAAAACTCCGTATAGATAAACCCTCGGAGGAGGTGGTTGCAAAAT 480  
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QY 1424 CATATGGCTTCAAGAGGAGCAGGCAAGCAGCTTAAGAACAAACCCCTTCAAGTTCT 1483  
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QY 1484 TCGTTCACCGTCTCAGCAGTCTCCGAGGGCTGTGGCTTAA 1524  
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 Db 541 TCGTTCACCGTCTCAGCAGTCTCCGAGGGCTGTGGCTTAA 581  
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RESULT 5  
 CD038332 718 bp mRNA linear EST 07-MAY-2003  
 LOCUS UTPPI004\_B04 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
 DEFINITION Arachis hypogaea cDNA clone UTPPI004\_B04 5', mRNA sequence.

CD038332  
 ACCESSION CD038332.1 GI:30420170  
 VERSION EST.  
 KEYWORDS Arachis hypogaea (peanut)  
 SOURCE Arachis hypogaea

ORGANISM Arachis hypogaea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
 Aeschynomeneae; Arachis.

REFERENCE 1 (bases 1 to 718)  
 AUTHORS Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.  
 and Lynch,R.E.  
 TITLE Generation and Analyses of ESTs for Arachis hypogaea  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Baozhu Guo  
 Molecular Genetics  
 USDA/ARS, Crop Protection and Management Research Unit  
 2747 Davis Rd., Tifton, GA 31794, USA  
 Tel: 229-387-2334  
 Fax: 229-387-2321  
 Email: bguo@tifton.usda.gov  
 Seq primer: T3

## FEATURES

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/clone="UTPPI004_B04"
/tissue type="Immature pods"
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/lab_host="X11-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
/notes="vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
cDNA library has been constructed from peanut cultivar A13
(NC11XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lamda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
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ORIGIN

Query Match 36.0%; Score 548.6; DB 4; Length 718;  
Best Local Similarity 93.4%; Pred. No. 7.3e-140;  
Matches 621; Conservative 0; Mismatches 29; Indels 15; Gaps 4;

QY 875 GTGCCACGAGAGGAAATACGATGAAGATGAATATGAATACGATGAAGAG----- 927  
DB 1 GTCCCGACGAGAGGAGATACGATGAAGATGAATATGAATATGAATGAGAGGAGGC 60

QY 928 -----GATGAAGCGGTGGCAGGGGAAGCAGAGCGAGGGGAATGGTATTGAAGAGACGA 982  
DB 61 AACAAATAGAGAGCGGTGGCAGGGGAAGCAGAGCGAGCGCAATGGCATTTGAGGAGACCA 120

QY 983 TCTGCACCGCAAGTGTAAAGAAACATTTGGTGAAGACAGATCCCTGACATCTACAACC 1042  
DB 121 TCTGCACCGCAAGTGTAAAGAAACATTTGGTGAAGACAGATCCCTGACATCTACAACC 180

QY 1043 CTCAAGCTGGTTCACTCAAAATGCCAACCGATCTCAACCTTCTAATACATTTAGTGGCTTG 1102  
DB 181 CTCAAGCTGGTTCACTCAAAATGCCAACCGAGCTCAACCTTCTAATCTTAGTGGCTTG 240

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QY 1163 CCACCCACACAGCATATATCGATTGAGGGAGGGGCTCAGTGCAGTCTGTCGACCA 1222  
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QY 1223 GCACCGCAACACAGTGTACGACGAGAGCTTCAAGAGGGGTCACTGCTTGTGGTGGCAC 1282  
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QY 1283 AG-AACTTCCCGTCTGCGTGAAGAGTCCAGAGCGAGAACTTCGAATACGTGGCATTAAG 1341  
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QY 1342 ACAGACTCAAGGCCACGATAGCAACCTCCGCGGTGAACCTCCCTCATAGATACCTTG 1401  
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QY 1402 CC--GGAGGAGGTGGTTCGAAATTCATATGGCTCCAAAGGGGAGCAGGAGGCGCTTAA 1460  
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QY 1461 GAACAACAA--CCCTTTCAAGTCTTCGTTCCACCGTCTCAGCAGTCTCCGAGGGCTGTGG 1519

Db 601 GAACAACAAACCCCTTCAAGTCTTCGTTCCACCGTCTGAACAGTCTCTGAGGCGCTGTGG 660

QY 1520 CTTAA 1524

Db 661 CTTAA 665

RESULT 6  
CO897496

LOCUS CO897496

DEFINITION EST00001 Peanut Lambda Express library Arachis hypogaea cDNA 5', mRNA sequence.

ACCESSION CO897496

VERSION CO897496.1 GI:51237286

KEYWORDS EST.

SOURCE Arachis hypogaea (peanut)

ORGANISM Arachis hypogaea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.

REFERENCE 1 (bases 1 to 553)  
Yan, Y.S.; Wang, L.; Zhong, Y.J. and Huang, S.Z.  
Expressed sequence tags of mid-matured cotyledons of peanut  
Unpublished (2004)  
Contact: Shangzhi Huang  
Plant Development and Molecular Biology  
Sun Yat-sen University, Department of Biology and Biotechnology  
Guangzhou, 510275, China  
Tel: (860) 02084036592  
Email: YYS903@yahoo.com.cn  
Seq primer: pTriplEx2 Forward.  
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ORIGIN

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Matches 508; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 39 CCTCAATGCGCAGAGACCTGACAATCGCATTTGAATCAGAGGGCGGTTACATTGAGACTTG 98  
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QY 99 GAACCCCAACAAACAGAGGTTGCAATGCGCGCGGCTCGCCCTCTCTCGTTAGTCTCCG 158  
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QY 159 CGCAACGCGCTTCGTAGGCGCTTCTACTCCATGCTCCCGAGAGATCTTATCCAGCA 218  
DB 121 CGCAACGCGCTTCGTAGGCGCTTCTACTCCATGCTCCCGAGAGATCTTATCCAGCA 180

QY 219 AGAAGGGGATACTTTGGGTTGATATTCCTCGTGTCTCTAGACACTATGAAGAGCTCA 278  
DB 181 AGAAGGGGATACTTTGGGTTGATATTCCTCGTGTCTCTAGACACTATGAAGAGCTCG 240

QY 279 CACACAAGGTCTCGATCTCAGTCCCAAGAGACCAACCAAGACGTCTCAAGGAGAAACCA 338  
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QY 339 AAGCCCAACAGCAACGAGATAGTCAACAGAGGTGACCGCTTTCGATGAGGGTATCTCAT 398  
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 361 TGCAGTCCACCGGTGTTCTTCTTGGATGTACAAAGCAGCAGACACTGATGTTGTC 420  
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 459 TGTCTCTTACTGACACCAACACACACACACACACACACACACACACACACACAC 518  
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 421 TGTCTCTTACTGACACCAACACACACACACACACACACACACACACACACACAC 480  
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RESULT 7  
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 DEFINITION  
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 Arachis hypogaea cDNA clone UTPI005\_C08 5', mRNA sequence.  
 ACCESSION  
 CD038301  
 VERSION  
 CD038301.1 GI:30420139  
 KEYWORDS  
 EST.  
 SOURCE  
 Arachis hypogaea (peanut)  
 ORGANISM  
 Arachis hypogaea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
 Aeschynomeneae; Arachis.  
 1 (bases 1 to 602)  
 Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.  
 and Lynch, R. E.  
 Generation and Analyses of ESTs for Arachis hypogaea  
 Unpublished (2003)  
 Contact: Baozhu Guo  
 Molecular Genetics  
 USDA/ARS, Crop Protection and Management Research Unit  
 2747 Davis Rd., Tifton, GA 31794, USA  
 Tel: 229-387-2334  
 Fax: 229-387-2321  
 Email: bguo@tifton.usda.gov  
 Seq primer: T3.  
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 /notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;  
 cDNA library was constructed from peanut cultivar A13  
 (NCV11X84). A13 has resistance to Aspergillus infection  
 and drought tolerance. The immature pods that developed to  
 R6 stage were collected from different plants, and placed  
 into liquid N2 immediately and stored in -80°C freezer.  
 Total RNA was isolated with TRIzol-Reagent  
 ultrapur (GIBCOBRL). mRNA was extracted and library  
 total RNA (Promega). cDNA synthesis and library  
 construction followed the protocol of by ZAP-cDNA Gigapack  
 III Gold cloning kit (Stratagene). The cDNA above 500bp  
 were collected after size-fraction. The inserts were  
 directionally cloned into Uni-ZAP XR vector using XhoI  
 EcoRI sites adaptors. The lambda library was packed into  
 phages using Gigapack III Gold (Stratagene). The  
 un-amplified library was used to excise pBluescript

phagemids from the Uni-ZAP XR vector, and the phagemids  
 was used to transform the host bacteria SOLR. The library  
 was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN  
 Query Match 28.6%; Score 436; DB 4; Length 602;  
 Best Local Similarity 95.7%; Pred. No. 9.1e-109; Indels 0; Gaps 0;  
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 Db 1 CTCAAACCTGCCAAGCATCTCAACCTTCTTAATCTTAGTGGCTTGGACCTAGTGTGAA 60  
 QY 1117 TATGGAATCTCTACAGGAATGATTTGTCGCTCACTACACACCAACGACACAGC 1176  
 Db 61 TATGGAATCTCTACAGGAATGATTTGTCGCTCACTACACACCAACGACACAGC 120  
 QY 1177 ATCATATATCGATTGAGGGGACGGCTCACGTGCAAGTCGTGGACAGCAACGGCAACAGA 1236  
 Db 121 ATCATATATGCAATTGAGGGGACGGCTCACGTGCAAGTCGTGGACAGCAACGGCGACAGA 180  
 QY 1237 GTGTACGACGAGAGCTTCAAGAGGTCACGTGCTTGTGTGGTCCACAGAACTTCGCGCTC 1296  
 Db 181 GTGTTTCGACGAGAGCTTCAAGAAGTCACGTGCTTGTGTGGTCCACAGAACTTCGCGCTG 240  
 QY 1297 GCTGGAAAGTCCAGAGCGAGAACTTCGAATACGTGGCACTTCAAGACAGACTCAAGGCC 1356  
 Db 241 GCTGGAAAGTCCAGAGCGAGAACTTGAATACGTGGCACTTCAAGACAGACTCAAGGCC 300  
 QY 1357 AGCATAGCCAACTCCGCCGTGAAACTCCGTATAGATAAAGCTGCCGAGGAGGTGGTT 1416  
 Db 301 AGCATAGCCAACTAGCCGCTGAAACTCTTCATAGATAAAGCTGCCGAGGAGGTGGTT 360  
 QY 1417 GCAAAATTCATATGGCTTCCAAAGGGAGCAGGCAAGCAGCTTAAGAAACAAACACCCCTTC 1476  
 Db 361 GCAAAATTCATATGGCTTCCAAAGGGAGCAGGCAAGCAGCTTAAGAAACAAACACCCCTTC 420  
 QY 1477 AGTCTTCTGTTCCACCGTCTCAGCAGTCTCCGAGGCGTGTGCTTAA 1524  
 Db 421 AAGTCTTCTGTTCCACCGTCTCAGCAGTCTCTGAGGGCTGTGGCTTAA 468

RESULT 8  
 CD038222  
 LOCUS  
 DEFINITION  
 Arachis hypogaea cDNA clone UTPI004\_B11 5', mRNA sequence.  
 ACCESSION  
 CD038222  
 VERSION  
 CD038222.1 GI:30420060  
 KEYWORDS  
 EST.  
 SOURCE  
 Arachis hypogaea (peanut)  
 ORGANISM  
 Arachis hypogaea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;  
 Aeschynomeneae; Arachis.  
 1 (bases 1 to 532)  
 Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.  
 and Lynch, R. E.  
 Generation and Analyses of ESTs for Arachis hypogaea  
 Unpublished (2003)  
 Contact: Baozhu Guo  
 Molecular Genetics  
 USDA/ARS, Crop Protection and Management Research Unit  
 2747 Davis Rd., Tifton, GA 31794, USA  
 Tel: 229-387-2334  
 Fax: 229-387-2321  
 Email: bguo@tifton.usda.gov  
 Seq primer: T3  
 Location/Qualifiers  
 1. .532  
 /organism="Arachis hypogaea"  
 /mol\_type="mRNA"





## ORIGIN

Query Match 24.4%; Score 372; DB 4; Length 679;  
Best Local Similarity 92.9%; Pred. No. 4.6e-91;  
Matches 390; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1105 CTTAGTGTGGAATATGGAATCTCTACAGGAATGCAATGTTTTCGCTCACTACACACC 1164  
|||  
Db CCTGAGGCTGCAGGAATTCGGCAGGAGGGAATGCAATGTTTTCGCTCACTACACACG 105

QY 1165 AACGCACACAGCATATATCATTCAGGGGAGGGCTCACGTGCAAGTCGTGGACAGC 1224  
|||  
Db 106 AACGCACACAGCATATATCATTCAGGGGAGGGCTCATGTGCAAGTGGTGGACAGC 165

QY 1225 AACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTCACTGTCTTGTGGTCCACAG 1284  
|||  
Db 166 AACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTCACTGTCTTGTGGTCCACAG 225

QY 1285 AACTTCGCGTGCCTGGAAGTCCCGAGGAGCAACTTCGAATACGTGGCAATTCAGACA 1344  
|||  
Db 226 AACTTCGCGTGCCTGGAAGTCCCGAGGAGCAACTTCGAATACGTGGCAATTCAGACA 285

QY 1345 GACTCAGGCCAGCATAGCAACCTCGCGGTGAAACTCCGTCATAGTAACTCCGCG 1404  
|||  
Db 286 GACTCAGGCCAGCATAGCAACCTCGCGGTGAAACTCCGTCATAGTAACTCCGCGCG 345

QY 1405 GAGGAGTGTGTCGAATTCATATGGCTCCAAAGGAGGAGCAAGGAGCTTAAAGAAC 1464  
|||  
Db 346 GAGGAGTGTGTCGAATTCATATGGCTCCAAAGGAGGAGCAAGGAGCTTAAAGAAC 405

QY 1465 AACAAACCCCTTCAAGTTCCTTCACCGTCTCAGCAGTCTCCGAGGGCTGTGGCTTAA 1524  
|||  
Db 406 AACAAACCCCTTCAAGTTCCTTCACCGTCTCAGCAGTCTCCGAGGGCTGTGGCTTAA 465

## RESULT 12

BQ123409  
LOCUS BQ123409.1 GI:20175371  
DEFINITION Medicago truncatula cDNA clone pGLSD-32121, mRNA  
ACCESSION BQ123409  
VERSION BQ123409.1  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
REFERENCE 1 (bases 1 to 906)  
AUTHORS Grusak, M.A., Samac, D., Town, C.D., Van Aken, S., Utterback, T., Cheung, F., and Fraser, C.M.  
TITLES ESTs from late stage developing seeds of Medicago truncatula  
JOURNAL Unpublished (2002)  
COMMENT Contact: Grusak, M.A.  
USDA/ARS Children's Nutrition Research Center  
Baylor College of Medicine  
1100 Bates Street, Houston, TX 77030-2600, USA  
Tel: 713 798 7044  
Fax: 713 798 7078  
Email: mgrusak@bcm.tmc.edu  
TIGR sequence name: MTRAQ59TK More information is available at:  
www.medicago.org  
Seq primer: Sknod (CTA gAA CTA gtg GAT CC).  
FEATURES  
source location/Qualifiers  
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/tissue\_type="Immature seeds"  
/dev\_stage="25 to 35 days after pollination"

/lab\_host="XLOLR"

/clone\_lib="GLSD"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:  
XhoI; Immature seeds, collected from pods ranging in age  
from 25 to 35 days after pollination, were harvested from  
greenhouse-grown plants. Seed were removed and separated  
from pod walls and immediately frozen in liquid nitrogen.  
Seeds throughout the age range were pooled for mRNA  
extraction. cDNA was prepared from polyA+ enriched RNA.  
The cDNA was directionally ligated into the Unizap XR  
vector from Stratagene and packaged using Gigapack III  
Gold packaging extracts. Plasmids containing cDNA inserts  
were excised from the recombinant lambda-Zap phage using  
Ex-assist helper phage and propagated in XLOLR cells."

## ORIGIN

Query Match 21.7%; Score 330.4; DB 3; Length 906;  
Best Local Similarity 63.5%; Pred. No. 1.6e-79;  
Matches 540; Conservative 0; Mismatches 301; Indels 9; Gaps 2;

QY 680 GAGCAGCAAGAAAGAAAGAAAGTGGAAACATCTTCAGCGGCTTCACGCCGAGT 739  
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Db 47 GAGGAAGGAAACAAACAAAGTAATGAAGGAGGCAACATTTTCAGTGGCTTCAAGAGGATT 106

QY 740 TCTGGAACAAGCCTTCCAGGTTGACGACAGACAGATAGTGCAAAACCTTAAGAGGCGAGA 799  
|||  
Db 107 TCTTGAAGATGCAATTGAACGTGA---ACAGGCATATAGTTGAAAAAATTTCAAGGCGAGGA 163

QY 800 CCGAGAGTCAAGAGAGGAGGAGCCATTTGCACAGTGAGGGGAGGCTTCAGATCTTGAGCC 859  
|||  
Db 164 ATGAAGACAGGAGAAAGGAGGCCATTTGCAAGTGGAGGAGGACTCAGCATCATGAGCC 223

QY 860 C-----AGATAGAAAGAGACGTCGCCAGAAAGAGGAATACGATGAAGATGAATATG 913  
|||  
Db 224 CTCGAGAGAGACAAACACCCACCCAGCAGACAGATGAAGATGAAGATGAAGAGG 283

QY 914 AATACGATGAAGAGGATAGAAAGCGTGGCAGGGGAAGCAGCAGCGGGGAATGTTATTG 973  
|||  
Db 284 ATGAGTGGAGGCCACATCATCAGAAAGCAGAAAGAGAAAGGCAACACCGTCTTG 343

QY 974 AAGAGACGATCTGCACCGCAAGTGTCTAAAGAGACATTTGGTAGAAACAGATCCCCTGACA 1033  
|||  
Db 344 CGGAAACAATTTGCACTGCCAGGCTTCACCAAGACATGTTCTCATCTTCACTACCTGACA 403

QY 1034 TCTCAACCCCTCAAGCTGTTTCACTCAAAACCTGCCAACGATCTCAACCTTCTAATCTTA 1093  
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Db 404 TCTCAACCCCTCAAGCTGTTTCACTCAAAACCTGCCAACGATCTCAACCTTCTAATCTTA 463

QY 1094 GTGGCTTGGACCTAGTGTCTGAATATGGAATCTCTTACAGGAATGCAATGTTTGTGCTC 1153  
|||  
Db 464 GTGGCTTGAAGACTCAGTGTCTGAGCATGGAACCTCTCCACAGAAATGCTATGTTCTCCAC 523

QY 1154 ACTCAACACCAACCGCAGCAGCATATATCGATTGAGGGGAGCGGCTCACGTGCAAG 1213  
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Db 524 ACTCAACCTCAATGCAAAACAGCATAATATGTCATTTGAATGGACGTGCAAGGCTCAAG 583

QY 1214 TCGTGACAGCAACCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGCTCAGTGTGTTG 1273  
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Db 584 TAGTGAACCTGCAATGGCAACACTGTGTTTCGATGAGGAACATAGAACTGGCGGTGATGA 643

QY 1274 TGGTGCCACAGAACTTTCGCGCTGCTGGAAAGTCTCCAGAGGAGAACTTCGAAATACGTGG 1333  
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Db 644 TGGTGCCACAAACCTTTCGCTGTCAGCAAAAATCAGTGAAGCAGACAGGTTTCACTTATGTTT 703

QY 1334 CATTCAAGACAGACTCAAGGCCAGCATAGCAAACTCCCGGTGAAAACCTCGTCTATAG 1393  
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Db 704 CATTCAAGACCAATGATTAATGCCCAATTTGCCAGGCTTGCAGGACACAACTCCACTCTAA 763

QY 1394 ATAACTCGCGGAGGAGTGGTTTGGAAATTCATATATGCGCTCCAAAGGAGGAGCAAGGC 1453  
|||  
Db 764 GTGGTATGCCAGTGGATGTGCTTTCAGCTACATTCACATGACAGAGATGAGCAAGGC 823

QY 1454 AGCTTAAGAAACAAACACCCCTTCAAGTCTTCGTTCCACCGTCTCAGCAGTCTCCGAGGG 1513

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||||| 824 AGCTCAAAACAACTCTTTTAAATTTCTAGTTCACCCCGTGAGTCGGAACGCAGAG 883
||| 1514 CTGTGGCTTA 1523
||| 884 CTGCAGCTTA 893

RESULT 13
BQ123283
LOCUS
DEFINITION
BQ123283 974 bp mRNA linear EST 17-APR-2002
EST608859 GLSD Medicago truncatula cDNA clone pGLSD-3IN1, mRNA
sequence.
ACCESSION
VERSION BQ123283
KEYWORDS
SOURCE
ORGANISM Medicago truncatula (barrel medic)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 974)
Grusak,M.A., Samac,D., Town,C.D., Van Aken,S., Utterback,T.,
Cheung,F. and Fraser,C.M.
ESTs from late stage developing seeds of Medicago truncatula
Unpublished (2002)
Contact: Grusak, M.A.
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713 798 7044
Fax: 713 798 7078
Email: mgrusak@bcm.tmc.edu
TIGR sequence name: MTRAO73TK More information is available at:
www.medicago.org
Seq primer: SKnod (CTA gAA CTA gtg GAT CC).
Location/Qualifiers
1..974
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="pGLSD-3IN1"
/tissue_type="Immature seeds"
/dev_stage="25 to 35 days after pollination"
/lab_host="XL0LR"
/clone_lib="GLSP"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. cDNA was prepared from polyA+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-zap phage using
Ex-assist helper phage and propagated in XL0LR cells."

ORIGIN
Query Match 21.1%; Score 321.6; DB 3; Length 974;
Best Local Similarity 63.7%; Pred. No. 4.4e-77;
Matches 524; Conservative 0; Mismatches 289; Indels 9; Gaps 2;

QY 680 GACGACACAGAGAGAAACGAGGTGGAAACATCTTTCAGCGGCTTCACGCCGAGT 739
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DB 102 GAGGAAGGGAACACACAGAAAATGAGGAGGCAACATTTTCAGTGGCTTCAAGAGGATT 161
|||
QY 740 TCCTGGAACAGGCTTCCAGGTTGACGACAGACAGATAGTGCAAAACCTTAAGAGCGCAGA 799
|||
DB 162 TCTTGAAGATGCTTGAACGT--GAACAGGCATATAGTTGAAAACTTCAAGGCAGGA 218
|||
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QY 800 CCGAGAGTGAAGAGAGGAGCCATTGTGACAGTGAAGGGAGGCCTCAGAATCTTTGAGCC 859
|||
DB 219 ATCAAGACCAGGAGAGGAGCCATTGTCAAAGTGAAGGAGACTCAGCATCATGAGCC 278
|||
QY 860 C-----AGATAGAAGAGACGTCGCCGACGAAGAAGAGGAATACGATGAAGATGAATATG 913
|||
DB 279 CTCAGAGAGACAAACACGCCACCCAGCAGACAGATGAAGATGAAGATGAAGAGG 338
|||
QY 914 AATACGATGAAGAGGATAGAAGGCGTGGCAGGGGAAGCAGCGGGAATGGTATTG 973
|||
DB 339 ATGAGTGGAGGCCACATCATCAGAAAAGCAGAAAGAGAAAAGAGAAAGGCAACGGTCTTG 398
|||
QY 974 AAGAGACGATCTGCACCGCAAGTGTAAAAAGAACATTTGGTAGAAACAGATCCCTTGACA 1033
|||
DB 399 CGGAAACAAATTTGCACTGCCAGGCTTCACCGAACATGGTCTCATCTTCACCTTGACA 458
|||
QY 1034 TCTACAACCTCAAGCTGGTTCACTCAAAATGCGCAACGATCTCAACCTTCTAATACTTA 1093
|||
DB 459 TCTACAACCTCAAGCTGGTAGAATCAAACTATCACCAGCTTCGACCTCCAGCTCTCA 518
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QY 1094 GTGGGCTTGGACCTAGTGTGAATATGAAATCTCTACAGGAATCATTTGTTTGCCTC 1153
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DB 519 GTGGGCTAAGACTCAGTGTGAGCATGGAATCTCCACAGAAATGCTATGTTGTTCCAC 578
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QY 1154 ACTACAACACCAACCGCACACAGCATATATCGATTGAGGGACGGCTCAGCTGCAAG 1213
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DB 579 ACTACAATCTCAATGCAAAACAGCATATATTTGGCATTTGAATGGACGTGCAAGGCTACAAG 638
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QY 1214 TCGTGACAGCAACCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGCTCAGTGTCTTG 1273
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QY 1274 TGGTGCCACAGAACTTTCGCGTGTGGAAAGTTCACAGACGCGAGAACTTCGAAATACGTGG 1333
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DB 699 TCGTGCCACAAACTTTGCTGTTCAGCAAAAATCAGTGAGCGCACAGGTTCACTTATGTTT 758
|||
QY 1334 CATTCAAGACAGACTCAAGGCCAGCATAGCCAACTCCCGGTGAAAACCTCCGTCTCATAG 1393
|||
DB 759 CATTCAAGACCAATGATATATGCCCAATTCGACAGGCTTCAGGAGCACAACTCCACTCTAA 818
|||
QY 1394 ATAACTGCGGAGGAGGTGGTTGCAAAATTCATATATGCTTCCAAAGGGAGCAGGCAAGC 1453
|||
DB 819 GTGGTATGCCAGTGGATGTGCTTGCAGCTACATTTCAACATGGACAGGAATGAGGCGAGC 878
|||
QY 1454 AGCTTAAGAACAAACCCCTTCAAGTTCTTGTTCACCGT 1495
|||
DB 879 AGCTCAAAAACAACTCTCTTTAATTTCTAGTTTACCCCGT 920
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RESULT 14
BQ123283
LOCUS
DEFINITION
ACCESSION
VERSION BQ123283
KEYWORDS
SOURCE
ORGANISM Medicago truncatula (barrel medic)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 886)
Grusak,M.A., Samac,D., Town,C.D., Van Aken,S., Utterback,T.,
Cheung,F. and Fraser,C.M.
ESTs from late stage developing seeds of Medicago truncatula
Unpublished (2002)
Contact: Grusak, M.A.
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
```



Tel: 713 798 7044  
Fax: 713 798 7078  
Email: mgrusak@bcm.tmc.edu  
TIGR sequence name: MTRBM60TK  
More information is available at: www.medicago.org  
Seq primer: SKmod (CTA GAA CTA gtg gat CC).

FEATURES  
source

1. .886  
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/notes="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Immature seeds, collected from pods ranging in age from 25 to 35 days after pollination, were harvested from greenhouse-grown plants. Seed were removed and separated from pod walls and immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

## ORIGIN

Query Match 20.7%; Score 316.2; DB 4; Length 886;  
Best Local Similarity 63.2%; Pred. No. 1.3e-75;  
Matches 538; Conservative 0; Mismatches 303; Indels 10; Gaps 3;  
QY 680 GAGCAGCAAGAAGAAAGAAACGAGGTGGAAACATCTTTCAGCGGCTTCACCCGGAGT 739  
DB 40 GAGGAAGGGAACAAACGAAGAAATGAAGAGGCAACATTTTCAGTGGCTTCAAGAGGAT 99  
QY 740 TCTGTGAACAAGCTTCCAGGTGTGACACAGACAGATAGTGCACAAACCTTAAGAGGCGAG 799  
DB 100 TCTTGAAGATGATTTGAACGT---GAACAGGCATATAGTTGAAACATTTCAAGGCGAGA 156  
QY 800 CCGAGAGTGAAGAAGAGGAGGCATTTGTGACAGTGAGGGAGCGCTCAGAAATCTTCAGCC 859  
DB 157 ATGAACACAGGAGAGAGGAGCCATTTGTCAAAGTGGAGGAGACTCAGCATCATGAGCC 216  
QY 860 C-----AGATAGAAAGACGCTGCGCAGCAAGAGGAATACGATGAAGATGAATATG 913  
DB 217 CTCAGAGAGACAAACAACGCCACCCAGCAGACAGATGAAGAAGATGAAGATGAAGAGG 276  
QY 914 AATACCATGAAGAGGATAGAGCGGTGGAGGGAGCAGAGCGGGGGAATGGTATTG 973  
DB 277 ATGAGTGGAGGCCACATCATATCAAAAGCAGAAAGAGAAAGAGGCAACAGCGTCTTG 336  
QY 974 AAGAGACGATCTGCACCGCAAGTGTCTAAAGAAACATTTGTGTAAGAACAGATCCCTGACA 1033  
DB 337 CGGAACAATTTGCATCTGCCAGGCTTCACCAAGAACATGTTCTCATCTTATCACCTGACA 396  
QY 1034 TCTAACCCCTCAAGCTGGTTCTACTCAAACTGCCAACGATCTCAACCTTCTTAATCTTA 1093  
DB 397 TCTAACCCCTCAAGCTGGTTAGTAATCAAACTATATCACCAGCTTCGACCTCCCGAGCTCTCA 456  
QY 1094 GGTGGCTTGGACCTAGTGTGATATGGAATCTCTACAGGATGCAATGTTTGTGCTC 1153  
DB 457 GGTGGCTTAAGACTTCAGTGTGAGCATGGAATCTCCACAGAAATGCTATTTGTTCCAC 516  
QY 1154 ACTAACACCAACGACACAGCATCATATATCGATTGAGGGAGCGGGCTCAGCTCAAG 1213  
DB 517 ACTACATCTCATGCAACAGCATATATTTGCAATTTGATGACCTGCAAGGCTACAG 576  
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Db 577 TAGTGAATGCAATGCAACACACTGTGTCGATGAGGAACATAGAACTGCGCGTCATTGA 636  
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Db 637 TCGTGCCACAAACATTTGCTGTTGCGACAAATTCAGTGACGACAGGTTTCACTTATGTTT 696  
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Db 697 CATTCAAGACCAATGATATGCGCAATTCGCCAGGCTTCAGGAGCACAAATCCACTCTAA 756  
QY 1394 ATAACTCGCGGAGGAGGTGTTGCAAAATCATATGCGCTCCAAAGGAGCAGCAAGCC 1453  
Db 757 GTGGTATGCCAGTGGATGTGCTTTCAGCTACATTCACATGGAAGAAATGAGGCAAGC 816  
QY 1454 AGCTTAAGAACAAACACCCCTTCAAGTTCCTTCGTTCCACCGTCTCAGCAGTCTCCGAGGG 1513  
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QY 1514 CTGTGGCTTAA 1524  
Db 876 CTGCAGCTTAA 886

RESULT 15  
CA858492

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

CA858492 861 bp mRNA linear EST 18-DEC-2002  
EST635747 GLSD Medicago truncatula cDNA clone pGLSD-38K19, mRNA  
sequence.  
CA858492  
CA858492.1 GI:27232856  
EST.  
Medicago truncatula (barrel medic)

Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 861)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Grusak, M.A., Samac, D., Town, C.D., Van Aken, S., Utterback, T.,  
Cheung, F. and Fraser, C.M.  
ESTs from late stage developing seeds of Medicago truncatula  
Unpublished (2002)  
USDA/ARS Children's Nutrition Research Center  
Baylor College of Medicine  
1100 Bates Street, Houston, TX 77030-2600, USA  
Tel: 713 798 7044  
Fax: 713 798 7078  
Email: mgrusak@bcm.tmc.edu  
TIGR sequence name: MTRBS70TK  
More information is available at: www.medicago.org  
Seq primer: SKmod (CTA GAA CTA gtg gat CC).

FEATURES  
source

1. .861  
/organism="Medicago truncatula"  
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/dev\_stage="25 to 35 days after pollination"  
/lab\_host="XL0LR"  
/clone\_lib="GLSD"  
/notes="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Immature seeds, collected from pods ranging in age from 25 to 35 days after pollination, were harvested from greenhouse-grown plants. Seed were removed and separated from pod walls and immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts

were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

## ORIGIN

	Query Match	20.68;	Score 314;	DB 4;	Length 861;
	Best Local Similarity	64.08;	Pred. No. 5.4e-75;		
	Matches 525; Conservative	0;	Mismatches 285;	Indels 10;	Gaps 3;
Qy	680	GAGCAGACAAAGAAGAAAAA	CGAAGGTGAAAACATCTT	CAGCGGCTTCACGCCGGAGT	739
Dd	45	GAGNAAGGGAACAACAAGAAA	TGAAGGACACATTTT	CAGTGGCTTCAAGAGGATT	104
Qy	740	TCTGTGAAACAGCCCTTCCAG	GTTCACGACACAGATAGTG	TGC AAAACCTTAAGAGGCGAGA	799
Dd	105	TCTTGG AAGATG CATTTGAAC	CGT---GAACAGGCCATATAG	TGTGAAAAACTTCAAAGGCAGGA	161
Qy	800	CCGAGAGTGAAGAGAGGGAG	CCCATCTGTGACGTGAGGG	GAGGCCCTCAGAAATCTTTGAGCC	859
Dd	162	ATGAAGACCAGGAGAGGGAG	CCCATTTGTCAAAGTGGAA	GAGGNACTCAGCATCATGAGCC	221
Qy	860	C-----AGATAGAAAGAG	ACGTGCCACGAAGAAGAG	AATACGATGAAGATGAATATG	913
Dd	222	CTCCAGAGAGACAACAACGC	CACCACCCAGCACACAAG	ATGAAGATGAAGATGAAGAGG	281
Qy	914	AATACGATGAAGAGGATAGA	AGGCGTGGCAGGGGAAC	CAGAGCGAGGGGGAATGTTATG	973
Dd	282	ATGAGTGGAGGCCACATCAT	CAGAAAAAGCAGAGAGAA	GAGAAAGGCAACAACGGTCTTG	341
Qy	974	AAGAGACGATCTGCACCGC	AAAGTCTATAAAGAAACAT	TGGTAGAAAAACAGATCCCCCTGACA	1033
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Qy	1034	TCTACAAACCTCAAGCTGT	TTCACTAAAAC TGCCAAC	AGATCTCAACCTTCTTAATCTTA	1093
Dd	402	TCTACAAACCTCAAGCTGT	AGATACTAAAACATATC	ACCAGCTTCGACCTCCCAGCTCTCA	461
Qy	1094	GGTGGCTTGACCTPAGTGC	TGAATATGGAATCTCTAC	AGAAATGCAATGTGTTGTCGCTC	1153
Dd	462	GGTGGCTTAAGACTCAGT	GTGAGCATGGAACCTTCC	CACAGAAATGCTATGTTGTTCCAC	521
Qy	1154	ACTACAAACCAACGCACAC	GACATCATATATCGATT	GAGGGGACGGGCTCAGTGCAGG	1213
Dd	522	ACTACAATCTCAATGC	AAAAAGCATAATATTTGG	CATTTGAATGGACGTGCAAGGCTACAAG	581
Qy	1214	TCGTGGACACGACGCAAC	GAGGTGTACGACGAGGAG	CTTCAAGSGGTCACTGCTGCTG	1273
Dd	582	TAGTGAACCTGCAATGG	CAACACTGTGTTCAGTAG	GAACTAGAAAGCTGGCCGTCATTGA	641
Qy	1274	TGTTGCCACAGAACTTCG	CCCGTCGCTGGAAAGTCCC	CAGAGCGAACTTCGAATACGTGG	1333
Dd	642	TCGTGCCACAAAAC TT	TGCTGTTGCAGCAAAA	TCAAGTGAGCGACAGGTTTCACTTATGTTT	701
Qy	1334	CATTCAAGACAGACTCA	AGGCCACAGATAGCCAA	CCCTCGCGGTGAAAACTCCGTCATAG	1393
Dd	702	CATTCAAGACCAATGAT	AATAGCCCAATTTGCC	AGGCTTGCAGGACACAATCCACTCTAA	761
Qy	1394	ATRAACCTGCCGGAGG	AGTGGTTCGCAAAATTC	ATATGCGCTTCAAAGGGAGCAGGCAAGGC	1453
Dd	762	GTGGTATGCCCATGG	ATGTGCTTCGACTACAT	-TCACATGGACAGAAATGAGGGCAGGC	820
Qy	1454	AGCTTAAGAAACAACA	ACCCCTTCAAGTTCTT	TCGTTCCACC	1493
Dd	821	AGCTCAAAAACAACAAT	CTCTTTTAAATTTCT	TAGTTCCACC	860

Search completed: June 24, 2006, 00:18:46  
Job time : 7833.57 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:43:18 ; Search time 237.534 Seconds  
(without alignments)  
12004.877 Million cell updates/sec

Title: US-10-728-051-3

Perfect score: 1524

Sequence: 1 cggcagcaaccggaggagaa.....ctccgagggtgtggcttaa 1524

Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq:\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq:\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq:\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq:\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/ina/8 COMB.seq:\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq:\*
- 8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq:\*
- 9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq:\*
- 10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1391.2	91.3	1853	3	US-09-715-036-4
2	517.4	34.0	1446	3	US-09-108-010B-13
3	517.4	34.0	1446	3	US-09-758-652-13
4	517.4	34.0	1446	3	US-10-684-651-13
5	513	33.7	1488	3	US-09-108-010B-11
6	513	33.7	1488	3	US-09-758-652-11
7	513	33.7	1488	3	US-10-684-651-11
8	513	33.7	1743	3	US-09-762-381-1
9	505	33.1	1746	3	US-09-805-694B-15
10	504	33.1	1458	3	US-09-108-010B-12
11	504	33.1	1458	3	US-09-758-652-12
12	504	33.1	1458	3	US-10-684-651-12
13	198	13.0	1551	3	US-09-108-010B-15
14	198	13.0	1551	3	US-09-758-652-15
15	198	13.0	1551	3	US-10-684-651-15
16	153.2	10.1	1689	3	US-09-108-010B-14
17	153.2	10.1	1689	3	US-09-758-652-14
18	153.2	10.1	1689	3	US-10-684-651-14
19	142	9.3	1706	3	US-09-462-720-1
20	136.6	9.0	1685	2	US-08-486-721A-1
21	133	8.7	1679	3	US-10-053-410-5
22	132.2	8.7	1556	2	US-08-486-721A-2
23	114.6	7.5	3113	2	US-08-146-422-20

ALIGNMENTS

RESULT 1

US-09-715-036-4 ; Sequence 4, Application US/09715036 ; Patent No. 6943010

GENERAL INFORMATION:

APPLICANT: DODO, HORTENSE W.

APPLICANT: ARNTZEN, CHARLES J.

APPLICANT: KONAN, KOFFI N'DA

APPLICANT: VIQUEZ, OLGA

TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN

TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS

FILE REFERENCE: 072121/0104

CURRENT APPLICATION NUMBER: US/09/715, 036

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 60/167,255

PRIOR FILING DATE: 1999-11-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 1853

TYPE: DNA

ORGANISM: Arachis hypogaea

US-09-715-036-4

Query Match	91.3%	Score 1391.2;	DB 3;	Length 1853;
Best Local Similarity	95.4%	Pred. No. 0;		
Matches 1454;	Conservative	0;	Mismatches 68;	Indels - 2;
Gaps	2;			
QY	2	GGCAGCAACGGAGGAGAACGGGTGCCAGTTCACAGCGCCTCAATGCCAGAGACCTTGACA	61	
Db	71	GGCAGCAGCGGAGGAGAGATGCGTCCAGCGCCTCAATGCCAGAGACCTTGACA	130	
QY	62	ATCGCATTTGAATCAGAGGCGGTTCATTTGAGATTGGAAACCCCAACACAGAGTTGC	121	
Db	131	ACCGCATTTGAATCAGAGGCGGTTCATTTGAGATTGGAAACCCCAACACAGAGTTGC	190	
QY	122	AATGCCCGCGGTTCGTCCTCTCGCTTAGTCTCCGCGCAACGCCCTTCGTAGGCCCTT	181	
Db	191	AATGCCCGCGGTTCGTCCTCTCGCTTAGTCTCCGCGCAACGCCCTTCGTAGGCCCTT	250	
QY	182	TCTACTCCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAGGATACTTTGGGTGA	241	
Db	251	TCTACTCCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAGGATACTTTGGGTGA	310	
QY	242	TATTCCCTGGTTGCTCTAGACACTATGAGAGGCTCACACAGGCTCGTCGATCTCAGT	301	

Db 311 TATTCCTGGTGTCTCTAGCACATATGAAGAGCCTGCACAAAGAGACGCCGATATCAGT 370  
Qy 302 CCCAAGAGCCACCAAGACGFTCTCAAGGAGAAGACCAAGCCCAACAGCAACGAGATAGTC 361  
Db 371 CCCAAGAGCCACCAAGACGFTTTCGAAGAGAAGACCAAGCCCAACAGCAACGAGATAGTC 430  
Qy 362 ACCAAGAGTGCACCGTTTCGATGAGGTGATCTCATTCGAGTTCGCCCGGTGTCCT 421  
Db 431 ACCAAGAGTGCACCGTTTCAATGAGGGTGATCTCATTCGAGTTCGCCCGGTGTCCT 490  
Qy 422 TCTGGCTCTACAAAGCAGCAGACACTGATGTTGCTGTTTCTCTTACTGACACCAACA 481  
Db 491 TCTGGCTCTACAAAGCAGCAGACACTGATGTTGCTGTTTCTCTTACTGACACCAACA 550  
Qy 482 ACAACGACAAACCACTGTGATCAGTTCCTCCAGGAGATTCATATTTGGCTGGGAACACGGAGC 541  
Db 551 ACAACGACAAACCACTGTGATCAGTTCCTCCAGGAGATTCATATTTGGCTGGGAACACGGAGC 610  
Qy 542 AAGAGTCTTTAAGGTACCAAGCAACAAAGCAGACAAAGCAGACCAAGAGCTTACCATATA 601  
Db 611 AAGAGTCTTTAAGGTACCAAGCAACAAAGCAGACAAAGCAGACCAAGAGCTTACCATATA 670  
Qy 602 GCCCATACAGCCCGCAAGTCAGCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGAC 661  
Db 671 GCCCATACAGCCCGCATAGTTCGGCTAGACGAGAGCGTGAATTTGCCCTCGAGGAC 730  
Qy 662 AGCACAGCCCGCAGAGAACGAGCAGGACCAAGAAAGAAACGAAAGGTGGAACATCTTCA 721  
Db 731 AGCACAGCCCGCAGAGAACGAGCAGGACCAAGAAAGAAACGAAAGGTGGAACATCTTCA 790  
Qy 722 GCGGCTTCACGCCGAGTTCCTCGAACACAGCCTTCAGGTTGACGACAGACATAGTGC 781  
Db 791 GCGGCTTCACGCCGAGTTCCTCGAACACAGCCTTCAGGTTGACGACAGACATAGTGC 850  
Qy 782 AAAACCTAAGAGCGAGACCGAGAGTGAAGAGAGGAGCCATTGTGACAGTGAAGGGAG 841  
Db 851 AAAATCTGTGGGGGAGAACGAGAGTGAAGAGAGGAGCCATTGTGACGTTGAGGGAG 910  
Qy 842 GCCTCAGAAATCTTGAAGCCAGATAGAAAGAGAGCTGCCGACGAAAGAGGAATACGATG 901  
Db 911 GCCTCAGAAATCTTGAAGCCAGATAGAAAGAGAGTGCAGCAGAAAGAGGAATACGATG 970  
Qy 902 AGATGAATATGAATACGATGAAGAGATGAAGGCGTGCGAGGGAAGCAGAGGAGGG 961  
Db 971 AGATCAATATGAATACCATGAACAGATGGAAGGCGTGCGAGGGAAGCAGAGGCGGG 1030  
Qy 962 GGAATGGTATTGAAGAGACCATCTGCACCGCAAGTGTCTAAAAAGAAACATTGGTAGAAACA 1021  
Db 1031 GGAATGGTATTGAAGAGACCATCTGCACCGCATGTGTTAAAAAGAAACATTGGTAGAAACA 1090  
Qy 1022 GATCCCTGACATCTACAAACCTCA-AGCTGGTTCACTGAAACTGCGCAACGATCTCAAC 1080  
Db 1091 GATCCCTGACATCTAGCATCTCAGCGCTGGTTCACTGAAACTGCGC-ACGATCTCAAC 1149  
Qy 1081 CTTCTAATCTAGTGGCTTGACCTAGTGTGCTGAATATGAAATCTCTACAGGAATGCA 1140  
Db 1150 CTTCTAATCTAGTGGCTTGACCTAGTGTGCTGAATATGAAATCTCTACAGGAATGCA 1209  
Qy 1141 TTGTTTGTGCTCACTACAAACCAACGACACAGCATCATATATCGATTGAGGGGACGG 1200  
Db 1210 TTGTTTGTGCTCACTACAAACCAACGACACAGCATCATATATGATTGAGGGGACGG 1269  
Qy 1201 GCTCAGTGAAGTCTGAGCAGCAACGGCAACAGAGTGTACGAGGAGCTTCAAGAG 1260  
Db 1270 GCTCAGTGAAGTGTGAGCAGCAACGGCAACAGAGTGTACGAGGAGGCTTCAAGAG 1329  
Qy 1261 GGTCACTGCTGTGTGTGTCACAGAACTTCGCCGTGCTGGAAGTCCCAAGAGCGAAGC 1320  
Db 1330 GGTCACTGCTGTGTGTGTCACAGAACTTCGCCGTGCTGGAAGTCCCAAGAGCGAAGC 1389  
Qy 1321 TTCGAATACGTGGCATTTCAAGACAGACTCAAGGCCCAAGCATAGCAGCACTTCGCCGTGAA 1380  
Db 1390 TTCGAATACGTGGCATTTCAAGACAGACTTCAAGGCCCAAGCATAGCAGCACTTTGCCGTGAA 1449

## RESULT 2

US-09-108-010B-13  
; Sequence 13, Application US/09108010B  
; Patent No. 6362399  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; GARY MICHAEL FADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/108,010B  
; FILING DATE: 30-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/019,940  
; FILING DATE: JUNE 14,1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LYNNE M. CHRISTENBURY  
; REGISTRATION NUMBER: 30,971  
; REFERENCE/DOCKET NUMBER: BB-1071-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-5481  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1446 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-108-010B-13

Query Match 34.0%; Score 517.4; DB 3; Length 1446;  
Best Local Similarity 62.8%; Pred. No. 2.9e-139;  
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

Qy 5 AGCAACCGAGGAGAACGCGTGCAGTTCAGCGCTCAATGCGCAGAGACCTGACAAATC 64  
Db 71 AGCAGCCACAGCAAAACGAGTGCAGATCCAACGCTCAATGCGCTAAAAACCGGATAAC 130  
Qy 65 GCATTGAATCAGAGGGCGGTTACATTGAGACTTGGAAACCCCAACCAACAGAGTTCGAAT 124  
Db 131 GTATAGAGTCAGAGGTGGCTTCATTGAGACATGGAAACCCCTAACCAACAGCCATTCCAGT 190



Matches		954;	Conservative	0;	Mismatches	421;	Indels	144;	Gaps	4;
QY	5	AGCAACGGAGGAGAA	CGGTG	CCAGTTC	CGAGTTC	CAATG	CGCAG	AGACCT	TGCAATC	64
Db	71	AGCAGCCACAGCAAAA	CGAGT	GCAGAT	CCAAAGC	CTCAAT	GCCCTA	AAACCG	GATAACC	130
QY	65	GCATTCAATCAGAGGG	GGTTA	CATTG	AGACTT	GGAAACC	CCACCA	ACCGAG	GTTCGAAT	124
Db	131	GTATAGAGTCAGAAGG	TGGCTT	CATTG	AGACAT	TGGAAAC	CCCTAA	CAAGCC	ATTCAGT	190
QY	125	GGCCCGCGTCCGCTCT	CTCGCTT	AGTTC	CTCCCGC	CAACG	CCCTTC	GTAGC	CTTTCT	184
Db	191	GTGCCGGTGTGCTCT	CTCGCT	GCACCT	CAACCG	CAAGC	CCCTTC	GCAGAC	CTTCC	250
QY	185	ACTCCAAATGCTCCCA	AGGAGAT	CTTCAT	CCAGCA	AGGAAG	GGGAT	ACTTTT	GGTGGT	244
Db	251	ACACCAACGCTCCCA	AGGAGAT	CTACAT	CCAAAG	GTAGT	GTGTA	TTTTT	TGGCAT	310
QY	245	TCCCTGGTTGCTCTA	GACACT	ATGA	AGAGC	CTCAC	ACAA	AGGT	CGTCAG	304
Db	311	TCCCGGTTGTCTCTA	GACAT	TTGA	AGGCT	-----	-----	-----	-----	342
QY	305	AAAGACCACCAAGAC	GTCTC	CAAG	AGAG	AGAC	CAAA	AGCC	AAACAG	364
Db	343	-----	-----	-----	-----	-----	-----	-----	-----	382
QY	365	AGAAGTGCACCGTTT	CGATG	AGGGT	ATCTAT	TGGAG	TTCC	ACCG	GGTGTG	424
Db	383	AGAAGATCTATCACT	TTCAG	AGAGG	GTGAT	TGAT	TGC	AGT	GCACCG	442
QY	425	GGCTCTACACACGAC	CACAT	GATG	TTG	TGCT	GTCT	TTCT	TACTG	484
Db	443	GGATGTACAAATGA	AGACAC	TCCT	GTG	TTG	TG	CGG	TTTCT	502
QY	485	ACGACAAACAGCTTG	ATCAG	TTC	CCAG	GAGT	TCA	ATT	TGG	544
Db	503	TCAGAAACAGCTCG	ACAGT	CGCT	AGAG	ATTC	TAT	CTTG	CTGG	562
QY	545	AGTTCTTAGGTACCA	AGCAACA	AGAG	CAGACA	AAAG	AGCA	AGAG	CGTT	604
Db	563	AGTTCTTAGGTACCA	AGCAACA	AGAG	CAGACA	AAAG	AGCA	AGAG	CGTT	595
QY	605	CATACAGCCGCAAG	TAGT	CAGC	CTAG	ACA	AGAG	CGT	GATTT	664
Db	596	-----	-----	-----	-----	-----	-----	-----	-----	604
QY	665	ACAGCCGACAGAGAC	GACGAG	CAAGA	AGAA	CAAG	AGT	TGGA	AAACAT	724
Db	605	AAAGCCAGAAAGGAA	AGCGT	CAGCA	AGAA	AGAA	AGAA	AGAG	GAGC	664
QY	725	GCTTCAGCGGAGTT	CTTGAA	CAAC	AGCCTT	CCAG	TTG	ACG	ACACAG	784
Db	665	GCTTCGCGCGGAAT	CTTGAA	CAAT	GCCTTC	---G	TCGT	GGAC	AGCAG	721
QY	785	ACCTAAGAGCGAGAC	CGAGT	TGA	AGAG	GGAG	CCATT	GTG	CAGT	844
Db	722	AGCTAAGTGTGAAGA	AGAAAG	AGAG	AGAG	AGG	GTG	CCATT	GTG	781
QY	845	TCAGAAATCTTGAGC	CCAGAT	TAGAA	AGAG	AGCT	CCG	ACG	AGAG	904
Db	782	TCAGCGTGATAAG	CCCA	CCAG	AGAG	AGC	CAACA	AGAC	CCG	841
QY	905	ATGAATATGATACG	ATGA	AGAG	ATAG	AGCG	TG	CGAG	GAAG	964
Db	842	CAGATTGTGACGAA	AGAA	CAAA	CAAT	-----	-----	-----	-----	886
QY	965	ATGGTATTGAAGAG	CATCT	GAC	CGCA	AGT	GCT	TAAA	AGAA	1024
Db	887	ATGGCATGTACGAG	ACCA	TTTG	CAC	ATG	AGAT	CTGC	CAAC	946
QY	1025	CCCTGACATCTTCA	ACCCCT	CAAG	CTGG	TTTCA	CTCA	AAAT	CTG	1084
Db	947	CACCTGACATCTT	CAACCC	CTCA	AGCT	GGT	AGCAT	CAAC	CCG	1006

## RESULT 4

US-10-684-651-13  
; Sequence 13, Application US/10684651  
; Patent No. 6828491  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; GARY MICHAEL FADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/684,651  
; FILING DATE: 14-Oct-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/758,652  
; FILING DATE: 11-Jan-2001  
; APPLICATION NUMBER: 60/019,940  
; FILING DATE: JUNE 14,1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LYNNE M. CHRISTENBURY  
; REGISTRATION NUMBER: 30,971  
; REFERENCE/DOCKET NUMBER: BB-1071-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-5481  
; TELEFAX: 302-773-0164



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/019,940  
FILING DATE: JUNE 14, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: LYNE M. CHRISTENBURY  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1071-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1488 base pairs  
TYPE: nucleic acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-108-0108-11

Query Match 33.7%; Score 513; DB 3; Length 1488;  
Best Local Similarity 62.7%; Pred. No. 5.5e-138;  
Matches 968; Conservative 0; Mismatches 425; Indels 150; Gaps 5;  
QY 5 AGCAACGGGAGGAGCGGTGCGAGTTCAGCGCCTCAATGCGAGAGACCTGACAATC 64  
DB 71 AGCAGCCTCAGCAAAACGAGTGCAGATCCAAAACCTCAATGCGCCTCAAAACCGGATAACC 130  
QY 65 GCATTGAATCAGAGGGCGGTTCATTGAGACTTGGAAACCCCAACAAACAGGAGTTCGAAT 124  
DB 131 GTATAGATCAGAGGAGGGCTCATTTGAGACATGGAACCTCAACAAAGCCATTCCAGT 190  
QY 125 GCGCGGGGTGCGCCTCTCTCGTCTAGTCTCCGCGCGCAAGCCCTTCGTAGCCCTTTCT 184  
DB 191 GTCCCGGTGTGCGCCTCTCTCGTCTAGCCTCAACCGCAACGCGCTTCGTAGACCTTCCT 250  
QY 185 ACTCCATGTCCTCCAGGAGATCTTCATCCAGCAAGGAGGGGATATCTTTGGGTGATAT 244  
DB 251 ACACCAACGGTCCCAAGGAATCTATCCAAAGGTAAAGGTATTTTGGCATGATAT 310  
QY 245 TCCTCTGTTCTCTAGACACTATGAAGAGCCTCACACACAAGGTCTCGTCACTCTCAGTCCC 304  
DB 311 ACCCGGGTGTCTAGACATTTGAAGGCGCTCA----- 344  
QY 305 AAAGACCAACAGAGCTTCCAGGAGAGAGACCAAGGCCCAACAGCAACGAGATAGTCAAC 364  
DB 345 -----ACAACCTCAACAAAGAGGACAAAGCAGCAGACCAACAGACCGTCAAC 391  
QY 365 AGAAGGTGCAACCGTTCGATGAGGGGTGATCTCATTTGCGTTCACCGGTGTTGCTTTCT 424  
DB 392 AGAAGATCTATACTTCAGAGAGGGGTGATTTGATCGCAGTGCCTACTGGTGTGCAATGGT 451  
QY 425 GGCTCTAACACGACCAACGACACTGATGTTGCTGTTCTTTACTGACACCAACAACA 484  
DB 452 GGATGTACAACAATGAAGACACTCTCTGTTGTCGCGTTCATATTATGACACCAACAGCT 511  
QY 485 ACACCAACAGCTGTGATGATGTTCCCGAGGAGATTCATTTGGCTGGGAACACCGGCAAG 544  
DB 512 TGGAGAACCAGCTCGACGATGCTAGGAGATTTCTATCTTGTGCGGAACCAAGAGCAAG 571  
QY 545 AGTTCTTAAGGTACCAACAGCAACAGCAGCAAAAGCAGACGAAGAGCTTACCATATAGCC 604  
DB 572 AGTTCTTAATATCAGCAAG----- 594  
QY 605 CATAACGCGCAAGTTCAGCCTAGACAGAGAGCGTGAATTTAGCCCTTCGAGGACAGC 664  
DB 595 -----CAAGGAGGTCAATC 607  
QY 665 ACAGCGCAGAGACGAGGAGGACAGAAAGAAACGAGGTGGAATCTTCAGCG 724  
DB 608 AAAGCCAGAAAGGAAAGCATCAGCAAGAAAGAAACGAAAGGAGCGCATATTTAGTG 667  
QY 725 GCTTCAGCGGGAGTTCTCTGGAAACAAGCCTTCAGGTTGACGACAGACAGATAGTCAAA 784

DB 668 GCTTCACCTCGAAATTTCTTGGAACTGCTTTCAGCGT---GGACAAGCAGATAGCGAAA 724  
QY 785 ACTTAAGAGCGAGACCGAGAGTGAAGAAGAGGGAGCCATTGTGACAGTGTAGGGAGGCC 844  
DB 725 ACTCAAGAGGAGAGAACGAAGGGGAGAGCAAGGGAGCCATTGTGACAGTGAAGAGAGGTC 784  
QY 845 TCAGATCTTTAGCCCA-----GATAGAAAGAGAGCTGCCGACGAGAGAGGAAT 895  
DB 785 TGAGCGTGATAAAACCCACCGGACGAGCAGCAACAAAGACCCAGGAGAGAGAGAGAG 844  
QY 896 AGCATGAAGATGAATA-----TGAATACGATGAAGAGGATAGAAGCGGTG 940  
DB 845 AAGAAGAGGATGAGAAGCCACAGTGCAGGGTAAAGACAAACACTGCCAACGCCCGAG 904  
QY 941 GAGGGGAGAGAGAGGAGCGGGGAGTGTATTGAAGAGAGGATCTGCACCGCAAGTGCTA 1000  
DB 905 GAAGCCAAAGCAAAAGCAGAGAAATGGCAATTTGACGAGACCATATGACCATGAGACTTC 964  
QY 1001 AAAAGAACATTTGGTAGAAACAGATCCCTGACATCTACAAACCTCAAGCTGGTTCACTCA 1060  
DB 965 GCCAACACATTTGGCCAGACTTCATCACCTTGACATCTACAAACCTCAAGCGGTAGCGTCA 1024  
QY 1061 AAATGCCCAACGATCTCAACCTTTCTAATATCTTAGGTGGCTTGACACCTAGTGTGAATATG 1120  
DB 1025 CAACCGCCACAGCCTTGACTTCCAGCCCTCTCGTGGCTCAGACTCAGTGTGCTGTTG 1084  
QY 1121 GAAATCTTACAGGAATGCAATTTGTTGCTCCTACATACAAACCAACGACGACAGCATCA 1180  
DB 1085 GATCTCTCGCAGAAATGCAATTTGCTGCCACACTACAACTGAAACGCGAACAGCATAA 1144  
QY 1181 TATATCGATTGAGGGAGCGGCTCAGTGCAGTCTGTCGACAGCAACGCAACAGAGTGT 1240  
DB 1145 TATACCATTTGAATGAGCGGCATTTGATACAGTGTGTAATTGCAACGGTGAGAGTGT 1204  
QY 1241 ACACGAGAGGCTTCAAGAGGGTCACTGCTTGTGTGTCACAGAACTTTCGCGCTGCTG 1300  
DB 1205 TTGATGAGAGCTGCAAGAGGGACGGTGTGATCTGTCACAAAACCTTTGTGTGCTG 1264  
QY 1301 GAAAGTCCAGAGCGAGAACTTCGAATACGTGCAATTCAGACAGACTCAAGGCCAGCA 1360  
DB 1265 CAAGATCAGAGTGAACACTTCGAGTATGTGTCATTCAAGACCAATGATACACCATGA 1324  
QY 1361 TAGCAACCTCGCGGTGAAACCTCGTCAATACATAAACCTGCCGAGGAGGTGGTTGCAA 1420  
DB 1325 TCGGCACTTTGAGGGGCAAACTCATTTGTAACGATTTACCAGAGAGAGTATTTCAGC 1384  
QY 1421 ATTATATGCGCTTCCAAAGGGAGCAGGCAAGGAGCTTAAGAAACAACACCCCTTCAAGT 1480  
DB 1385 ACATTTCAACCTTAAAGGCCAGCAGGCGAGATAAAGAAACAACACCCCTTCAAGT 1444  
QY 1481 TCTTCGTTCCAGCTCTCAGCAGTCTCCGAGGGCTGTGGCTTA 1523  
DB 1445 TCCTGGTTCCACCTCAGGAGTCTCAGAAGAGAGCTGTGGCTTA 1487

RESULT 6  
US-09-758-652-11  
; Sequence 11, Application US/09758652  
; Patent No. 6703544  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; APPLICANT: GARY MICHAEL PADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA



ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WINDOWS 95  
SOFTWARE: MICROSOFT WORD 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,652  
FILING DATE: 11-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/019,940  
FILING DATE: JUNE 14,1996  
ATTORNEY/AGENT INFORMATION:  
NAME: LYNN M. CHRISTENBURY  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1071-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1488 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-758-652-11

Query Match 33.7%; Score 513; DB 3; Length 1488;  
Best Local Similarity 62.7%; Pred. No. 5.5e-138;  
Matches 968; Conservative 0; Mismatches 425; Indels 150; Gaps 5;

QY 5 AGCAACCGGAGGAGCGCTGCGCAGTTCCAGCCCTCAATGCCAGAGACCTGACAAATC 64  
DB 71 AGCAGCTCAGCAAAACGAGTGCAGATCAAAACCTCAATGCCCTCAAAACCGGATAACC 130  
QY 65 GCATTGAATCAGAGGGCGGTACATTGAGACTTGGAAACCCCAACAAACGAGGTTTCAAT 124  
DB 131 GTATAGATCAGAAGGAGGCTCATTTGAGACATGGAACCTTAACAAACGACCTTCCAGT 190  
QY 125 GCGCGGCGTGCCTCTCTCGTTAGTCTCCGCGCAACGCGCTTTCGTAGGCGCTTCT 184  
DB 191 GTCCGCGTGTGCGCTCTCTCGTGCACCCCTCAACCGCAACGCGCTTTCGTAGACCTTCT 250  
QY 185 ACTCCATGCTCCCGAGGAGTCTTATCCAGCAAGAGGAGTACTTTGGGTTGATAT 244  
DB 251 ACACCAACGCTCCCGAGGAAATCTACATCCAAAGGTAAGGTAATTTTGGCATGATAT 310  
QY 245 TCCTCGTTGCTCTAGACACTATGAGAGGCTCACACAAAGGTCGTGATCTCAGTCCC 304  
DB 311 ACCCGGTTGCTCTAGACACTTTGAAGAGCTCA----- 344  
QY 305 AAAGACCAACAGACGTTCTCAAGGAGAGAACCAAGCCCAACAGCAACGAGATAGTCAAC 364  
DB 345 -----ACAACCTCAACAAGAGGACAAAGCAGCAGACACCAAGACCGTCAAC 391  
QY 365 AGAAGGTGACCGTTTCGATGAGGAGTATCTATTGCGATTCCTCCCGGTTGCTTCT 424  
DB 392 AGAAGATCTATACTTCAGAGAGGGGATTTGATCGCAGTGCCTACTGTTGTCATGGT 451  
QY 425 GGCCTACACAGCAGCAGCACTGATGTTGCTGTTTCTCTTACTGACACCAACAACA 484  
DB 452 GGATGTACACATGAGACACTCTCTGTTGTTGCTTCTATATTGACACCAACAGCT 511  
QY 485 ACACCAACAGCTTGATCAGTCCCGAGGAGTTCATTTGGCTGGGAACACGAGCAAG 544  
DB 512 TGGAGAACCAAGCTCGACAGATGCTTAGGAGATTTCTATCTTGTCTGGGAACCAAGCAAG 571  
QY 545 AGTTCTTAGTACCAGCAACAAGCAGACAAAGCAGCAAGAGCTTACCATATAGCC 604  
DB 572 AGTTCTTAAATATCAGCAAG----- 594

## RESULT 7

US-10-684-651-11  
; Sequence 11, Application US/10684651  
; Patent No. 6828491  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; GARY MICHAEL FADER

QY 605 CATAAGCCGCAAAAGTCAGCTAGACAGAGAGCGTGAATTTAGCCCTCGAGGACAGC 664  
DB 595 -----CAAGGAGGTCAATC 607  
QY 665 ACAGCCGAGAGAACGAGCAGGAGCAAGAAAGAAACGAGAGGTGGAAACATCTTACGCG 724  
DB 608 AAAGCCAGAAAGGAAAGCATCAGCAAGAAAGAAACGAGAGGAGGAGCATATTTAGTG 667  
QY 725 GCTTACGCGCGGAGTTCCTGGAACAGCCCTTCCAGGTTGACGACAGACAGATAGTGA 784  
DB 668 GCTTACCCCTGGAATTTTGAACATCATTCAGCGT---GGACAGCAGATACCGAA 724  
QY 785 ACCTAAGAGCGGAGACCGAGAGTGAAGAGAGGAGGACATTTGTGACAGTGAAGGAGGCC 844  
DB 725 ACCTAAGAGGAGAGACGAGAGGAGGAGCAACAGGAGGCCATTTGTGACAGTGAAGAGG 784  
QY 845 TCAGATCTTTGAGCCCA-----GATAGAAGAGACGTCGCCGACGAAGAGAGGAAT 895  
DB 785 TGAGCGGTATAAAACCCACCGACGAGCAGCAACAAAGACCCCGAGGAAGAGGAAG 844  
QY 896 ACGATGAAGATGAATA-----TGAATACGATGAAGAGGATAGAGAGGCGTG 940  
DB 845 AAGAAGAGGATGAAGAGCCACAGTGCAGGGTAAAGACAAACCTGCAACGCCCGAG 904  
QY 941 GCAGGGGAGCAGAGGCGGGGAAATGGTATTGAAGAGAGCGATCTGCACCGCAAGTGCTA 1000  
DB 905 GAAGCCAAAGCAAAAGCAGAGAAATGGCATTCAGGAGACCATATGCACCATGAGACTTC 964  
QY 1001 AAAAGAACATTTGTAGAAACAGATCCCTTCACATCTACAAACCTCAAGCTGTTTCACTCA 1060  
DB 965 GCCACAACATTTGGCCAGACTTCATCACTGACATCTACAAACCTCAAGCGCGTAGCGTCA 1024  
QY 1061 AAAGTCCCAACGATCTCAACCTTCTAATCTAGTGGCTTGGACCTAGTGTGCTGAATATG 1120  
DB 1025 CAACCGCCACGACCTTGACTTCCAGCCCTCTCTGCGCTCAGACTCAGTGTGCTGAGTTG 1084  
QY 1121 GAAATCTCTACAGAAATGCAATTTGTCGCTCACTACAAACCAACGACGACACAGCATCA 1180  
DB 1085 GATCTCTCCGCAAGAAATGCAATGTTCTGCGCCACACTACACCTGAACGCGCAACAGCATAA 1144  
QY 1181 TATATCGATTGAGGGAGCGGCTCAGTGCAGTCTGAGCAGCAACGCGCAACAGAGTGT 1240  
DB 1145 TATACGATTTGAATGGACGGGCAATTGATACAGTGGTGAATTTGCAACGCGTGAGAGAGTGT 1204  
QY 1241 ACCACGAGAGCTTCAAGAGGCTCAGTGTCTTGTGTCACAGAACTTCGCGCTGCTG 1300  
DB 1205 TTGATGAGAGCTGCAAGAGGAGCGGTGCTGATCGTGCCCAAAACCTTTGTGTTGCTG 1264  
QY 1301 GAAAGTCCGAGAGCGAGAACTTCGAAATACGTGGCATTTCAAGACAGACTCAAGGCCACGCA 1360  
DB 1265 CAAGATCAGAGTGAACACTTCGAGTATGTGTCATTCAAGACCAATGATACACCCATGA 1324  
QY 1361 TAGCCAACTTCGCGGTGAAACTCCGTCATAGATTAACCTGCGCGGAGGAGGTGGTTGCAA 1420  
DB 1325 TCGGCACTCTTTCAGGGGCAAACTCATTTGTAACGCAATTTACAGAGGAAGTATTGAGC 1384  
QY 1421 ATTATATGCTCCAAAGGAGCAGCAGGAGCTTAAAGAACAAACAAACCCCTTCAAGT 1480  
DB 1385 ACATTTCAACCTTAAAGAGCCAGGCGGAGGAGATTAAGAAACAAACCCCTTCAAGT 1444  
QY 1481 TCTTCGTTCCACCGCTCTCAGCAGTCTCCGAGGCGCTGTGGCTTA 1523  
DB 1445 TCCTGTTCCACCTCAGGAGTCTCAGAGAGAGCTGTGGCTTA 1487

TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
CLASSES OF SOYBEAN SEED  
PROTEIN GENES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WINDOWS 95  
SOFTWARE: MICROSOFT WORD 7.0A

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/684,651  
FILING DATE: 14-Oct-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,652  
FILING DATE: 11-Jan-2001  
APPLICATION NUMBER: 60/019,940  
FILING DATE: JUNE 14,1996

ATTORNEY/AGENT INFORMATION:  
NAME: LYNNE M. CHRISTENBURY  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1071-A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1488 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-684-651-11

Query Match 33.7%; Score 513; DB 3; Length 1488;  
Best Local Similarity 62.7%; Pred. No. 5.5e-138;  
Matches 968; Conservative 0; Mismatches 425; Indels 150; Gaps 5;

QY	5	AGCAACCGGAGGAGAACGCGCTGCCAGTTCAGCGCCTCAATGCGCAGAGACCTTGACAATC	64
DB	71	AGCAGCCTCAGCAAAACGAGTGCAGATCCAAAACCTCAATGCGCTCAAAACCGGATAACC	130
QY	65	GCATTGAATCAGAGGGCGGTTACATTGAGACTTGGAAACCCCAACACAGGAGTTGGAAT	124
DB	131	GTATAGAGTCAGAAGGAGGGCTCATTGAGACATGGAACCCCTAACAACAGCCATTCCAGT	190
QY	125	GCGCCGCGTGCCTCTCTCGCTTAGTCTCCGCGCAACGCCCTTCGTAGGCGCTTCT	184
DB	191	GTCCCGGTGTGCGCTCTCTCGCTGACCCCTCAACCGCAACGCCCTTCGTAGACCTTCCT	250
QY	185	ACTCCCAATGTCCCGAGGAGTCTTCATCCAGCAAGGAGGAGTACTTTGGGTGATAT	244
DB	251	ACACCAACGTTCCCGAGGAATCTACATCCNACAAGGTAAGGGTATTTTGGCATGATAT	310
QY	245	TCCTTGGTGTCTCTAGACATATGAAGAGGCTTCAACACAGGTCGTCTCAGTCCC	304
DB	311	ACCGGGTGTCTCTAGCACATTTGAAGAGGCTCA-----	344
QY	305	AAAGACCAACAGACGCTCCAGGAGAGAACCAAGCCCAACAGCAACGAGATAGTCACC	364
DB	345	-----ACAACTTCAACAAAGAGAGCAAGACGAGACCAAGACCGTCCACC	391
QY	365	AGAAGGTGACCGGTTTCGATGAGGGTGTATCTATTGCAAGTTCCACCGGTTGCTTTCT	424
DB	392	AGAAGATCTATACTTCAGAGAGGGTGTATTGATCGCAGTGCCTTACTGTGTTGATGGT	451

QY	425	GGCTCTAACACGACACGACACTGATGTTGTTGCTGTTTCTTCTACTGACACCAACA	484
DB	452	GGATGTACAAACAATGAAGACACTCTCTGTTGTTGCGCTTTCTATTATGACACCAACAGCT	511
QY	485	ACGACAAACAGCTTGTATCAGTTCCTCCAGGAGATTCAATTTGGCTGGAAACACCGAGCAAG	544
DB	512	TGAGAACACAGCTCGACAGATGCTTAGAGATTCTATCTTGTGGGAACCAAGAGCAAG	571
QY	545	AGTTCTTAAGGTACCAAGCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATATAGCC	604
DB	572	AGTTTCTAAAATATCAGCAAGAG-----	594
QY	605	CATACAGCCGCAAAAGTCAGCTAGCCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGACAGC	664
DB	595	-----	607
QY	665	ACAGCCGACAGAGAAACGAGCAGGACAGAAAGAAAGAAACGAAGGTGGAACATCTTCAGCG	724
DB	608	AAAGCCAGAAAGGAAGCATCAGCAAGAGAGAAACGAAGGAGGAGCATATTGAGTG	667
QY	725	GCTTCACGCGGAGTTCTTGGAAACAAAGCCTTCCAGGTTGACGACACAGACAGATAGTCAAA	784
DB	668	GCTTCACCTCGGAATTTCTTGGAAACATGCAATTCAGCGT---GGCAACAGCAGATAGCGAAA	724
QY	785	ACCTAAGAGCGCAGACCGAGAGTGAAGAGAGGAGGAGCCATTGTGACAGTGAAGGGAGGCC	844
DB	725	ACCTAAGAGGAGAGAACGAAGGGAAGACAAGGGAGCCATTGTGACAGTGAAGAGGAGTTC	784
QY	845	TCAGAAATCTTGAGCCCA-----GATAGAAAGAGAGCGTGCCGACGAGAGAGGAAT	895
DB	785	TGAGCGTGATAAAACCAACCCACGAGCAGCAACAAGAGACCCAGGAAGAGAGAAAG	844
QY	896	ACGATCAAGATGAATA-----TGAAATACGATGAAGAGGATAGAAGGCGTG	940
DB	845	AAGAAGAGATGAGAAGCCACAGTGCAAGGGTAAAGACAAACACTGCCAACGCCGCCGAG	904
QY	941	GCAGGGAGACGAGGAGGAGGGAATGGTATTGAAGAGAGATCTGCACCAGGAGTCTA	1000
DB	905	GAAGCCAAAGCAAAAGCAGAAATGGCAATTCACGAGACCATATGCCACCATGAGACTTC	964
QY	1001	AAAAGAAACATTTGGTAGAAACAGATCCCTTGACATCTACACCCCTCAAGCTGGTTCACTCA	1060
DB	965	GCACAAACATTTGCCAGACTTCATCACTGACATCTACAACCCCTCAAGCCGCTAGCGTCA	1024
QY	1061	AACTGCGCAACGATCTCAACCTCTTAATCTTAGTGGCTTGACACTAGTCTGATGATG	1120
DB	1025	CAACCGCCACACGCTTGACTTCCAGCCCTCTCGTGGCTCAGACTCAGTGTGAGTTG	1084
QY	1121	GAATCTCTACAGGAATGCAATTTGTCGCTCACTACAACCAACCAACGACACAGCATCA	1180
DB	1085	GATCTCTCCGCAAGATGCAATGTTGTCGCCACACTACAACCTGAAGCCGCAACAGCATAA	1144
QY	1181	TATATCGATTGAGGGGACGGGCTCAGCTGCAAGTCGTGGACAGCAACGCGCAACAGAGTGT	1240
DB	1145	TATACGCAATTGAATGACGGGCATTTGATAACAAGTGGTGAATTTGCAACCGTGAGAGAGTGT	1204
QY	1241	ACAGAGGAGCTTCAAGAGGTCACGTGCTTGTGTTGCCACAGACACTTCGCGTCCCTG	1300
DB	1205	TTGATGAGAGAGCTGCAAGAGGGAACGGGTGCTGATCGTGGCCACAAACCTTTGTGGTGCTG	1264
QY	1301	GAAAGTCCACGAGCGAGAACTTCGAATACGTGGCATTTCAAGACAGACTCAAGGCCACGCA	1360
DB	1265	CAAGATCAGAGATGACAACTTCGAGTATGTGTCTTCAAGACCAATGATACACCATGA	1324
QY	1361	TAGCCAACTCTCGCGGTGAAAACTCCGTCATAGATAAACCTGCGGAGAGGAGTGTGCAAA	1420
DB	1325	TCGCACTCTTGCAGGGGCAAACTCATTTGTGAACGCAATTTACCAGAGGAAAGTGAATTCAGC	1384
QY	1421	ATTATATGCGCTTCCAAAGGAGGAGCAGGAGGAGCTTAAAGAACAAACAAACCCCTTCAAGT	1480
DB	1385	ACACTTTCAACCTTAAAGAAAGCCAGCAGCGCCAGGAGAGATTAAGAAACAAACCCCTTCAAGT	1444



; APPLICANT: Kinney, Anthony  
; TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans  
; FILE REFERENCE: BB1432 US NA  
; CURRENT APPLICATION NUMBER: US/09/805,694B  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/189,823  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 15  
; LENGTH: 1746  
; TYPE: DNA  
; ORGANISM: Glycine max  
; US-09-805-694B-15

Query Match 33.1%; Score 505; DB 3; Length 1746;

Best Local Similarity 62.4%; Pred. No. 1.2e-135;

Matches 963; Conservative 0; Mismatches 430; Indels 150; Gaps 5;

QY	5	AGCAACGGAGGAGGAGCGGTCCAGTTCAGCGCCTCAATGCGCAGAGACCTGCAATC	64
DB	125	AGCAGGCTCAGCAAAACGAGTGCAGATCCAAAACCTCAATGCCCTCAAAACCGGGTAACC	184
QY	65	GCATTGAATCAGAGGCGGTTACATTGAGACTTTGGAAACCCCAACACACAGGAGTTTCAAT	124
DB	185	GTATAGATCAGAAAGAGGGCTCATTTGAGACATGGAAACCTAACAACAAGCCATTCAGT	244
QY	125	GCGCGCGGTGCGCCTCTCTCGTTAGTCTCGCCGCGCAACGCCCTTCGTAGGCCCTTCT	184
DB	245	GTGCGGCTGTGCGCTCTCTCGTGCACCTCAACCGCAAGGCCCTTCGTAGACCTTCT	304
QY	185	ACTCCTGCTCCCGAGGAGATCTTATCCAGCAAGGAGGGGATTTGGTTGATAT	244
DB	305	ACACCAACGGTCCCGCAAGAAATCTATCAACAAGGTAAAGGTTATTTTGGCATGATAT	364
QY	245	TCCCTGGTTGCTTAGACACTATGAAGAGCCTCACACAAAGGTCGTGATCTCAGTCCC	304
DB	365	ACCGGGTGTCTAGCACATTTGAAGGCTCA-----	398
QY	305	AAAGACCAACAGAGCTTCCAGGAGAGAGACCAAGCCCAACAGCAAGATAGTCAAC	364
DB	399	-----ACAACCTCAACAAGAGAGCAAAAGCAGCAGCACCACAGACCGTCACC	445
QY	365	AGAGGTGACCGTTTCGATGAGGTGATCTATTGCGATTCACCGGTTCGTTCTTCT	424
DB	446	AGAAGATCTATAACTCCAGAGAGGGTATTTGATCGCAGTGCCTACTGGTTGTCATGGT	505
QY	425	GGCTCTACCAACGACCAACGACACTGATGTTGTTGCTCTTTCTTTACTGACACCAACA	484
DB	506	GGATGTACAACATGAAGACACTCTCTGTTGTTGCGGTTTCTATTATGACACCAACAGCT	565
QY	485	ACGACAAACAGCTTGATTCAGTTCGCCAGGAGATTCATTTGGCTGGGAACAGGCAAG	544
DB	566	TGAGAAACAGCTCGACAGCAGATGCTTAGGAGATTTCTATCTTGGGAAACCAAGAGCAAG	625
QY	545	AGTTCTTAAGTACAGCAGCAACAGCAGCAACAGCAGCAAGAGCTTACCATATAGCC	604
DB	626	AGTTCTTAAGTATCAGCAAG------	648
QY	605	CATACAGCCGCAAAAGTTCAGCTAGACAGAGAGCGGTGAATTTAGCCCTTCGAGGACAGC	664
DB	649	-----CAAGGAGGTATC	661
QY	665	ACAGCGCAGAGAACGACGAGGACAGAGAGAGAAACGAGGTGGAACATCTTCAGCG	724
DB	662	AAAGCCAGAAAGGAAAGCATTCAGCAAGAGAGAAACGAAAGGAGCAGCATATTGAGTG	721
QY	725	GCTTCAGCGCGAGTTCTCGAAACAGCCTTCCAGGTTGACGACAGCAGATAGTCAAA	784
DB	722	GCTTCAGCGCGAGTTCTCGAAACAGCCTTCCAGGTTGACGACAGCAGATAGCAGAA	778
QY	785	ACCTAAGAGCGCAGACCGAGGTGAAGAGAGGAGGACCATTTGACAGTGAAGGGAGGCC	844

DB	779	ACCTCAAGGAGAGAACGAAGGGGAAGACAAGGAGCCATTGTGACAGTGAAGGAGGTC	838
QY	845	TCAGAAATCTTGAGCCCA-----GATAGAAAGAGAGCTGCCGACGAAGAGAGGAAT	895
DB	839	TGAGCGTGATAAAACCCACCGGACGAGCAACAAGAGACCCAGGAAGAGGAAG	898
QY	896	ACGATGAAGATGAATA-----TCAATACGATGAAGAGGATAGAAGCGGTG	940
DB	899	AAGAAGAGGATGAGAAAGCCACAGTGCAGGGTAAAGACAACACTGCCAACGCCCGGAG	958
QY	941	GCAGGGAAAGCAGAGGAGGAGGGGAATGGTATTGAAGAGAGCATCTGCACCGCAAGTGCTA	1000
DB	959	GAAGCCAAAGCAAAAGCAGAGAAATGGCATTTGACGAGAGACCATATSCACCATGAGACTTC	1018
QY	1001	AAAAGAAATTTGGTAGAAAACAGATCCCTGACATCTAACAACCTCAAGCTGGTCACTCA	1060
DB	1019	GCCACAACATTTGGCCAGACTTCATCACTGACATCTACAACCTCAAGCGGTAGCGTCA	1078
QY	1061	AAACTGCCAACGATCTCAACCTTCTAATACTTAGGTGGCTTGACCTAGTGTGAATATG	1120
DB	1079	CAACCCCAACAGCCTTGACTTCCAGCCCTCTCGTGGCTCAGACTCAGTGTGGATTGG	1138
QY	1121	GAAATCTTACAGGAATGCAATTTGTCGCTCACTTACAACACCAACGACACAGCATCA	1180
DB	1139	GGTCTCTCGCAAGAAATGCAATTTGTCGCCACACTTACAACCTGAACGCGAACAGCATAA	1198
QY	1181	TATATCGATTGAGGGAGCGGCTCAGTGCAGTCAAGTCTGTGACAGCAACGCAAGAGTGT	1240
DB	1199	TATACGATTTGAATGGACGGGCAATTTGATACAAGTGGTGAATTCGAACGCGTAGAGAGTGT	1258
QY	1241	ACGACGAGGAGCTTCAAGAGGGTCACTGCTTGTGTGTGTCACAGAACTTCGCGCTCGCTG	1300
DB	1259	TTGATGGAGAGCTGCAAGAGGAGCGGTGCTGATCTGTCACCAAAAATTTGTTGGTGGCTG	1318
QY	1301	GAAAGTCCAGAGCGAGAACTTCGAATACGTGGCATTTAAGACAGACTCAAGGCCCGCAGCA	1360
DB	1319	CAAGATCAGAGTGAACAATTCGAGTATGTGTCATTCAAGACCAATGATACACCCATGA	1378
QY	1361	TAGCCAACTCGCGGTGAAAACCTCGTATAGATAAATCTGCCGAGGAGGTGGTTGCAA	1420
DB	1379	TCGGCACTTTGCAGGGGCAAACTCATTTGTAACGCAATTTACCAGAGGAGTGAATTCAGC	1438
QY	1421	ATTCTATATGGCTTCCAAAGGAGCAGGCAAGGAGCTTAAGAAACAACAACCCCTTCAAGT	1480
DB	1439	ACACTTCAACCTAAAAGCCAGCAGCCAGCAGATTAAGAACAACAACCCCTTCAAGT	1498
QY	1481	TCTTCTTCCACGCTCTCAGCAGTCTCCGAGGGCTGTGGCTTA	1523
DB	1499	TCTGTGTTCCACTCCTCAGGAGTCTCAGAGAGAGCTGTGGCTTA	1541

## RESULT 10

US-108-010B-12

; Sequence 12, Application US/09108010B

; Patent No. 6362399

; GENERAL INFORMATION:

; APPLICANT: ANTHONY JOHN KINNEY

; APPLICANT: GARY MICHAEL FADER

; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC

; CLASSES OF SOYBEAN SEED

; PROTEIN GENES

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95



ADDRESSEE: E. J. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 19898

## COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WINDOWS 95  
SOFTWARE: MICROSOFT WORD 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,652  
FILING DATE: 11-Jan-2001

## CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/019,940

FILING DATE: JUNE 14,1996

## ATTORNEY/AGENT INFORMATION:

NAME: LYNNE M. CHRISTENBURY

REGISTRATION NUMBER: 30,971

REFERENCE/DOCKET NUMBER: BB-1071-A

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-5481

TELEFAX: 302-773-0164

## INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1458 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-758-652-12

Query Match 33.1%; Score 504; DB 3; Length 1458;  
Best Local Similarity 62.0%; Pred. No. 2.2e-135;  
Matches 943; Conservative 0; Mismatches 450; Indels 129; Gaps 4;

QY 5 AGCAACCGGAGGAGAACGGGTCCAGTTCAGCGCTCAATGCGCAGAGACCTGCAATC 64  
DB 62 AGCAGGCACAGCAAAATGAGTGCAGATCCAAAAGCTGAATGCCCTCAAAACGGATAACC 121

QY 65 GCATTGAATCAGAGGGGGTTACATTGAGACTTGGAAACCCCAACACACAGGAGTTCGAAT 124  
DB 122 GTATAGATCGGAAGGTGGGTTCAITGAGACATGGAAACCCCTAACAACAGCCCAITCCAGT 181

QY 125 GCGCCGGCGTGCCTCTCTCGCTTAGTCTCCTCCGCGCAACGCCCTTCGTAGGCCCTTTCT 184  
DB 182 GTGCCGGTGTGCCCTCTCTCGCTGCACCCCTTAACCGCAATGCCCTTCGTAGACCTTCCT 241

QY 185 ACTCCAAATGTCCTCCAGGAGATCTTCATCCAGCAAGAGGGGATACCTTTGGGTGATAT 244  
DB 242 ACACCAACGGTCCCGAGAAATACATACAAAGGTAATGTAATTTTGGCATGATAT 301

QY 245 TCCCTGGTGTCTAGACACTATGAAGAGCTTACACACAGGTTCGTTCAGTCTCAGTCCC 304  
DB 302 TCCCGGGTGTCTAGACTTATCAAGAGCCGCA----- 335

QY 305 AAAGACCACCAAGACGTCTCCAAGGAGAGACCAAAAGCCCAACAGCAACAGATAGTCACC 364  
DB 336 -----AGAAATCTCAGCAACGAGGACGAGGCCAGAGCCCAAGACCGTCACC 382

QY 365 AGAAGGTGACCGTTTCGATGAGGGGTGATCTCATTTGAGTTCCTCCACGGGTGCTTTCT 424  
DB 383 AAAAGGTACATCGCTTCAGAGAGGGGTGATTTGATTCGCAAGTGCCTACTGGGTGTCATGGT 442

QY 425 GCGCTTACACAGCACGACACTGATGTTGCTGTTTCTTACTGACACCAACAACA 484  
DB 443 GGATGTACAAACAATGAAGACACTCCTGTTGTCGGTTTCTATATTTGACACCAACAGCT 502

QY 485 ACACCAACCAAGCTTGATCAGTTCCTCCAGGAGATTCAAATTTGGCTGGGAACCGGAGCAAG 544

RESULT 12

US-10-684-651-12

Sequence 12, Application US/10684651  
Patent No. 6828491  
GENERAL INFORMATION:  
APPLICANT: ANTHONY JOHN KINNEY  
APPLICANT: GARY MICHAEL FADER  
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
CLASSES OF SOYBEAN SEED  
PROTEIN GENES  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WINDOWS 95  
SOFTWARE: MICROSOFT WORD 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/684,651  
FILING DATE: 14-Oct-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,652  
FILING DATE: 11-Jan-2001  
APPLICATION NUMBER: 60/019,940  
FILING DATE: JUNE 14,1996  
ATTORNEY/AGENT INFORMATION:  
NAME: LYNNE M. CHRISTENBURY  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1071-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1458 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-684-651-12

Query Match 33.1%; Score 504; DB 3; Length 1458;  
Best Local Similarity 62.0%; Pred. No. 2.2e-135;  
Matches 943; Conservative 0; Mismatches 450; Indels 129; Gaps 4;  
QY 5 AGCAACCGAGGAGAACGGTGCAGTCCAGCGCCTCAATGCCAGAGACCTGACAATC 64  
DB 62 AGCAGGCACAGCAAAATGATGCCAGATCCAAAAGCTGAATGCCCTCAAAACCGGATAAC 121  
QY 65 GCATTGAATCAGAGGCGGTACATTGAGACTTGGAAACCCCAACACACAGGAGTTCGAAT 124  
DB 122 GTATAGATCGGAAGTGGTTCATTGAGACATGGAAACCTTAACAACAGCCATTCCAGT 181  
QY 125 GCGCCGCGTGCCTCTCTCGTTAGTCTTCGCGCCGCAACGCCCTTCGTAGGCCCTTCT 184  
DB 182 GTCCGCGTGTGCCCTCTCTCGTGCACCCCTTAACCGCAATGCCCTTCGTAGACCTTCT 241  
QY 185 ACTCCATGTCCTCCAGGAGATCTTCATCAGCAAGAGGGGATACTTTGGTTGATAT 244  
DB 242 ACACCAACGCTCCCGAGGAATCTACATACAACAGGTAATGGTATTTTGGCATGATAT 301  
QY 245 TCCCTGTTCTCTAGACACTATGAAGAGCCTCACACACAAGGTCTCGATCTCAGTCCC 304  
DB 302 TCCCGGTTGCTTAGCACTTATCAAGAGCCGA----- 335  
QY 305 AAAGACCACCAAGACGCTCTCCAGGAGAGAACCAAGCCCAACAGCAGATAGTCACC 364

DB 336 -----AGAAATCTCAGCAACAGGAGCAGAACCCAGAGGCCCAAGACCGTCACC 382  
QY 365 AGAAGGTGCACCGTTTTCGATGAGGGTGATCTCATTCAGTTCCACCGGTGTTGCTTCT 424  
DB 383 AAAAGGTACATCGCTTCAGAGAGGGTGATTTGATCCAGTGCCCTACTTGGTGTTCATGGT 442  
QY 425 GGCTCTACAACGACCAACGACACTGATGTTGTTGCTGTTCTTCTTACTGACCAACAACA 484  
DB 443 GGATGTACAACAATGAAGACACTCTCTGTTGTCGCGTTCTATTTACACCAACAGCT 502  
QY 485 ACAGAAACGAGCTTGATCAGTTCCTCCAGGAGATTCAATTTGGCTGGGAACACGAGCAAG 544  
DB 503 TGGAGAACGAGCTCGACCAAGTGCCTAGGAGATTCTATCTTCTGGGAACCAAGAGCAAG 562  
QY 545 AGTTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGACAAAGAGCTTACCATATAGCC 604  
DB 563 AGTTTCTAAATATCAGCAGCAG----- 585  
QY 605 CATACAGCCCGCAAGTTCAGCCTTAGACAAGAGAGCGTGAAATTTAGCCCTTCGAGGACAGC 664  
DB 586 -----CAGCAAGGAGGTT 598  
QY 665 ACAGCCGACAGAAACGAGCAGGACAGAAAGAAAGAAACCAAGGTGAAACATCTTCAGCG 724  
DB 599 CCAAAAGCCAGAAAGGAAAGCAACRAAGAAAGAAACCAAGGAAAGCAACATATTGAGTG 658  
QY 725 GCTTCACGCGGAGTTCTTGGAAACAGCCTTCCAGGTTCACGACAGACAGATAGTCAAA 784  
DB 659 GCTTCGCCCTTGAATTTCTTGAAGAAAGCGTTC---GGCGTGAACATGCAATAGTAGAA 715  
QY 785 ACCTAAGAGCGGAGACCGAGAGTGAAGAGAGGGAGCCATTGTGACAGTGAAGGGAGGCC 844  
DB 716 ACCTAAGGTGAGAACGAAGAGGAGGATAGTGGAGCCATTGTGACAGTGAAGAGGAGTTC 775  
QY 845 TCAGAAATCTTGAGCCAG---ATAGAAAGAGAGCTGCCACGAGAGAGGAAATAGCATG 901  
DB 776 TAAGAGTCAAGTCCAGCCATGAGGAGCCACAGCAAGAAGAAGATGATGATGATGAGG 835  
QY 902 AAGATGAATATGAATACGATGAAGAGGATAGAGGCGTGGCAGGGGAAGCAGAGGAGGG 961  
DB 836 AAGAGCGCACAGTGCCTGGAGACAGACAAGGTTGCCAACGCCAAAGCAAGAGAGCA 895  
QY 962 GGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGCTTAAAGAAACATTTGGTGAACA 1021  
DB 896 GAAATGGCATTTGATGAGACCATTTGCACAATGAGACTTCGCCCAAAACATTTGGTCAGA 955  
QY 1022 GATCCCTGACATCTACAACCCCTCAAGCTGGTTCACTCAAAACTGCCAACGACGCTTCAAC 1081  
DB 956 CATCACCTGACATCTACAACCCCTCAAGCTGGTAGCATCAACCCGCCACGAGCTTGA 1015  
QY 1082 TTCTAATACTTAGTGGCTTGGACCTTAGTCTGAATATGGAATCTCTACAGGAATGCAT 1141  
DB 1016 TCCAGCCCTTGCTTCTTCAAACTCAGTGCCAGTATGGATCCTCCGCAAGATGCTA 1075  
QY 1142 TGTTTGTCTCCTACACACCAACGACACAGCATCATATATCATTTGAGGGGACGG 1201  
DB 1076 TGTTGTCGCCACATACACCCCTGAAACGCAACAGCATAATATACGCAATTTGAATGGCGGG 1135  
QY 1202 CTCAGCTGCAAGTGTGGAGCAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1261  
DB 1136 CATTTGTAAGTGGTGAATTGCAATTTGGTGAAGAGTGTTTGATGGAGAGTGTCAAGAG 1195  
QY 1262 GTCAGCTGCTTGGTGGCCACAGAACTTCGCGTCCGAAAGTCCGAGAGGAGAACT 1321  
DB 1196 GAGGGGTGCTGATCTGTTCCACAAACCTTTGGCGTGGCTGCAAAATCCAGAGGCACTA 1255  
QY 1322 TCGAATACCTGGCATTTCAAGACAGACTCAAGGCCCAAGCAGATAGCCAACTTCGCGGTGAA 1381  
DB 1256 TTGAGTATGTGATTTCAAGACCAATGATAGACCTTCGTAACCTTCGAGGGGCA 1315  
QY 1382 ACTCCGCTATAGATAACCTTCGCGGAGGAGGTGGTTGCAAAATTCATATGCGCTCAAGGG 1441  
DB 1316 ACTCATTTGTAAGCGATTTGCCAGAGGAGTGTATTCAGCACACTTTTAAACCTTAAGAGCC 1375

QY 1442 AGCAGCAGGAGCTTAAGAACAAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAGC 1501  
Db 1376 AGCAGCCAGGAGGTTGAAGAACAAACCCCTTTCAGCTTCCCTTGTTCACCCCTCAGGAGT 1435  
QY 1502 AGTCTCCGAGGCTGTGGCTTA 1523  
Db 1436 CTCAGAGGAGCTGTGGCTTA 1457

RESULT 13  
US-09-108-010B-15  
; Sequence 15, Application US/09108010B  
; Patent No. 6362399  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; GARY MICHAEL FADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/108,010B  
; FILING DATE: 30-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/019,940  
; FILING DATE: JUNE 14,1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LYNNE M. CHRISTENBURY  
; REGISTRATION NUMBER: 30,971  
; REFERENCE/DOCKET NUMBER: BB-1071-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-5481  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1551 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-108-010B-15  
Query Match 13.0%; Score 198; DB 3; Length 1551;  
Best Local Similarity 51.4%; Pred. No. 1e-46;  
Matches 699; Conservative 0; Mismatches 600; Indels 61; Gaps 8;

QY 14 AGGAGAACGGTCCAGGCTCAATCGCAGAGACCTGACAAATCGCATTTGAAT 73  
Db 86 AGTTCAACGAGTGCCAACTCAACAACTCAACGGTTGGAAACCCGACACCGGTTAGT 145  
QY 74 CAGAGGGCGGTTACATTGAGACTTGGAAACCCCAACACAGGAGTTTGAATGCGCCGGCG 133  
Db 146 CCGAAGTGGTCTTATTGAACATGAACTCTCAACACCCCTGAGCTGCAATGCGCCGGTG 205  
QY 134 TCGCCCTCTCTCGTTAGTCTCGGCGGCAACGCCCTTCGTAGGCCCTTCTACTCCAAATG 193  
Db 206 TCACCTGTTTCAAAACGACCCCTCAACCGCAACGGCTCCCACTTGGCCATCTTACTTACCTT 265

QY 194 CTCCCAGGAGATCTTCATCCAGCAAGGAGGGATACCTTTGGTTGATATATTCCTCGGTT 253  
Db 266 ATCCCAATGATCATTTGCTGTTCAAGGAGAGGAGCAATTTGATTTGCAATTCGGGAT 325  
QY 254 GTCCTAGACACTATGAAGAGCCTTCACACAAGGTCGTGATCTCAGTCCCAAGAACAC 313  
Db 326 GTCCGAGAGCGTTTGAGAGCCACA-----ACAAC 355  
QY 314 CAAGAGCTCTCCAAGGAGAGACCAAGCAACAGCAAGAGATAGTACCAGAGGTC 373  
Db 356 AATCAAGCAGAAGAGGCTCAAGGTCACAGCAGCAACTACAAGACAGTACCAGAGATTC 415  
QY 374 ACCGTTTCGATGAGGCTGATCTCATTTGCAAGTTCCCAACCGGTGTTGCTTCTTGCTTACA 433  
Db 416 GTCACCTTCAATGAAGGAGACGTACTAGTATTCCTCTTGCTGTTCTTACTGACCTATA 475  
QY 434 AGCACACGACACTGATGTTGTTGTTCTTACTGACACCAACAACAACAGCAAC 493  
Db 476 ACACTGGCGATGAACCCAGTTGTTGCCATCAGTCTCTTGACACCTCCAACCTTCAACAATC 535  
QY 494 AGCTTGATCAGTTCCCGAGGAGATTCAATTTGCTGGGAACACGGAGCAAGAGTTCTTAA 553  
Db 536 AGCTTGATCAAAACCCAGAGTATTTACCTTTGCTGGGAACCCAGATATAGAGCATCCCG 595  
QY 554 GGTACCAGCAACAAAGCAGACAAAGCAGACGAAGCTTTACCATATAGCCCATACAGCC 613  
Db 596 AGACCATGCAAA--CAGCAGCAGCAGAGAGTATGTTGGACGCAACGAGGGGCAACA 653  
QY 614 CGCAAAGTCAGCTTAGACAAGAG--AGCTGTAATTTAGCCTCTCGAGGACAGCACAGCCG 672  
Db 654 CCGACAGCAGGAGGAAGAGTGGCAGTGTCTCAGTGGCTTCAGCAAAACATTTCTTAGC 713  
QY 673 AGAAGACGAGCAGGACAAGAAAGAAAGAGGTGGAAACATCTTTCAG---CGGCTT 728  
Db 714 ACAATCTTTCAACACCAACGAGGACACACTGAGAAACTTCGCTTCCAGATGACGAAG 773  
QY 729 CACGCCGAGTTCTTGGAAACAAGCCTTCAGAGTTGACGACAGACAGATAGTGCAAAACCT 788  
Db 774 GAAGCAGATCGTGACAGTGGAGGGGCTCAGCGTTATCAGCCCCAAGTGGCAAGAACA 833  
QY 789 AAGAGCGAGACCGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAAGGGGAGGCTCAG 848  
Db 834 AGAAGACGAAGACGAAGACGAAGAATATGGAACGAGCGCCCTCTTATCTCTCAGC 893  
QY 849 AATCTTTGAGCCAGATAGAAAGAGAGCTGCC---GACGAAGAGAGGAATATCAGATCAAGA 905  
Db 894 AGACCAAGCCATGGAAAGCATGAAGATGACGAGGACGAGGACGAAGAGAGATCAACC 953  
QY 906 TGAATATGAATACGATGAAGAGGATAGAAG-----CGTGGCAGGGG 947  
Db 954 TCGTCTGATCACCTCCACAGCGCAAGCAGGCCCCGAACAACAAGAACCCAGCTGGAAG 1013  
QY 948 AAGCAGAGCGGGGAATGGTATTGAAGAGCAGATCTGCACCGCAAGTGTCTTAAAGAA 1007  
Db 1014 AGGATGTAGACTAGAAATGGGGTTGAGGAAATATTTGCACCATGAAGCTTCACGAGAA 1073  
QY 1008 CATTTGGTAGAAACAGATCCCTGACATCTACAACCTCTCAAGCTGTTCACTCAAAACTGC 1067  
Db 1074 CATTTGCTGCCCTTACGTTGCTGACTTCTACAACCCAAAGCTGGTGGCATAGCACCT 1133  
QY 1068 CAACGATCTCAACCTTCTAATATCTTAGTGGCTTGGACCTAGTGTGAATATATGAAATCT 1127  
Db 1134 CAACAGTCTCACCTCCAGCCCTCCGCAATTCGGACTCAGTGGCCCAATATTTGTCCT 1193  
QY 1128 CTACAGGAATGATTTGTTGTCCTCAACACCAAGCAGCAGCATCATATATCG 1187  
Db 1194 CTACAGGAATGGAATTTACTCTCCAGATTGGAACTTGAACCGCAACAGTGTGACG-ATGA 1252  
QY 1188 ATTGAGGGGACGGGCTCAGCTGCAAGTCTGTGACAGCAACCGCAACAGAGTGTACGACGA 1247  
Db 1253 CTCAGGGGAAGG--AAGAGTTAGAGTGGTGAATCTGCCAAGGAATGCAAGTGTTCAGCG 1310  
QY 1248 GGAGCTTCAAGAGGGTCAAGTCTTGTGTGGTCCACGAAGACTTCGCGCTCGCTGGAAGTC 1307



Db 1311 TGAGCTAAGGAGGGAACAATTGCTAGTGGTCCGACAGACCCGCGTGGCTGAGCAAGG 1370  
QY 1308 CCAGAGCGAGAACTTCGAATACGTGGCAATCAAGACAGAC 1347  
Db 1371 GGGAGAACAGGATTGGAATATGATGTTCAAGACACAC 1410

RESULT 14  
US-09-758-652-15  
; Sequence 15, Application US/09758652  
; Patent No. 6703544  
; GENERAL INFORMATION:  
; APPLICANT: GARY MICHAEL FADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/758,652  
; FILING DATE: 11-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/019,940  
; FILING DATE: JUNE 14,1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LYNNE M. CHRISTENBURY  
; REGISTRATION NUMBER: 30,971  
; REFERENCE/DOCKET NUMBER: BB-1071-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-5481  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1551 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-758-652-15

Query Match 13.0%; Score 198; DB 3; Length 1551;  
Best Local Similarity 51.4%; Pred. No. 1e-46;  
Matches 699; Conservative 0; Mismatches 600; Indels 61; Gaps 8;

QY 14 AGGAGAACGGTCCAGTTCAGCGCTCAATGCGCAGAGACTGCAATCGCAATGAAT 73  
Db 86 AGTTCAACGAGTGCCAACTCAACACCTCAACCGCTTGGAAACCGGACCCGCGGTTGAGT 145  
QY 74 CAGAGGGCGTTACATTGAGACTTGGNAACCCCAACACCGAGGTTGCAATGCGCGCG 133  
Db 146 CGAAGGTTGCTCTATTGAAACATGAACTCTCAACACCTGAGCTGCAATGCGCGGTG 205  
QY 134 TCGCCCTCTCTCGCTTAGTCTCCGCGCAACCGCTTCTAGGCTCTTCTACTCCAATG 193  
Db 206 TCACTGTTCCAAACGCAACCTCAACCGCAACGGCTCCCACTTGGCCATCTTACTTACCTT 265  
QY 194 CTCCCCAGGAGATCTTCATCCAGCAAGGAGGATATCTTGGGTTGATATTCCTTGTT 253

Db 266 ATCCCAAAATGATCATTTGTGTTCAAGGGAAGGAGCAATTTGATTTTCATTTTCCGGAT 325  
QY 254 GTCTTAGACACATATGAAGAGCCCTCACACACAAGGTGTCGATCTCAGTCCCAAGACAC 313  
Db 326 GTCCCGAGAGTTTGAAGGCCACA-----ACAA 355  
QY 314 CAAGACGTCTCAAGGAGAGACCAAAAGCCAAAGCAAGAGATAGTACCAGAAGTGC 373  
Db 356 AATCAAGCAGAGAGGCTCAAGGTCAAGCAGCACTACAAGACAGTACCAGAAGATTC 415  
QY 374 ACCGTTTCGATGAGGGTGATCTCATTTGACAGTCCCAAGGTTGCTTTCTTGGCTCTACA 433  
Db 416 GTCACTTCAATGAAGGAGAGCTACTAGTATCTCTTGGTGTCTTACTGACCTATA 475  
QY 434 ACGACCACGACACTGATGTTGTTGCTTCTTACTGACACCAACCAACCAAGCAAC 493  
Db 476 AACTGGGATGNAACGATTTGGCATGTCCTCTTGACACTCAACTTCAACATC 535  
QY 494 AGCTTGATCAGTTCCCGAGGAGATTCAATTTGGCTGGGAACACGGAGCAAGATTCTTAA 553  
Db 536 AGCTTGATCAAAACCCAGAGATTATTTACTTCTGGAAACCCAGATATAGACATCCCG 595  
QY 554 GGTACCAGCAACAAAGCAGACAAAGCAGAGAAAGCTTTACCATATAGCCCATACAGCC 613  
Db 596 AGACCATGCAACAA--CAGCAGCAGCAGAGAGTCTATGTTGGACGCAAGCAGGGCAACA 653  
QY 614 CGCAAGTCAGCTAGACAAAGAG--AGCGTGAATTTAGCCCTCGAGGACGACAGCCGC 672  
Db 654 CGACAGCAGGAGGAAGAGGTGGCAGTGTCTCAGTGGCTTCAGCAACATTTCTTAGC 713  
QY 673 AGAGAACGAGCAGGGAAGAAAGAAACGAGGTGGAAACAATCTTCAG-----CGCTT 728  
Db 714 ACAATCTTCAACACCAACGAGGACACAGTGGAAACTTCGGTCTCCAGATCAGCAAG 773  
QY 729 CAGCGCGAGTTCCTGGAACAAGCTTCCAGGTTGACGACAGACAGATAGTGGAAAACCT 788  
Db 774 GAAGCAGATCGTACAGTGGAGGAGGCTCAGCGTTATCAGCCCAAGTGGCAAGACA 833  
QY 789 AAGAGCGAGACCGGAGAGTGAAGAGAGGAGGACCATTTGTGACAGTCAAGGAGGCTCAG 848  
Db 834 AGAAGACGAGAGAGAGACGAAGACGAAGATATGGAACGACGCCCTTTATCTCTCAGC 893  
QY 849 AATCTTTGAGCCAGATAGAAAGAGACGTGCC---GACGAAGAGAGAGAAATACGATGAAGA 905  
Db 894 ACGACCAACCCATGGAAGCATGAAGATCAGCAGGACGAGGACGAAGAGAAATCAACC 953  
QY 906 TGAATATGAATACGATGAAGAGATAGAAG-----CGTGGCAGGGG 947  
Db 954 TCGTCTGATCACCTCCACAGCAGCAAGCAGGCGCCGAAACCAACAAAGACCCAGTGAAG 1013  
QY 948 AAGCAGAGCAGGGGAATGGTATTGAAGAGACGATCTCAGCCGCAAGTCTTAAAGAA 1007  
Db 1014 AGGATGTCAGACTAGAAATGGGGTTAGGAAATATTTGACCATGAAGCTTCAAGGAA 1073  
QY 1008 CATTTGTAGAAACAGATCCCTTGACATCTACAACCTCAAGCTGGTTCCTCAAAACTGC 1067  
Db 1074 CATTTGCTCCCTTCAAGGCTGACTTCTACAACCCAAAGCTGGTGGCTTAGCACCT 1133  
QY 1068 CAAAGATCTCAACCTTCTAATATCTTAGTGGCTTGGACCTAGTGTGTAATATGGAATCT 1127  
Db 1134 CAACAGTCTCAACCTTCCAGCCCTCCGCAATTTGAGACTCAGTGGCCAAATATGTTGCT 1193  
QY 1128 CTACAGGAATGATTTGTTGTCGCTCACTACAACCAACGACGACAGCATATATATCG 1187  
Db 1194 CTACAGGAATGGAATTTACTCTCCAGATTGGAATTTGAACGCAACAGTGTGACG-ATGA 1252  
QY 1188 ATTGAGGGACGGGCTCAGCTCAAGTCTGTGACAGCAACCGCAACAGAGTGTACGACGA 1247  
Db 1253 CTCGAGGGAAGG--AAGAGTTAGAGTGTGTAAGTCCCAAGGGAATGCAAGTGTTCGACGG 1310  
QY 1248 GGAGCTTCAAGAGGCTCAGCTTGTGTTGTCACAGAACTTCGCGCTCGCTGGAAAGTC 1307  
Db 1311 TGAGCTAAGGAGGAGCAATTTGCTAGTGGTGGCAGAAACCCCGCGTGGCTGAGCAAGG 1370

QY 1308 CCAGAGCGAGAACTTCGAATACGTGCGCAATTCAGACAGAC 1347  
 Db 1371 GGGAGAACAAAGGATGGAAATATGTAGTGTCAAGACACAC 1410

RESULT 15

US-10-684-651-15  
 ; Sequence 15, Application US/10684651  
 ; Patent No. 6828491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ANTHONY JOHN KINNEY  
 ; APPLICANT: GARY MICHAEL FADER  
 ; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
 ; CLASSES OF SOYBEAN SEED  
 ; PROTEIN GENES  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
 ; STREET: 1007 MARKET STREET  
 ; CITY: WILMINGTON  
 ; STATE: DELAWARE  
 ; COUNTRY: UNITED STATES OF AMERICA  
 ; ZIP: 19898  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: DISKETTE, 3.50 INCH  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
 ; SOFTWARE: MICROSOFT WORD 7.0A  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/684,651  
 ; FILING DATE: 14-Oct-2003  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/758,652  
 ; FILING DATE: 11-Jan-2001  
 ; APPLICATION NUMBER: 60/019,940  
 ; FILING DATE: JUNE 14,1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: LYNNE M. CHRISTENBURY  
 ; REGISTRATION NUMBER: 30,971  
 ; REFERENCE/DOCKET NUMBER: BB-1071-A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 302-992-5481  
 ; TELEFAX: 302-773-0164  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1551 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 US-10-684-651-15

Query Match 13.0%; Score 198; DB 3; Length 1551;  
 Best Local Similarity 51.4%; Pred. No. 1e-46;  
 Matches 699; Conservative 0; Mismatches 600; Indels 61; Gaps 8;  
 QY 14 AGGAGAACGGTCCAGTTCAGCGCCTCAATGCGCAGAGACCTGACAAATCGCAATTGAAT 73  
 Db 86 AGTTCACAGAGTCCCACTCAACAACTCAACGGTTGGAACCCGACCACCGCGTTGAGT 145  
 QY 74 CAGAGGCGGTTACATTGAGACTTGGNAACCCCAACACACAGGAGTTCGAATGCGCGCGG 133  
 Db 146 CCGAAGGTGCTTATTGAAACATGGAACCTCAACACCCCTGAGCTGCAATGCGCGCGTG 205  
 QY 134 TCGCCCTCTCGCTTAGTCTCGCGCAACGCCCTTGTAGGCTTTCTACTTCCAATG 193  
 Db 206 TCACTGTTTCCAAACGACCCCTCAACCGCAACGGCTCCCACTTGCACATCTTACTTACCTT 265  
 QY 194 CTCCCAGGAGATCTTCATCCAGCAAGGAAGGGGATCTTTGGTGTGATATCCCTGGTT 253

Db 266 ATCCCAATGATCATTTGTCGTTCAAGGAGAGGAGCAATTTGATTTTCATTTCCGGAT 325  
 QY 254 GTTCCTAGACACTATGAAGAGCCTCACAACAAGGTTCGTGATCTCAGTCCCAAGACAC 313  
 Db 326 GTCCCGAGACGTTTGAGAGGCCACA-----ACAA 355  
 QY 314 CAAGAGCTCTCAAGGAGAGAACCAAGGCAACAGCAAGAGTAGTCACCAAGAGTGC 373  
 Db 356 AATCAAGCAGAAGAGGCTCAGGTCAACAGCACTACAAGACAGTCAACAGAGATTTC 415  
 QY 374 ACCGTTTCGATGAGGTTGATCTCATTTGCAAGTTCACACCGGTTGTTCTTGCTCTACA 433  
 Db 416 GTCACTTCAATGAAGGAGACGTACTAGTATTCCTTGGTGTCTTACTTGACCTATA 475  
 QY 434 AGACCAACGACACTGATGTTGTTGTTCTTCTTACTGACACCAACCAACAGCAACACC 493  
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 QY 614 CGCAAGTCAAGCTAGACAAAG--AGCGTGAATTTAGCCCTCGAGGACAGACAGCCCG 672  
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 QY 673 AGAGAACGAGCAGGACCAAGAAAGAAAAACGAAGTGGAAACATCTTCAG----CGCTT 728  
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Job time : 251.534 secs



GenCore version 5.1.9  
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main.\*

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- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524	100.0	1524	3	US-09-731-375A-3
2	1524	100.0	1524	6	US-10-728-806-5
3	1524	100.0	1524	9	US-10-100-303A-89
4	1524	100.0	1524	9	US-10-728-323-3
5	1524	100.0	1524	9	US-10-728-051-3
6	1524	100.0	1524	10	US-10-899-551-5
7	1391.2	91.3	1853	10	US-10-958-324-4
8	517.4	34.0	1446	3	US-09-758-652-13
9	517.4	34.0	1446	8	US-10-684-651-13
10	517.4	34.0	1446	8	US-10-757-074-13
11	517.4	34.0	1446	8	US-10-757-155-13
12	517.4	34.0	1446	8	US-10-757-667-13
13	517.4	34.0	1446	10	US-10-508-263-27
14	517.4	34.0	1673	8	US-10-425-114-7280
15	517.4	34.0	1689	8	US-10-425-114-8531
16	517.4	34.0	1694	8	US-10-425-114-8592
17	517.4	34.0	1697	8	US-10-425-114-7583

18	517.4	34.0	1766	8	US-10-424-599-28860	Sequence 28860, A
19	515.8	33.8	1671	8	US-10-425-114-7594	Sequence 7594, Ap
20	513	33.7	1431	10	US-10-409-993-2	Sequence 2, Appli
21	513	33.7	1434	10	US-10-409-993-16	Sequence 16, Appl
22	513	33.7	1458	10	US-10-409-993-10	Sequence 10, Appl
23	513	33.7	1488	3	US-09-758-652-11	Sequence 11, Appl
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25	513	33.7	1488	8	US-10-757-074-11	Sequence 11, Appl
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37	513	33.7	1729	8	US-10-425-114-8164	Sequence 8164, Ap
38	513	33.7	1730	8	US-10-425-114-8133	Sequence 8133, Ap
39	513	33.7	1834	8	US-10-424-599-28863	Sequence 28863, A
40	511.4	33.6	1458	10	US-10-409-993-14	Sequence 14, Appl
41	511.4	33.6	1729	8	US-10-425-114-8584	Sequence 8584, Ap
42	505	33.1	1746	3	US-09-805-694B-15	Sequence 15, Appl
43	505	33.1	1746	9	US-10-922-732-15	Sequence 15, Appl
44	504	33.1	1458	3	US-09-758-652-12	Sequence 12, Appl
45	504	33.1	1458	8	US-10-684-651-12	Sequence 12, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-731-375A-3  
; Sequence 3, Application US/09731375A  
; Publication No. US20030035810A1  
; GENERAL INFORMATION:  
; APPLICANT: Caplan, Michael  
; TITLE OF INVENTION: Microbial Delivery System  
; FILE REFERENCE: 2002834-0100  
; CURRENT APPLICATION NUMBER: US/09/731,375A  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/195,035  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Atachis hypogaea  
US-09-731-375A-3

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Best Local Similarity		100.0%;	Pred. No. 0;		
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				Indels	0;
				Gaps	0;
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Db	1	CGGCAGCAACCGGAGGAGAACGGTCCAGTTC	CGCGCTCAATGCGAGACCTGAC	60	
Qy	61	AATCGCATTTGAATCAGAGGGCGGTTACATTTGAGACTTGGAAACCCCAACACAGGAGTTTC	120		
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Qy	121	GAATGCGCGGCTCGCCCTCTCTCGCTTAGTCTCGCGGCAACGCCCTTCGTAGGCCT	180		
Db	121	GAATGCGCGGCTCGCCCTCTCTCGCTTAGTCTCGCGGCAACGCCCTTCGTAGGCCT	180		
Qy	181	TTCTACTCAATGCTCTCCAGGAGATCTTTCATCCAGCAAGGAGGACTTTTGGGTTG	240		
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; Sequence 5, Application US/10228806
; Publication No. US20030049237A1
; GENERAL INFORMATION:
; APPLICANT: Bannon, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions
; TITLE OF INVENTION: to Allergy
; FILE REFERENCE: 2002834-0043
; CURRENT APPLICATION NUMBER: US/10/228,806
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-228-806-5

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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; Sequence 89, Application US/10100303A
; Publication No. US20030202980A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction
; FILE REFERENCE: 2002834-0166
; CURRENT APPLICATION NUMBER: US/10/100,303A
; CURRENT FILING DATE: 2002-03-18
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Atachis hypogaea, Prot/Nucleo Ara h 3
US-10-100-303A-89
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Query Match 100.0%; Score 1524; DB 7; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CGGCAGCAACCGGAGAGAACGCGTGCCAGTTCCAGCGCTCAATCGCAGAGACCTGAC 60
QY 61 AATCGCATTTGAATCAGAGGCGGTTTACATTGAGACTTTGGAACCCCAACCAACAGGAGTTC 120
Db 61 AATCGCATTTGAATCAGAGGCGGTTTACATTGAGACTTTGGAACCCCAACCAACAGGAGTTC 120
QY 121 GAATGCGCGGCGTCCCTCTCTCGCTTAGTCTTCCGCGCAACGCCCTTCGTAGGCCT 180
Db 121 GAATGCGCGGCGTCCCTCTCTCGCTTAGTCTTCCGCGCAACGCCCTTCGTAGGCCT 180
QY 181 TTCTACTCTCAATGCTCCCGCAGGAGATCTTCATCCAGCAAGGAGGATCTTTGGGTTG 240
Db 181 TTCTACTCTCAATGCTCCCGCAGGAGATCTTCATCCAGCAAGGAGGATCTTTGGGTTG 240
QY 241 ATATTCCCTGGTTGCTTAGACACTATGAAGAGCCTCACACACAAGGTCGTCTGATCTCAG 300
Db 241 ATATTCCCTGGTTGCTTAGACACTATGAAGAGCCTCACACACAAGGTCGTCTGATCTCAG 300
QY 301 TCCCAAGACCAACGAAGAGCTCTCCAGGAGAAAGACAAAGCCCAACAGACAGATAGT 360
Db 301 TCCCAAGACCAACGAAGAGCTCTCCAGGAGAAAGACAAAGCCCAACAGACAGATAGT 360
QY 361 CACCAAGAGTGCACCGTTTCGATGAGGAGTATCTCATTTGCAGTTCGCCCGGTGTGCT 420
Db 361 CACCAAGAGTGCACCGTTTCGATGAGGAGTATCTCATTTGCAGTTCGCCCGGTGTGCT 420
QY 421 TTCTGGCTCTACAACGACCAACGACACTGATGTTGTTGCTGTTTCTTACTGACACCAAC 480
Db 421 TTCTGGCTCTACAACGACCAACGACACTGATGTTGTTGCTGTTTCTTACTGACACCAAC 480
QY 481 AACACAGCAACACAGTTGATCAGTTCCCGCAGAGATTCAAATTTGGCTGGGAACACGGAG 540
Db 481 AACACAGCAACACAGTTGATCAGTTCCCGCAGAGATTCAAATTTGGCTGGGAACACGGAG 540
QY 541 CAAGAGTTCTTAAGGTACCCAGCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATAT 600
Db 541 CAAGAGTTCTTAAGGTACCCAGCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATAT 600
QY 601 AGCCCATACAGCCGCAAGTACGCTTAGCAAGAGAGCGTGAATTTAGCCCTCGAGGA 660
Db 601 AGCCCATACAGCCGCAAGTACGCTTAGCAAGAGAGCGTGAATTTAGCCCTCGAGGA 660
QY 661 CAGCAGCGCAGAGAACGACAGACAGACAGACAGACAGACAGACAGACAGATCTTTC 720
Db 661 CAGCAGCGCAGAGAACGACAGACAGACAGACAGACAGACAGACAGATCTTTC 720
QY 721 AGCGGCTTCACGCGGAGTTCCTGGAAACAAAGCCCTTCAGGTTGACACAGACAGATAGTG 780
Db 721 AGCGGCTTCACGCGGAGTTCCTGGAAACAAAGCCCTTCAGGTTGACACAGACAGATAGTG 780
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QY 781 CAAAACCTTAAGAGCGAGACCGAGAGTGAAGAAGAGGAGGCCATTGTGACAGTGAAGGGA 840
Db 781 CAAAACCTTAAGAGCGAGACCGAGAGTGAAGAAGAGGAGGCCATTGTGACAGTGAAGGGA 840
QY 841 GGCCTCAGAATCTTGAGCCCGAGATAGAAAGAGACGTGCCGACGAAGAAGAGGAATACGAT 900
Db 841 GGCCTCAGAATCTTGAGCCCGAGATAGAAAGAGACGTGCCGACGAAGAAGAGGAATACGAT 900
QY 901 GAAGATGAATATGAATACATGAGAGGATAGAGGCGTGGCAGGGAAGCAGAGCGAG 960
Db 901 GAAGATGAATATGAATACATGAGAGGATAGAGGCGTGGCAGGGAAGCAGAGCGAG 960
QY 961 GCGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGTCTAAAAGAAACATTGGTAGAAAC 1020
Db 961 GCGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGTCTAAAAGAAACATTGGTAGAAAC 1020
QY 1021 AGATCCCTTGACATCTACAACCCCTCAAGCTGTGTTCTCACTCAAACTGCCAACGATCTCAAC 1080
Db 1021 AGATCCCTTGACATCTACAACCCCTCAAGCTGTGTTCTCACTCAAACTGCCAACGATCTCAAC 1080
QY 1081 CTTCTAATACTTAGTGGCTTGGACCTAGTGTGCTGAATATGGAATCTCTACAGGAATGCA 1140
Db 1081 CTTCTAATACTTAGTGGCTTGGACCTAGTGTGCTGAATATGGAATCTCTACAGGAATGCA 1140
QY 1141 TTGTTTGTGCTCACTACAAACCCACGACACAGCATCATATATCGATTGAGGGGACGG 1200
Db 1141 TTGTTTGTGCTCACTACAAACCCACGACACAGCATCATATATCGATTGAGGGGACGG 1200
QY 1201 GCTCAGTGCAGTCTGGACAGCAACCGGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1260
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QY 1261 GGTACAGTGTGTGTGCGCAAGAACTTCGCCGTGCTGGAAAGTCCAGAGCGAGAAC 1320
Db 1261 GGTACAGTGTGTGTGCGCAAGAACTTCGCCGTGCTGGAAAGTCCAGAGCGAGAAC 1320
QY 1321 TTCGAATAGTGCATTTCAAGACAGACTCAAGGCCAGAGATAGCCAACTCGCCGCTGAA 1380
Db 1321 TTCGAATAGTGCATTTCAAGACAGACTCAAGGCCAGAGATAGCCAACTCGCCGCTGAA 1380
QY 1381 AACTCCGTGCATAGATAACCTGCGGAGGAGTGGTTCGAAATTCATATATGCGCTCCAAAGG 1440
Db 1381 AACTCCGTGCATAGATAACCTGCGGAGGAGTGGTTCGAAATTCATATATGCGCTCCAAAGG 1440
QY 1441 GAGCAGGCAAGGAGCTTGAAGAACAAACCAACCCCTTCAAGTTCTTCAAGTTCTTCAAG 1500
Db 1441 GAGCAGGCAAGGAGCTTGAAGAACAAACCAACCCCTTCAAGTTCTTCAAGTTCTTCAAG 1500
QY 1501 CAGTCTCCGAGGCGTGTGGCTTAA 1524
Db 1501 CAGTCTCCGAGGCGTGTGGCTTAA 1524
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RESULT 4

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US-10-728-323-3
; Sequence 3, Application US/10728323
; Publication No. US2004020894A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0232
; CURRENT APPLICATION NUMBER: US/10/728,323
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/731,375
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 3
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Arachis hypogaea
; US-10-728-323-3

Query Match      100.0%; Score 1524; DB 9; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCAGAACCGGAGAGAACCGCGTCCAGTTCACAGCGCTCAATCGCAGAGACCTGAC 60
Db 1 CGGCAGAACCGGAGAGAACCGCGTCCAGTTCACAGCGCTCAATCGCAGAGACCTGAC 60
QY 61 AATCGCATTTGAATCAGAGGCGGTTACATTGAGACTTTGGAACCCCAACACAGGAGTTT 120
Db 61 AATCGCATTTGAATCAGAGGCGGTTACATTGAGACTTTGGAACCCCAACACAGGAGTTT 120
QY 121 GAATGCGCGGCGTTCGCCCTCTCTCGCTTAGTCTCCGCGCAACCGCCCTTCGTAGGCCT 180
Db 121 GAATGCGCGGCGTTCGCCCTCTCTCGCTTAGTCTCCGCGCAACCGCCCTTCGTAGGCCT 180
QY 181 TTCTACTCAATGCTCTCCAGGAGATCTTCAATCCAGCAAGAGGAGTACTTTGGGTTG 240
Db 181 TTCTACTCAATGCTCTCCAGGAGATCTTCAATCCAGCAAGAGGAGTACTTTGGGTTG 240
QY 241 ATATTTCCCTGGTGTCTTAGACACTATGAAGAGGCTTCACACAAAGGTCGTGATCTCAG 300
Db 241 ATATTTCCCTGGTGTCTTAGACACTATGAAGAGGCTTCACACAAAGGTCGTGATCTCAG 300
QY 301 TCCCAAGAACCCACCAAGAGAGTCTTCCAAAGGAGAGACCAAAGGCCAACAGAGATAGT 360
Db 301 TCCCAAGAACCCACCAAGAGAGTCTTCCAAAGGAGAGACCAAAGGCCAACAGAGATAGT 360
QY 361 CACCAGAGAGTGACCGTTTCGATGAGGAGTGTCTCAATTCAGTTCCTCCACCGTGTGCT 420
Db 361 CACCAGAGAGTGACCGTTTCGATGAGGAGTGTCTCAATTCAGTTCCTCCACCGTGTGCT 420
QY 421 TTCTGCTCTTACAACCAACCAACGACACTGATGTTGTTGTTGTTCTTCTACTGACACCAAC 480
Db 421 TTCTGCTCTTACAACCAACCAACGACACTGATGTTGTTGTTGTTCTTCTACTGACACCAAC 480
QY 481 AACCAACGACCAACCCAGCTTGTATCAGTTTCCCAGGAGATTCAATTTGGTGGGAAACGAG 540
Db 481 AACCAACGACCAACCCAGCTTGTATCAGTTTCCCAGGAGATTCAATTTGGTGGGAAACGAG 540
QY 541 CAAAGATGTTTAAAGTACCAGCAACAAAGCAGACAAAGCAGACGAAAGAGCTTACCATAT 600
Db 541 CAAAGATGTTTAAAGTACCAGCAACAAAGCAGACAAAGCAGACGAAAGAGCTTACCATAT 600
QY 601 AGCCCATACAGCCCGCAAAAGTACAGCTAGACAAAGAGAGCGTCAATTTAGCCCTTCGAGGA 660
Db 601 AGCCCATACAGCCCGCAAAAGTACAGCTAGACAAAGAGAGCGTCAATTTAGCCCTTCGAGGA 660
QY 661 CAGCAGAGCGCAGAGAACGAGCAGACCAAGAGAGAGAGAAACCAAGAGTGGAAACATCTTC 720
Db 661 CAGCAGAGCGCAGAGAACGAGCAGACCAAGAGAGAGAGAAACCAAGAGTGGAAACATCTTC 720
QY 721 AGCGGCTTCAACCGCGAGTTCCTGGAAACAGCCCTTCAGGTTGACACAGACAGATAGTG 780
Db 721 AGCGGCTTCAACCGCGAGTTCCTGGAAACAGCCCTTCAGGTTGACACAGACAGATAGTG 780
QY 781 CAAAACCTTAAGAGCGGAGACCGGAGAGTGAAGAAGAGGAGGCCATTGTGACAGTGAAGGGA 840
Db 781 CAAAACCTTAAGAGCGGAGACCGGAGAGTGAAGAAGAGGAGGCCATTGTGACAGTGAAGGGA 840
QY 841 GGCCTCAGAATCTTGAGCCCGAGATAGAAAGAGACGTCGCCGACGAAGAAGAGGAATACGAT 900
Db 841 GGCCTCAGAATCTTGAGCCCGAGATAGAAAGAGACGTCGCCGACGAAGAAGAGGAATACGAT 900
QY 901 GAAGATGAATATGAATACGATGAAGAGGATAGAGGCGTGGCAGGGAAGCAGAGCGAG 960
Db 901 GAAGATGAATATGAATACGATGAAGAGGATAGAGGCGTGGCAGGGAAGCAGAGCGAG 960
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QY 961 GGAATGGTATTGAAGAGAGCGATCTGCACCGCAAGTCTAAAAAGAACATTTGGTAGAAAC 1020  
DB 961 GGAATGGTATTGAAGAGAGCGATCTGCACCGCAAGTCTAAAAAGAACATTTGGTAGAAAC 1020  
QY 1021 AGATCCCTGACATCTACAACTTCAAGCTGGTTCACCTCAAACTGCGCAAGATCTCAAC 1080  
DB 1021 AGATCCCTGACATCTACAACTTCAAGCTGGTTCACCTCAAACTGCGCAAGATCTCAAC 1080  
QY 1081 CTTCTAATCTAGTGGCTTGCACCTAGCTAGTGGTTCATATGAAATCTCTACAGGAATGCA 1140  
DB 1081 CTTCTAATCTAGTGGCTTGCACCTAGCTAGTGGTTCATATGAAATCTCTACAGGAATGCA 1140  
QY 1141 TTGTTTGTCTCACTACAACTTCAAGCTGGTTCACCTCAAACTGCGCAAGATCTCAAC 1200  
DB 1141 TTGTTTGTCTCACTACAACTTCAAGCTGGTTCACCTCAAACTGCGCAAGATCTCAAC 1200  
QY 1201 GCTCAGTGCAGTCTGAG 1260  
DB 1201 GCTCAGTGCAGTCTGAG 1260  
QY 1261 GGTCACTGCTTGTGTCACAG 1320  
DB 1261 GGTCACTGCTTGTGTCACAG 1320  
QY 1321 TTGGAATACGTGGCATTCAAG 1380  
DB 1321 TTGGAATACGTGGCATTCAAG 1380  
QY 1381 AACTCCGTCTAGATCACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
DB 1381 AACTCCGTCTAGATCACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
QY 1441 GAGCAGGAG 1500  
DB 1441 GAGCAGGAG 1500  
QY 1501 CAGTCTCCGAGGAG 1524  
DB 1501 CAGTCTCCGAGGAG 1524

## RESULT 5

US-10-728-051-3  
; Sequence 3, Application US/10728051  
; Publication No. US20040234548A1  
; GENERAL INFORMATION:  
; APPLICANT: Caplan, Michael J.  
; APPLICANT: Bottomly H., Kim  
; APPLICANT: Sosin B., Howard  
; APPLICANT: Burks A., Wesley  
; APPLICANT: Sampson A., Hugh  
; TITLE OF INVENTION: Microbial Delivery System  
; FILE REFERENCE: 2002834-0222  
; CURRENT FILING DATE: 2003-12-04  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,035  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea  
US-10-728-051-3

Query Match 100.0%; Score 1524; DB 9; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCAGCAACCGGAGGAG 60

DB 1 CGGCAGCAACCGGAGGAG 60  
QY 61 AATCGGATTTGAATCAGAGGCGGTTTACATTTGAGACTTTGNAACCCCAACACCAAGAGAGTTC 120  
DB 61 AATCGGATTTGAATCAGAGGCGGTTTACATTTGAGACTTTGNAACCCCAACACCAAGAGAGTTC 120  
QY 121 GAATGCGCGGCGCTCCCTCTCTCGCTTAGTCTCTCGCGCGCAACGCGCTTCTGTTAGGCTT 180  
DB 121 GAATGCGCGGCGCTCCCTCTCTCGCTTAGTCTCTCGCGCGCAACGCGCTTCTGTTAGGCTT 180  
QY 181 TTCTACTTCAATGCTCTCCAGGAGATCTTTCATCCAGCAAGGAGAGGAGATCTTTGGGTTG 240  
DB 181 TTCTACTTCAATGCTCTCCAGGAGATCTTTCATCCAGCAAGGAGAGGAGATCTTTGGGTTG 240  
QY 241 ATATTTCCCTGGTTCCTAGACACTATGAAGAGCTTACACCAAGAGTCTGCTGATCTCAG 300  
DB 241 ATATTTCCCTGGTTCCTAGACACTATGAAGAGCTTACACCAAGAGTCTGCTGATCTCAG 300  
QY 301 TCCCAAGACACCAAGT 360  
DB 301 TCCCAAGACACCAAGT 360  
QY 361 CACCAGAGAGTGCACCGTTTCGATGAGGAGTCTCTCATTTGCACTTCCACCGGTTGCT 420  
DB 361 CACCAGAGAGTGCACCGTTTCGATGAGGAGTCTCTCATTTGCACTTCCACCGGTTGCT 420  
QY 421 TTCTGCTCTACACGACACGACACTGATTTGTTGCTGTTCTCTTACTGACACCAAC 480  
DB 421 TTCTGCTCTACACGACACGACACTGATTTGTTGCTGTTCTCTTACTGACACCAAC 480  
QY 481 AACACGACCAACCGAGTTCAGTTCCTCCAGGAGATTCATTTGGTGGGAAACACGAGAG 540  
DB 481 AACACGACCAACCGAGTTCAGTTCCTCCAGGAGATTCATTTGGTGGGAAACACGAGAG 540  
QY 541 CAAGAGTCTTTAAGGTACCAAGCAACAAAGCAGACAAAGCAGAGAGAGAGAGAGAGAGAG 600  
DB 541 CAAGAGTCTTTAAGGTACCAAGCAACAAAGCAGACAAAGCAGAGAGAGAGAGAGAGAGAG 600  
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DB 601 AGCCCATACAGCCCGCAAGAGTCCAGCTAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
QY 661 CAGCAGCGCAG 720  
DB 661 CAGCAGCGCAG 720  
QY 721 AGCGGCTTCACGCGGAGTTCCTGGAAACAAAGCCTTCCAGGTTGACAGACAGAGAGAGAG 780  
DB 721 AGCGGCTTCACGCGGAGTTCCTGGAAACAAAGCCTTCCAGGTTGACAGACAGAGAGAGAG 780  
QY 781 CAAAACCTAAGAGGCGAG 840  
DB 781 CAAAACCTAAGAGGCGAG 840  
QY 841 GGCCTCAGAACTTTGAGCCAGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
DB 841 GGCCTCAGAACTTTGAGCCAGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 901 GAAGATGAATATGAATACGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
DB 901 GAAGATGAATATGAATACGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 961 GGGAAATGGTATTGAAG 1020  
DB 961 GGGAAATGGTATTGAAG 1020  
QY 1021 AGATCCCTGACATCTACAACTTCAAGCTGGTTCATCTCAAACTGCCAACGATCTCAAC 1080  
DB 1021 AGATCCCTGACATCTACAACTTCAAGCTGGTTCATCTCAAACTGCCAACGATCTCAAC 1080  
QY 1081 CTTCTAATCTAGTGGCTTGGAG 1140

Db 1081 CTTCTAATACTTAGGTGGCTTGGACCTAGTGTGCTGAATATGAAATCTCTACAGGAATGCA 1140  
Qy 1141 TTGTTTGTGCTCACTACAACCAACGACACACAGCATCATATATCGATTGAGGGACGG 1200  
Db 1141 TTGTTTGTGCTCACTACAACCAACGACACACAGCATCATATATCGATTGAGGGACGG 1200  
Qy 1201 GCTCAGCTGCAAGTCGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1260  
Db 1201 GCTCAGCTGCAAGTCGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1260  
Qy 1261 GGTCAAGTCTGTTGGTGGCCACAGAACTTTCGCCGTGCTGGAAGTCCCGAGAGCGAGAAC 1320  
Db 1261 GGTCAAGTCTGTTGGTGGCCACAGAACTTTCGCCGTGCTGGAAGTCCCGAGAGCGAGAAC 1320  
Qy 1321 TTCGAATACGTGGCATTCGAAGCAGACTCAAGGCCACAGATAGCCAACTTCGCCGTGAA 1380  
Db 1321 TTCGAATACGTGGCATTCGAAGCAGACTCAAGGCCACAGATAGCCAACTTCGCCGTGAA 1380  
Qy 1381 AACTCCGTCTATAGATAACCTGCCGGAGGAGTGTGTTGCAAAATTCATATGGCCTCCAAAGG 1440  
Db 1381 AACTCCGTCTATAGATAACCTGCCGGAGGAGTGTGTTGCAAAATTCATATGGCCTCCAAAGG 1440  
Qy 1441 GAGCAGCGAAGGCAGCTTAAGAACAAACCCCTTCAAGTTCCTCGTTCACCGTCTCAG 1500  
Db 1441 GAGCAGCGAAGGCAGCTTAAGAACAAACCCCTTCAAGTTCCTCGTTCACCGTCTCAG 1500  
Qy 1501 CAGTCTCCGAGGGCTGTGCTTAA 1524  
Db 1501 CAGTCTCCGAGGGCTGTGCTTAA 1524

RESULT 6  
US-10-899-551-5  
; Sequence 5, Application US/10899551  
; Publication No. US20050063994A1  
; GENERAL INFORMATION:  
; APPLICANT: Caplan, Michael J.  
; APPLICANT: Burks, A. Wesley  
; APPLICANT: Sampson, Hugh A.  
; APPLICANT: Howard, Sosin B.  
; APPLICANT: Bottomly, Kim H.  
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction to Allergy  
; FILE REFERENCE: 2002834-0233  
; CURRENT APPLICATION NUMBER: US/10/899,551  
; CURRENT FILING DATE: 2004-07-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: species Arachis hypogaea  
US-10-899-551-5

Query Match 100.0%; Score 1524; DB 10; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCAGCAACCGGAGAGAACCGGTGCGAGTTCAGGGCCTCAATGGCGAGACCTGAC 60  
Db 1 CGGCAGCAACCGGAGAGAACCGGTGCGAGTTCAGGGCCTCAATGGCGAGACCTGAC 60  
Qy 61 AATCGCATTAATCAGAGGCGGTTCATTGAGACTTGGAAACCCCAACACCAAGGAGTTC 120  
Db 61 AATCGCATTAATCAGAGGCGGTTCATTGAGACTTGGAAACCCCAACACCAAGGAGTTC 120  
Qy 121 GAATGGCGCGCGTTCGCCCTCTCTCGCTTAGTCTCGCGCGCAACGCCCTTCGTAGCCCT 180  
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Qy 181 TTCTACTCBAATGTCCTCCAGGAGATCTTCATCCGCAAGGAAGGGGATACCTTTGGGTTG 240  
Db 181 TTCTACTCBAATGTCCTCCAGGAGATCTTCATCCGCAAGGAAGGGGATACCTTTGGGTTG 240

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Db 241 ATATTCCCTGGTGTCTAGACACTATGAAGAGCCTTCACACAAAGGTGTCGATCTCAG 300  
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Db 421 TTCTGGCTCTCAACAGCACCACTGATGTTGTTGCTGTTCTTCTACTGACACCAAC 480  
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Qy 541 CAAGAGTTCCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATAT 600  
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Db 661 CAGCAGCGCGCAGAGAACAGCAGACAAAGAAAGAAACGAAGGTGGAACATCTTC 720  
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Db 721 AGCGGCTTCACCGCGAGTTCCTTGGAAACAAAGCCTTCAGGTTGACACAGACAGATAGTG 780  
Qy 781 CAAAACCTAAGAGGCGGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAGGGGA 840  
Db 781 CAAAACCTAAGAGGCGGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAGGGGA 840  
Qy 841 GGCCTCAGAAATTTGAGCCAGATAGAAAGAGACGTGCCGACGAAGAAGGAATACGAT 900  
Db 841 GGCCTCAGAAATTTGAGCCAGATAGAAAGAGACGTGCCGACGAAGAAGGAATACGAT 900  
Qy 901 GAAGATGAATATGAATACGATGAAGAGGATAGAAAGCGTGGCAGGGAAGCAGGACGG 960  
Db 901 GAAGATGAATATGAATACGATGAAGAGGATAGAAAGCGTGGCAGGGAAGCAGGACGG 960  
Qy 961 GGGAAATGGTATTGAAGAGACGATCTGCAACCGCAAGTGTCTAAAAGAACATTGGTAGAAAC 1020  
Db 961 GGGAAATGGTATTGAAGAGACGATCTGCAACCGCAAGTGTCTAAAAGAACATTGGTAGAAAC 1020  
Qy 1021 AGATCCCTTGACATCTACAACCTCAAGCTGGTTCATCTCAAACTGCCACGATCTCAAC 1080  
Db 1021 AGATCCCTTGACATCTACAACCTCAAGCTGGTTCATCTCAAACTGCCACGATCTCAAC 1080  
Qy 1081 CTTCTAATACTTAGTGGCTTGGACCTAGTGTCTGAATATGGAATCTCTACAGGAATGCA 1140  
Db 1081 CTTCTAATACTTAGTGGCTTGGACCTAGTGTCTGAATATGGAATCTCTACAGGAATGCA 1140  
Qy 1141 TTGTTTGTGCTCACTACAACCAACGACACAGCATCATATATCGATTGAGGGACGG 1200  
Db 1141 TTGTTTGTGCTCACTACAACCAACGACACAGCATCATATATCGATTGAGGGACGG 1200  
Qy 1201 GCTCAGTGCAGTTCGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1260  
Db 1201 GCTCAGTGCAGTTCGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1260  
Qy 1261 GGTCAAGTCTGTTGGTGGCCACAGAACTTCGCCGTGCTGGAAGTCCCGAGCGAGAAC 1320  
Db 1261 GGTCAAGTCTGTTGGTGGCCACAGAACTTCGCCGTGCTGGAAGTCCCGAGCGAGAAC 1320  
Qy 1321 TTCGAATACGTGGCATTCGAAGCAGACTCAAGGCCACAGATAGCCAACTTCGCCGTGAA 1380

Db 1321 TTGGAATACGTGGCAATTAAGAGACAGACTCAAGGCCAGCATAGCCAACTCGCGGTGAA 1380  
Qy 1381 AACTTCGGTCTAGATACCTGCGGAGAGTGGTTCGAAATTCATATGCGCTCCAAAGG 1440  
Db 1381 AACTTCGGTCTAGATACCTGCGGAGAGTGGTTCGAAATTCATATGCGCTCCAAAGG 1440  
Qy 1441 GAGCAGCAAGGCGAGCTTAAGAAACAACCCCTTCAAGTTCCTCGTTCCACCGTCTCAG 1500  
Db 1441 GAGCAGCAAGGCGAGCTTAAGAAACAACCCCTTCAAGTTCCTCGTTCCACCGTCTCAG 1500  
Qy 1501 CAGTCTCCGAGGCTGTGGCTTAA 1524  
Db 1501 CAGTCTCCGAGGCTGTGGCTTAA 1524

## RESULT 7

US-10-958-324-4  
; Sequence 4, Application US/10958324  
; Publication No. US20050114924A1  
; GENERAL INFORMATION:  
; APPLICANT: DODO, HORTENSE W.  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: KONAN, KOFFI N'DA  
; APPLICANT: VIQUEZ, OLGA  
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN  
; FILE OF INVENTION: TRANSGENIC PEANUT SEEDS  
; FILE REFERENCE: 072121/0104  
; CURRENT APPLICATION NUMBER: US/10/958,324  
; CURRENT FILING DATE: 2004-10-06  
; PRIOR APPLICATION NUMBER: US/09/715,036  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/167,255  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1853  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea  
US-10-958-324-4

Query Match 91.3%; Score 1391.2; DB 10; Length 1853;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1454; Conservative 0; Mismatches 68; Indels 2; Gaps 2;  
Qy 2 GGCAACACCGAGGAGAACGCGTGCAGTTCAGCGCCTCAATGGCAGAGACCTTGACA 61  
Db 71 GGCAGCAGCCGAGGAGAAATGCGTGCAGTTCAGCGCCTCAATGGCAGAGACCTTGACA 130  
Qy 62 ATCGCATTTGAATCAGAGGGGGTTTACATTCAGACTTGGAAACCCCAACACAGGAGTTGC 121  
Db 131 ACCGATTTGAATCGAGGGGGTTTACATTCAGACTTGGAAACCCCAACACAGGAGTTGC 190  
Qy 122 AATGCGCGCGGTGCGCCCTCTCGTTAGTCTCGCGCCCAACGCGCCTTCGTAGGCGTT 181  
Db 191 AATGCGCGCGGTGCGCCCTCTCGTTAGTCTCGCGCCCAACGCGCCTTCGTAGGCGTT 250  
Qy 182 TCTACTCCAAATGTCCTCCAGAGATCTTCATTCAGAGAGAGAGGAGATCTTTGGGTTGA 241  
Db 251 TCTACTCCAAATGTCCTCCAGAGATCTTCATTCAGAGAGAGAGGAGATCTTTGGGTTGA 310  
Qy 242 TATTTCCTGCTGTCCTAGACACTATGAAGAGCTCACACAGGCTCGTCGATCTCAGT 301  
Db 311 TATTTCCTGCTGTCCTAGACACTATGAAGAGCTCGCACAAAGAGAGCGCCGATATCAGT 370  
Qy 302 CCCAAGACCCCAAGACGCTCTCCAGGAGAGAACCAAGCCCAACAGCAACAGAGATGTC 361  
Db 371 CCCAAGACCCCAAGACGCTTTCAGAGAGAGAACCAAGCCCAACAGCAACAGATGTC 430  
Qy 362 ACCAGAGGTGCACCGTTTCGATGAGGGTATCTCATTCAGTTCCTCCACCGGTGTCCTT 421  
Db 431 ACCAGAGGTGCACCGTTTCGATGAGGGTATCTCATTCAGTTCCTCCACCGGTGTCCTT 490

Qy 422 TCTGGCTCTACAAACGACGACGACCTGATGTTGTTGCTGTTTCTTCTTACTGACACCAACA 481  
Db 491 TCTGGCTGTACAAACGACGACGACCTGATGTTGTTGCTGTTTCTTCTTACTGACACCAACA 550  
Qy 482 ACAACGACAAACGAGCTTGATCTGCTCCAGGAGATTCAAATTTGGCTGGGAAACAGGAGC 541  
Db 551 ACAACGACAAACGAGCTTGATCTGCTCCAGGAGATTCAAATTTGGCTGGGAAACAGGAGC 610  
Qy 542 AAGAGTTCTTAAGGTACCAGCAACAAGCAGACAAAGCAGACGAAGAGCTTACCATATA 601  
Db 611 AAGAGTTCTTAAGGTACCAGCAACAAGCAGACAAAGCAGACGAAGAGCTTACCATATA 670  
Qy 602 GCCCATACAGCCCGCAAGGTAGCTAGACAAAGAGCGTGAATTTAGCCCTCGAGGAC 661  
Db 671 GCCCATACAGCCCGCATAGTTCGCCCTAGACGAGAGAGCGTGAATTTTCGCCCTCGAGGAC 730  
Qy 662 AGCAGAGCCGACAGAAACGAGGAGGACAGAAAGAAACGAAGGTGGAAACATCTTCA 721  
Db 731 AGCAGAGCCGACAGAAACGAGGAGGACAGAAAGAAACGAAGGTGGAAACATCTTCA 790  
Qy 722 GCGGCTTCAGCCGCGAGTTCTCTGAAACAAGCCTTCAGGTTGACGACAGACAGATAGTC 781  
Db 791 GCGGCTTCAGCCGCGAGTTCTCTGAAACAAGCCTTCAGGTTGACGACAGACAGATAGTC 850  
Qy 782 AAAACCTTAAGAGGCGAGACCGAGAGTGAAGAGGAGGAGCCATTGTGACAGTGAAGGAG 841  
Db 851 AAAATCTGTGGGCGAGACGAGAGTGAAGAGGAGGAGCCATTGTGACGTTGAGGAGGAG 910  
Qy 842 GCCTCAGAAATCTTGAAGCCAGATAGAAAGAGAGCTGCCGACGAGAGAGAAATACGATG 901  
Db 911 GCCTCAGAAATCTTGAAGCCAGATAGAAAGAGAGTGCAGGAGGAGGAGAGAGAAATACGATG 970  
Qy 902 AAGATCAATATGAATACGATGAAGAGATAGAGGCGTGCAGGAGGAGGAGGAGGAGG 961  
Db 971 AAGATCAATATGAATACGATGAAGAGATAGAGGCGTGCAGGAGGAGGAGGAGGAGG 1030  
Qy 962 GGAATGGTATTGAAGAGAGAGATCTGCACCCCAAGTCTAAAAAGAAACATTTGGTAGAAACA 1021  
Db 1031 GGAATGGTATTGAAGAGAGAGATCTGCACCCCAAGTCTAAAAAGAAACATTTGGTAGAAACA 1090  
Qy 1022 GATCCCTGACATCTCAACCCCTCA - AGCTGGTTTCACTCAAAACTGCAACGATCTCAAC 1080  
Db 1091 GATCCCTGACATCTCAACCCCTCACTCAGCGTGGTTTCACTCAAAACTGCAACGATCTCAAC 1149  
Qy 1081 CTTCTAATCTTAGTGGCTTGGACCTAGTCTGAAATATGAAATCTCTACAGAAATGCA 1140  
Db 1150 CTTCTAATCTTAGTGGCTTGGACCTAGTCTGAAATATGAAATCTCTACAGAAATGCA 1209  
Qy 1141 TTGTTTGTGCTCACTACAAACCAACGACACAGCATCATATATCGATTGAGGGAGCGG 1200  
Db 1210 TTGTTTGTGCTCACTACAAACCAACGACACAGCATCATATATGCAATTGAGGGAGCGG 1269  
Qy 1201 GCTCAGTGAAGTCTGACAGCAACGCGCAACAGAGTGTACGAGGAGGAGCTTCAAGAG 1260  
Db 1270 GCTCAGTGAAGTCTGACAGCAACGCGCAACAGAGTGTACGAGGAGGAGCTTCAAGAG 1329  
Qy 1261 GGTACGTTGTTGGTGCACAGAACTTCGCCGTGCTGGAAGTCCCAAGAGGAGAGAC 1320  
Db 1330 GGTACGTTGTTGGTGCACAGAACTTCGCCGTGCTGGAAGTCCCAAGAGGAGAGAC 1389  
Qy 1321 TTGGAATACGTGGCATTTAAGACAGACTCAAGGCCAGCATAGCCAACTTCGCCGCTGAA 1380  
Db 1390 TTGGAATACGTGGCATTTAAGACAGACTCAAGGCCAGCATAGCCAACTTTGCCGCTGAA 1449  
Qy 1381 AACTCCGTATAGATACTTCGCGAGGAGGTTGGTTCGAAATTCATATGCGCTTCAAGG 1440  
Db 1450 AACTCCGTATAGATACTTCGCGAGGAGGTTGGTTCGAAATTCATATGCGCTTCAAGG 1509  
Qy 1441 GAGCAGGAGGAGGAGGTTAAGACAAACCCCTTCAAGTTCCTCGTTCACCGCTCTCAG 1500  
Db 1510 GAGCAGGAGGAGGAGGTTAAGACAAACCCCTTCAAGTTCCTCGTTCACCGCTTCTCAG 1569

QY 1501 CAGTCTCCGAGGCTGTGGCTTAA 1524  
Db |||||||  
1570 CAGTCTCCGAGGCTGTGGCTTAA 1593

RESULT 8

US-09-758-652-13  
; Sequence 13, Application US/09758652  
; Patent No. US20010011377A1  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; GARY MICHAEL FADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95  
; SOFTWARE: MICROSOFT WORD 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/758,652  
; FILING DATE: 11-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/019,940  
; FILING DATE: JUNE 14,1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LYNE M. CHRISTENBURY  
; REGISTRATION NUMBER: 30,971  
; REFERENCE/DOCKET NUMBER: BB-1071-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-5481  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1446 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-758-652-13

Query Match 34.0%; Score 517.4; DB 3; Length 1446;  
Best Local Similarity 62.8%; Pred. No. 3.2e-154;  
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

QY 5 AGCAACGGAGGAGACGGCTGCAGTTCAGCGCCTCAATGCGCAGAGACCTGACAATC 64  
Db |||||||  
71 AGCAGCCACAGCAAAAACGAGTGCAGATCCAACGCCCTCAATGCCCTTAAACCGGATAACC 130  
QY 65 GCATTGAATCAGAGGGCGGTTACATTGAGACTTGGAAACCCCAACCAACCGAGGTTGGAAT 124  
Db 131 GTATAGATCAGAGGTGGCTTCATTGAGACATGGAACCTTAACAACAGCCATTCCAGT 190  
QY 125 GCGCCGGCGTGCCTCTCTCGTTAGTCTCCGCGCGCAACGCCCTTCGTAGGCCCTTTCT 184  
Db 191 GTCCGGTGTGCTCTCTCGTGCACCTCAACCGCAACGCCCTTCGACAGACCTTCTCT 250  
QY 185 ACTCCATGCTCCCGAGGAGATCTTCATCCAGCAAGGAGGATATCTTTGGGTGTGATAT 244  
Db 251 ACACCAACGCTCCCGAGGAGATCTACATCCAAAGAGTAGTGGTATTTTGGCATGATAT 310  
QY 245 TCCTCGTGTGCTAGACACTATGAGAGCGCTCACACAAAGGTGCTGATCTCAGTCCC 304

Db |||||||  
311 TCCCGGTTGTCTTAGCACATTTGAAGAGCCT----- 342  
QY 305 AAAGACCACCAAGACGTCTCCAAGGAGAAGACCAAAAGCCAAACAGCAACGAGATAGTACCC 364  
Db |||||||  
343 -----CAACAAAAGGACAAAGCAGCAGCGGCCCAAGACCGTCACC 382  
QY 365 AGAAGGTGACACCGTTTCGATGAGGGTGATCTCATTCAGTTCGCCCGGTGTTGCTTTCT 424  
Db 383 AGAAGATCTATCACCTTCAGAGAGGGTGATTTGATTCAGTGCCAAACCGGTTTGCATACT 442  
QY 425 GGCTCTCAACACGACACGACACTGATGTTGTTGCTGCTTTCTCTTACTGACACCAACAACA 484  
Db 443 GGATGTACAAACAATGAAGACACTCTCTGTTGTTGCGCTTTCTCTTATTGACACCAACAGCT 502  
QY 485 ACGACAACACGCTTGATCAGTTCCTCCAGGAGATTCATTTGGCTGGGAACACCGAGCAAG 544  
Db 503 TCAGAAACGAGCTCGACCATGCTCTAGGAGATTTCTATCTTGTCTGGAACCAAGAGCAAG 562  
QY 545 AGTTCTTAAGGTACACAGCAACAAAGCAGACAAAGCAGACGAAAGAGCTTACCATATAGCC 604  
Db 563 AGTTCTACAGTATCAGCCACAGACGACGCAAG----- 595  
QY 605 CATACAGCCCGCAAGCTCAGCCTTAGACAAGAGAGCGTGAAATTTAGCCTTCGAGGACAGC 664  
Db 596 -----GAGGTACTC 604  
QY 665 ACAGCCGACAGAAACGAGCAGGACAGAAAGAAACGAAAGTGGAAACATCTTCAGCG 724  
Db 605 AAAGCCAGAAAGGAAAGCGTTCAGAGAAAGAAAGAAACGAAAGGAGCGCATTTAGTG 664  
QY 725 GCTTACAGCGCGGAGTTCTTGGAAACAGCCTTCAGGTTGACGACAGACAGATAGTCAAA 784  
Db 665 GCTTCGCGCGGNAATCTTGGACATGCGTTC---GTCGTGGACAGCAGATAGTGAGAA 721  
QY 785 ACCTAAGAGCGCAGACCGAGAGTGAAGAAAGAGAGGAGCCATTGTGACAGTGAGGGGAGGCC 844  
Db 722 AGCTCAAGGTGAGAAACGAAAGAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 781  
QY 845 TCAGAACTTTCAGCCAGATAGAAAGAGAGCGTCCGACGAGAGAGGAGGAGGAGGAGGAGG 904  
Db 782 TCAGCGTGATAGCGCCACCCACCGAAGAGAGCAGCAACAAAGACCCGAGGAGAGAGAGAGC 841  
QY 905 ATGAATATGAATACGATGAGAGGATAGAAAGCGGTGGCAGGGGAAAGCAGAGCGAGGGGA 964  
Db 842 CAGATTGTGACGAGAAAGACAAACAT-----TGCCAAAGCCAAAGCAGAA 886  
QY 965 ATGGTATTGAAGAGAGCATCTGCACCGCAGTCTGCTAAAAGAACATTTGGTAGAAACAGAT 1024  
Db 887 ATGGCATTTGACGAGACCATTTGCACAAATGAGACTTCGCCACAAACATTTGGCCAGACTTCAT 946  
QY 1025 CCCTGACATCTACAAACCTTCAAGCTGGTTCACTCAAAACCTGCAACGATCTCAACCTTC 1084  
Db 947 CAGCTGACATCTTCAACCTTCAAGCTGGTAGCATCAACCGGTACCGCTCGACTTCC 1006  
QY 1085 TAATACCTTAGGTGGCTTGGACCTAGTCTGAAATATGAAATCTCTACAGAAATGCAATGT 1144  
Db 1007 CAGCCCTCTCGTGGCTCAAACTCAGTGGCCCGAGTTGGATCACTCCGCAAGAAATGCTATGT 1066  
QY 1145 TTGTCGCTCATCAACACCAACGACACAGCATCATATATTCGATTGAGGGGAGCGGCTC 1204  
Db 1067 TCGTGCACACTACAAACCTTGAACGCAACAGCATATATACGCAATTTGAATGGAGCGGCAT 1126  
QY 1205 ACGTCAAGTCTGAGGACGACCAACGCAACAGAGTGACGACGAGGAGCTTCAAGAGGGTC 1264  
Db 1127 TGGTACAGTGGTGAATTCGATGAGAGAGTGTGATGAGAGAGTCTCAAGAGGGAC 1186  
QY 1265 ACGTGTCTGTGGTGCACAGAACTTCGCGTCCGCTGAAAGTCCCAGAGAGCAACTTCG 1324  
Db 1187 AGGTGTTAATTTGTGCCACAAAACCTTTGCGGTGGCTGCAAGATCACAGAGCGCAACTTCG 1246  
QY 1325 AATACGTGGCATTCAGACAGACACTCAAGGCCAGCATAGCAACCTCGCCGGTGAAACT 1384

1247	AGTATGTTTCATTCAAGACCAATGATAGACCCCTCGATCGGCAACCTTGCAGGTGCAAACT	1306
Db		
1385	CCGTCATAGATAACCTGCCGAGGAGGTGGTTGCCAAATTCATATGGCCTCCAAAGGGAGC	1444
Qy		
1307	CATTGTTGAACGCAATTCGCCGAGGAAGTATTTCAGCAAACTTTTAACCTTAAGGAGGCAGC	1366
Db		
1445	AGGCAGGCGAGCTTTAGAACAAACACCCCTTCAGTTCTTCGTTCCACCGTCTTCACAGT	1504
Qy		
1367	AGGCCAGGCGAGGTCAGAAACAAACCCCTTCAGTTCTTCGTTCCACCTTAAGGAGTCTC	1426
Db		
1505	CTCCGAGGGCTGTGGCTTA	1523
Qy		
1427	AGAGGAGAGTTGTGGCTTA	1445
Db		

## RESULT 9

US-10-684-651-13  
; Sequence 13, Application US/10684651  
; Publication No. US20040064858A1  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; GARY MICHAEL FADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

US-10-684-651-13

Query Match 34.0%; Score 517.4; DB 8; Length 1446;  
Best Local Similarity 62.8%; Pred. No. 3.2e-154;  
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

Qy	5	AGCAACCGGAGGAGAACGGTGCCAGTTC	CGCGCCTCAATCGCGAGAGACCTGACAATC	64
Db	71	AGCAGCCACAGCAAAACGAGTGCCAGATC	CAACGCCTCAATGCCTTAAACCGGATTAACC	130
Qy	65	GCAATTGAATCAGAGGCGGGTTACAT	TGAGACTTGGAAACCCCAACAACGAGAGTTGCAAT	124



Db 887 ATGGCATTGAGGAGCACTTTGCACAAATGAGACTTCGCCCAACAATTTGGCCGAGACTTCAT 946  
QY 1025 CCCTGACATCTAACACCTCAAGCTGGTTTCACTCAAAATGCGCAAGATCTCAACCTTC 1084  
Db 947 CACCTGACATCTTCAACCTCAAGCTGGTAGCATCAACCGCTACCAGCTCGACTTCC 1006  
QY 1085 TAATACTTAGTGGCTTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCAATGT 1144  
Db 1007 CAGCCCTCTCGTGGCTCAAACTCAGTGGCCAGTTTGGATCACTCCGCAAGAATGCTATGT 1066  
QY 1145 TTGTCGCTCACTAACACCAACGCGCACACAGCATCATATATCGATTGAGGGGAGCGGCTC 1204  
Db 1067 TCGTGCCACACTAACCTGAACGCAACAGCATATATACGCAATTAATGGACGGGCAT 1126  
QY 1205 ACCTGCAAGTCTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264  
Db 1127 TGGTACAAGTGGTGAATTTGCAATGGTGAGAGAGTGTGTTGATGAGAGCTCGAAGAGGGAC 1186  
QY 1265 AGTGCTTGTGGTGCACAGAACTTGGCGTGGTGAAGTCCGAGAGGAGAACTTCG 1324  
Db 1187 AGTGTTAATTTGTGCCAACAACCTTTGCGGTGGTGCAGATCACAGAGCGCAACTTCG 1246  
QY 1325 AATACGTGGCATTCAAGACAGACTCAAGGCCAGCAAGAGTGTACGACGAGGAGCTTCAAGAACT 1384  
Db 1247 AGTATGTTTCAITCAAGACCAATGATAGACCTCGATCGCAACCTTGCAGGTGCAAACT 1306  
QY 1385 CCCTCATAGTAACCTGCCGGAGGAGTGGTTCGAAATTCATATGGCTCCAAAGGAGC 1444  
Db 1307 CATTGTTGAACGATTGCGGAGGAGTGTATCAGCAAACTTTTAACCTAAGAGGCGAGC 1366  
QY 1445 AGCAAGGAGCTTAAGAACAAACACCCCTTCAAGTTCCTTCAAGTTCACCGTCTCAGCAGT 1504  
Db 1367 AGCCAGGAGGCTCAAGAACAAACCCCTTTCAGCTTCTCGTTCACCTCAAGGAGTCTC 1426  
QY 1505 CTCGAGGCTGTGGCTTA 1523  
Db 1427 AGAGGAGGTTGTGGCTTA 1445

RESULT 11

US-10-757-155-13

; Sequence 13, Application US/10757155

; Publication No. US20040139503A1

; GENERAL INFORMATION:

; APPLICANT: ANTHONY JOHN KINNEY

; GARY MICHAEL FADER

; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC

; CLASSES OF SOYBEAN SEED

; PROTEIN GENES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10757,155

; FILING DATE: 14-Jan-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09758,652

; FILING DATE: 11-Jan-2001

; APPLICATION NUMBER: 60/019,940

; FILING DATE: JUNE 14,1996

; ATTORNEY/AGENT INFORMATION:

; NAME: LYNNE M. CHRISTENBURY

; REGISTRATION NUMBER: 30,971

; REFERENCE/DOCKET NUMBER: BB-1071-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 302-992-5481

; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1446 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

; US-10-757-155-13

Query Match 34.0%; Score 517.4; DB 8; Length 1446;

Best Local Similarity 62.8%; Pred. No. 3.2e-154;

Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

QY 5 AGCAACCGGAGGAGAACGCGTGCAGTTCAGGCGCCTCAATGCGCAGAGACTTGACAATC 64

Db 71 AGCAGCCACAGCAAAACGAGTGCAGATCCACGCTCAATGCCCTAAACCGGATAACC 130

QY 65 GCATTGAATCAGAGGGCGGTTCATTGAGACTTTGGAACCCCAACACAGAGTTCGAAT 124

Db 131 GTATAGAGTCAGAAGGTGGCTTCATTGAGACATGGAACCCCTAAACAACAGCCATTCCAGT 190

QY 125 GCGCCGCGTGCCTCTCTCGCTTAGTCTCCGCGCAACGCCCTTCGTAGGCGTTTCT 184

Db 191 GTCCCGGTGTGCGCTCTCTCGCTCAACCGCAACGCCCTTCGAGAGCTTCCT 250

QY 185 ACTCCAATGTCTCCAGGAGATCTTCATCCAGCAAGGAAGGGATCTTTGGGTGATAT 244

Db 251 ACACCAACGCTCCCGAGGAGATCTACATCAACAAGGTAGTGTATTTTGGCATGAT 310

QY 245 TCCTCGTTGTCTTAGACATATGAAGAGCCTCACACAAGGTGCTGATCTCAGTCCC 304

Db 311 TCCCGGTGTCTTAGACATTTGAAGAGCCT----- 342

QY 305 AAAGACCACCAAGACGCTCTCCAGGAGAGAACCAAGCCAAACAGACAGATAGTCACC 364

Db 343 -----CAACAAAAGGACAAAGCAGCAGCGCCCAAGACCGTCACC 382

QY 365 AGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTCAGTTCACCGGTTCGTTCTTCT 424

Db 383 AGAGATCTATCACTTCAGAGAGGGTGATTGATTCAGTGCACACCGGTTTGCATACT 442

QY 425 GGCTCTAACACGACACGACACTGTATGTTGTTGCTGTTCTTCTTACTGACACCAACA 484

Db 443 GGATGTACAAACATGAAGACACTCTCTGTTGTCGCTTCTCTTATTGACACCAACAGCT 502

QY 485 ACACAACACGCTTGATCAGTTCCTCCAGGAGATTCAATTTGGCTGGGAACACCGGCAAG 544

Db 503 TCCAGAACGAGCTCGACCATGCTTAGGAGATTCTATCTTCTGGGAACCAAGAGCAAG 562

QY 545 AGTTCTTAAGGTACACAGCAACAAAGCAGACGAAGAGCAGCAAGCTTACCATATAGCC 604

Db 563 AGTTCTACAGTATCAGCCACAGACGACGACGAG----- 595

QY 605 CATAAGCCCGCAAAAGTTCAGCTTAGACAAGAGAGCGTGAAATTTAGCCCTCGAGGACAG 664

Db 596 -----GAGGTACTC 604

QY 665 ACAGCCGACAGAACGAGCAGGACAGAAGAAACCAAGGTGGAACATCTTTCAGCG 724

Db 605 AAAGCCAGAAAGGAAAGCGTTCAGCAAGAGAAAGAAACCAAGGAGGACGATATTGAGTG 664

QY 725 GCTTCACGCGGAGTTCTCGGAACAGCCTTCAGGTTTCCAGGTTTCCAGACACAGATAGTCAAA 784

Db 665 GCTTCGCCCCGGAATTTCTTGGAACTGCGTTC---GTCGTGGACAGCGCAGATAGTGAA 721

QY 785 ACCTAAGAGCGGAGACCGGAGAGTGAAGAGAGGAGGCCATTTGTACAGTGTAGGGGAGGCC 844

Db 722 ACCTACAGCTGAGAACGAGGAGAGAGAGGGTCCATTGTGACAGTGAAGAGGTC 781  
Qy 845 TCAGAACTTTGAGCCAGATAGAAAGAGACGTCGCCAGCAAGAGAGGAAATACGATGAAG 904  
Db 782 TCAGCGTGATAAGCCACCACCGAAGAGCAGCAACAAGACCCGAGGAGAGGAGAAGC 841  
Qy 905 ATGAATATCAATACGATGAGAGGATAGAGGGGTGGCAGGGGAGCAGAGCGAGGGA 964  
Db 842 CAGATTGTACAGAGAAAGCAACAT- - - - -TGCCAAAGCCAAAGCAGAA 886  
Qy 965 ATGGTATTGAAGAGACGATCTGCACCGCAAGTGTCTAAAAAGAACATTGGTAGAAACAGAT 1024  
Db 887 ATGGCATTTGACAGACCATTTGCACATGAGACTTCGCCACACATTTGCCAGACTTCAT 946  
Qy 1025 CCCTGACATCTACAAACCTCAAGCTTGTTCTACTCAAACTGCGCAACGATCTCAACCTTC 1084  
Db 947 CACCTGACATCTCAACCTCAAGCTGGTAGCATCACAACCGCTACCGCTCGACTTCG 1006  
Qy 1085 TAATACTTAGTGGCTTGGACCTAGCTAGTCTGAATATGGAATCTCTACAGGAATGATTGT 1144  
Db 1007 CAGCCCTCTCGTGGCTCAAACTCAGTGCCTGAGTTGGATCACTCCGCAAGAAATGCTATGT 1066  
Qy 1145 TTGTGCTCACTACAAACACCAACGACACAGCATCATATATCGATTGAGGGGACGGCTC 1204  
Db 1067 TCGTGCCACACTACAACTGACGCAACAGCATATATACGATTGAATGAGCGGCAT 1126  
Qy 1205 AGTGCAAGTCTGTGGACAGCAACGCGCAACAGAGTGATGACGAGGAGCTTCAAGAGGTC 1264  
Db 1127 TGTACAAGTGGTGAATTCGAATGGTGAGAGAGTGTTCATGAGAGCTGCAAGAGGGAC 1186  
Qy 1265 AGTGCTTTGGTGCCACAGAACTTCGCGTGCCTGGAAGTCCAGAGCGGAACTTCG 1324  
Db 1187 AGTGTTAAATTTGGCCACAAACTTTTCGCTGCTGCAAGATCAGAGCGCAACTTCG 1246  
Qy 1325 AATACGTGCATTCAAGACAGACTCAAGGCCAGCATAGCAACCTTCGCGGTGAAAAC 1384  
Db 1247 AGTATGTTTCATTCAGACCAATGATAGACCTCGATCGCAACCTTGACGTTGCAACT 1306  
Qy 1385 CCGTCATAGATAACCTGCGGAGAGGAGTGTTCGCAAAATCATATGCGCTCCAAAGGAGC 1444  
Db 1307 CATTTGTTAAACGATTGCGGAGAGAGTGAATCAGCAAACTTTTAACTTAAGGAGGCAGC 1366  
Qy 1445 AGCAGGAGCTTAAAGCAACACCCCTTCAAGTCTTCGTTCCACCGTCTCAGCAGT 1504  
Db 1367 AGCCAGGAGGTCAGAAACAAACCCCTTTCAGTCTTCCTGTTCCACCTTAAGAGTCTC 1426  
Qy 1505 CTCGAGGGCTGTGGCTTA 1523  
Db 1427 AGAGGAGAGTTGTGGCTTA 1445

RESULT 12  
US-10-757-667-13

; Sequence 13, Application US/10/757667  
; Publication No. US20040139504A1  
; GENERAL INFORMATION:  
; APPLICANT: ANTHONY JOHN KINNEY  
; GARY MICHAEL FADER  
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC  
; CLASSES OF SOYBEAN SEED  
; PROTEIN GENES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/757,667  
; FILING DATE: 14-Jan-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/758,652  
; FILING DATE: 11-Jan-2001  
; APPLICATION NUMBER: 60/019,940  
; FILING DATE: JUNE 14,1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LYNNE M. CHRISTENBURY  
; REGISTRATION NUMBER: 30,971  
; REFERENCE/DOCKET NUMBER: BB-1071-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-5481  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1446 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
; US-10-757-667-13

Query Match 34.0%; Score 517.4; DB 8; Length 1446;  
Best Local Similarity 62.8%; Pred. No. 3.2e-154;  
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;  
Qy 5 AGCAACCGGAGGAGAACGGTCCAGTTCAGCGCTCAATGCGAGAGACCTGACAATC 64  
Db 71 AGCAGCCAGCAAGAAACGAGTGCCAGATCCAGCCTCAATGCCCTTAACCCGATTAAC 130  
Qy 65 GCATTGAATCAGAGGGCGGTTACATTGAGACTTTGGAACCCCAACACAGGAGTTGGAAT 124  
Db 131 GTATAGATCAGAGGTGGCTTCATTGAGACATGGAACCTTAACAACAAGCCATTCCAGT 190  
Qy 125 GGGCCGGGTGGCCCTCTCTCGTTAGTCTTCGCGCGCAAGCGCCTTCGTAGCGCTTCT 184  
Db 191 GTGCCGGTGTGGCCCTCTCTCGCTGCACCTCAACCGCAACGCCCTTCGCAGACCTTCCT 250  
Qy 185 ACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAGGAGATCTTTGGGTGATAT 244  
Db 251 ACACCAACGCTCCCGAGGAGATCTATCCAAACAGGTAGTGTATTTTGGCATGATAT 310  
Qy 245 TCCCTGGTTGTCTTAGACACTATGAAGAGCCTCACACAAAGGTGCTGATCTCAGTCCC 304  
Db 311 TCCCGGTTGTCTTAGACACTATTTGAAGAGCCT- - - - - 342  
Qy 305 AAAGACCAACAGACGCTCTCCAGGAGAGAACCAAGCCCAACAGCAACGAGATAGTCACC 364  
Db 343 - - - - -CAAAAAAGGACAAAGACAGCAGCGCCCAAGACCGTCACC 382  
Qy 365 AGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTCAGTTCCACCGGTGGTCTTCT 424  
Db 383 AGAAGATCTATCACTTCAGAGAGGGTGATTGATTGAGTGCACCGGTTCGATACT 442  
Qy 425 GGCTCTACAAACGACACGACACTGATGTTGTTGCTGTTCTTCTTACTGACACCAACA 484  
Db 443 GGATGTACAACAATGAAGACACTCCTGTTGTTGCGGTTTCTCTTATTGACACCAACAGCT 502  
Qy 485 ACAGAACCGAGTTGATCAGTTCGCCAGGAGATTCATTTGGCTGGGAACACCGAGCAAG 544  
Db 503 TCCAGAACCCAGCTCGACCAAGATGCCCTAGGAGATTTCTATCTTGTCTGGGAACCAAGAGCAAG 562  
Qy 545 AGTTCCTTAAGGTACCAAGCAAAAGCAGACAGCAAGAGAGCTTACCATATAGCC 604  
Db 563 AGTTCTTACAGTATCAGCCACAGACGACGACG- - - - - 595  
Qy 605 CATACAGCCCGCAAAAGTCCAGCTTAGACAGAGCGGTGAATTTAGCCCTCGAGGACAGC 664  
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Db 969 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCAACACCGCTACCAGCCTCGACTTCC 1028
Qy 1085 TAATACCTAGGTGGCTTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCATTGT 1144
Db 1029 CAGCCCTCTCGTGGCTCAAACTCAGTGGCCCGAGTTGGATCAGTCCGCAAGATGCTATGT 1088
Qy 1145 TTGTGCTCACTACAAACCAACGACACAGCATCATATATCGAATGAGGGGACGGGCTC 1204
Db 1089 TCGTGGCCACACTCAACCTGAACGCAACAGCATATATACGCATTGAATGGACGGGCAT 1148
Qy 1205 ACGTGAAGTCGTGGACAGCAACGGCAACAGAGTGTACGAGGAGCTTCAAGAGGGTC 1264
Db 1149 TGGTACAAGTGGTGAATTTGCAATGGTGAGAGAGTGTGTTGATGGAGAGCTCAAGAGGGAC 1208
Qy 1265 ACGTGTCTGTGGTGGCCACAACTTCGCGCTGGTGGAAAGTCCAGAGCGCAACTTCG 1324
Db 1209 AGGTGTTAATGTGGCCCAAACTTTTCGGTGGTGCAGATCAGAGAGCGCAACTTCG 1268
Qy 1325 AATACGTGGCAATCAAGACAGACTCAAGGCCAGCATAGCCAACTCGCGGTGAAAAC 1384
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Qy 1385 CCGTCATAGATAACCTGCGGAGAGGTGGTGGCAATTCATATGGCTCCAAAGGAGC 1444
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Qy 1445 AGCGAGGAGCTTAAAGCAACAAACCCCTTCAAGTTCCTGTTCCACCGTCTCAGCAGT 1504
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Qy 1505 CTCGAGGGGCTGTGGCTTA 1523
Db 1449 AGAGGAGAGTTGTGGCTTA 1467
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## RESULT 15

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US-10-425-114-8531
; Sequence 8531, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8531
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700757865_PLI
US-10-425-114-8531
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Query Match 34.0%; Score 517.4; DB 8; Length 1689;
Best Local Similarity 62.8%; Pred. No. 3.4e-154;
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;
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Db 105 AGCAGGCACACGAAAACGAGTGCAGATCCAAAGCGCTCAATGGCTCAAAACCGGATAACC 164
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Db 165 GTATAGAGTCAGAGGTGGCTTCATTGAGAGCATGGAAACCCCTAACAAAGCCATTCAGT 224
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Qy 125 GCGCGGCGTGGCGCTCTCTCGCTTAGTCTCTCGCGCGCAACGCCCTTCGTAGCCCTTTCT 184
Db 225 GTGCGGCTGTGCGCTCTCTCGCTGACCCCTCAACCGCAACGCCCTTCGAGACCTTCTCT 284
Qy 185 ACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATACTTTGGGTGATAT 244
Db 285 ACACCAACGCTCCCGAGGAGATCTACATCCAACAGGTAGTGGTATTTTGGCATGATAT 344
Qy 245 TCCTCGTGTGCTAGACACTATGAAGAGCCTCACACACAAGGTCTCGATCTCAGTCCC 304
Db 345 TCCCGGTTGTCTAGCACATTTTGAAGAGCT----- 376
Qy 305 AAAGACCAACAAAGACGCTCTCAAGGAGAGAACCAAGCCAAACAGCAACAGATAGTCACC 364
Db 377 -----CAACAAAAGGACAAAGCAGCAGCGGCCCAAGACCGTCACC 416
Qy 365 AGAAGTGCACCGTTTCGATGAGGGTGATCTCATTCAGTTCCACCGGTGTGCTTTCT 424
Db 417 AGAAGATCTATCACTTTCAGAGAGGGTGATTTGATTCAGTGCACCGGTTTTCATCT 476
Qy 425 GGCTCTACAAACGACCAACGACACTGATGTTGTTGCTGTTCTTCTTACTGACACCAACA 484
Db 477 GATGTACAACAATGAAGACACTCTCTGTTGTCGCTTCTCTTATTGACACCAACAGCT 536
Qy 485 AGCAACACAGCTTGATCAGTTCCCAGGAGATTTCAATTTGGCTGGGAACACGAGCAAG 544
Db 537 TCAGAAACAGCTCGACAGATGCTCTAGGAGATTCTATCTTGTGGGAACCAAGAGCAAG 596
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Qy 605 CATACAGCCCGCAAGTTCAGCTCAGTACAGAAAGAGCGTGCAATTTAGCCCTTCGAGGACAG 664
Db 630 -----GAGGTACTC 638
Qy 665 ACAGCCGACAGAAACGAGCAGGACAAAGAAAGAAACGAAAGGTGAAACATCTTCAGCG 724
Db 639 AAAGCCAGAAAGGAAAGCGTCAGCAAGAAAGAAAGAAACGAAAGGAGCAGCATATTCAGTG 698
Qy 725 GCTTCAGCGCGGAGTCTCTGGAACAAAGCCTTCAGGTTGACGACACACAGATAGTCAAA 784
Db 699 GCTTCGCGCCGGAATTTCTTGGAAACATGCGCTTC--GTCGTGACACAGGCAAGATAGAGAA 755
Qy 785 ACTTAAGCGCGAGACCGAGAGTGAAGAGAGAGGAGCGCATTTGTACAGTGAAGGAGGCGC 844
Db 756 AGCTACAGGTGAGAAACGAGAGAGAAAGAGAGAGGTTGCCATTGTGACAGTGAAGAGGTC 815
Qy 845 TCAGAACTTTGAGCCCGACATAGAAAGAGACGTGCGCAGCAAGAAAGAGGAATACGATGAAG 904
Db 816 TCAGCGTGATAAGCCCAACCGAAGAGCAGCAACAAAGACCCGAGGAAGAGGAGAAGC 875
Qy 905 ATGAATATGAATACGATGAAGAGGATAGAAAGCGGTGGCAGGGAAGCAGAGCGAGGGGA 964
Db 876 CAGATTGTGACGAGAAAGACAAACAT-----TGCCAAAGCCCAAGACAGAA 920
Qy 965 ATGGTATTGAAGAGACGATCTGCACCGCAAGTGCTAAAAAGAAACATTTGGTAGAAACAGAT 1024
Db 921 ATGGCAATGACGAGACCATTTGCACAAATGAGACTTCGCCACAAACATTTGCCAGACTTCAT 980
Qy 1025 CCCCTGACATCTACAAACCCCTCAAGCTGGTTCTACTCAAAACTGCCAACGATCTCAACCTTC 1084
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Qy 1085 TAATACTTAGTGGCTTGGACCTAGTGTGAATATGGAATCTCTACAGGAATGCATTCT 1144
Db 1041 CAGCCCTCTCGTGGGTCAAACTCAGTGGCCAGTTGGATCTCCGCAAGAAATGCTATGT 1100
Qy 1145 TTGTGCTCACTACAACACCAACGACACAGCATCATATATCGATTTGAGGGGACGGGCTC 1204
Db 1101 TGTGCCACACTACAACCTGAACGCAACAGCATATATACGCATTTGAATGACGGGCAT 1160
Qy 1205 ACGTGCAAGTCTGGGACAGCAACCGCAACAGAGTGTACGAGGAGAGCTTCAAGAGGGTC 1264
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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 18:21:18 ; Search time 33.1692 Seconds  
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Title: US-10-728-051-3

Perfect score: 1524

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications\_NA\_New.\*
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  - 2: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
  - 3: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
  - 4: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
  - 5: /EMC\_Celerra\_SID33/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
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  - 7: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
  - 8: /EMC\_Celerra\_SID33/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	33.7	1746	6	US-10-953-349-13162 Sequence 13162, A
2	504	33.1	1711	6	US-10-953-349-13154 Sequence 13154, A
3	354.4	23.3	1247	6	US-10-953-349-21829 Sequence 21829, A
4	170.4	11.2	1768	6	US-10-449-902-7351 Sequence 7351, Ap
5	168.4	11.0	1764	6	US-10-449-902-9966 Sequence 9966, Ap
6	160.6	10.5	1586	6	US-10-449-902-9937 Sequence 9937, Ap
7	145	9.5	1655	6	US-10-449-902-9923 Sequence 9923, Ap
8	137	9.0	1650	6	US-10-449-902-9995 Sequence 9995, Ap
9	137	9.0	1667	6	US-10-449-902-9890 Sequence 9890, Ap
10	133	8.7	1654	7	US-11-284-201-4 Sequence 4, Appli
11	107.2	7.0	1796	6	US-10-449-902-7968 Sequence 7968, Ap
12	44.8	2.9	1478	6	US-10-449-902-3323 Sequence 3323, Ap
13	40.4	2.7	261789	7	US-11-260-842-1 Sequence 1, Appli
14	40.2	2.6	1364	6	US-10-449-902-152 Sequence 152, App
15	40	2.6	1632	7	US-11-217-529-76067 Sequence 76067, A
16	39.4	2.6	760	6	US-10-953-349-10687 Sequence 10687, A
17	39	2.6	1725	6	US-10-449-902-18435 Sequence 18435, A
18	38.6	2.5	4316	6	US-10-517-441-9 Sequence 9, Appli
19	38.4	2.5	4316	6	US-10-517-441-537 Sequence 537, App
20	38.2	2.5	1987	6	US-10-449-902-28281 Sequence 28281, A
21	38.2	2.5	2185	6	US-10-449-902-6132 Sequence 6132, Ap
22	38	2.5	1977	7	US-11-217-529-647 Sequence 647, App
23	37.8	2.5	866	6	US-10-449-902-16667 Sequence 16667, A
24	37.8	2.5	1170	6	US-10-953-349-32139 Sequence 32139, A
25	37.8	2.5	1511	6	US-10-449-902-11220 Sequence 11220, A

ALIGNMENTS

RESULT 1

US-10-953-349-13162  
; Sequence 13162, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13162  
; LENGTH: 1746  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-953-349-13162

Query Match 33.7%; Score 513; DB 6; Length 1746;  
Best Local Similarity 62.7%; Pred. No 7.8e+149;  
Matches 968; Conservative 0; Mismatches 425; Indels 150; Gaps 5;

QY	5	AGCAACCGGAGAGAA	CGCGTCCAGTTC	CGCGCTCAATCGCGAGACCTGACAATC	64
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QY	65	GCATTGATCAGAGCG	GGTTACATTGAGACTTGGNAACCCCAACACACAGGAGTTCGAAT	124	
DB	185	GTATAGATCAGAAGG	AGGGCTCATTTGACATGGAACCCCTTAACAACAGCCATTCAGT	244	
QY	125	GGCGCGCGCTCGCCCT	CTCTCGCTTAGTCTCGCGCAACGCCCTTCGTAGGCCCTTCT	184	
DB	245	GTGCGCGTGTGCCCT	CTCTCGCTGACCCCTCAACCGCAACGCCCTTCGTAGACCTTCT	304	
QY	185	ACTCAATGCTCCCAG	GAGATCTTCATCCAGCAAGGAAGGGGATACTTTGGTTCATAT	244	
DB	305	ACACCAACCGTCCC	CAGGAAATCTACATCCAAACAGGTAAAGGTATTTTGGCATGATAT	364	
QY	245	TCCTTGGTGTCTAG	ACATATGAGAGCCTTCACACAAAGTCTCGATCTCAGTCCC	304	
DB	365	ACCCGGTGTCTTAG	CAACATTTGAAGACCTCA-----	398	
QY	305	AAAGACCAACCAAG	AGCTCTCCCAAGGAGAGACCAAGCCCAACGAGACGAGATAGTCACC	364	
DB	399	-----	-----ACNACCTCAACAAGAGGACAAAGCAGACACCAAGACCGTCACC	445	
QY	365	AGAAGGTGACCGTT	TCGATGAGGTGATCTCATTTGCAGTTCCCAACCGGTGTTGCTTCT	424	

Db 446 AGAAGATCTATACTTCAGAGAGGGTGAATTTGATCGCAGTGCCTACTGTGTTCATGGT 505  
Qy 425 GGCTCTCAACAGCAGCAGACATGATGTGTGCTGTCTTACTGACCAACAACA 484  
Db 506 GGATGTACAACAATGAAGACACTCCTGTGTGTCGCGTTTCTATTATTGACACCAAGCT 565  
Qy 485 ACACAAACAGCTTGATCAGTTCCTCCAGGAGATTCATTTGGCTGGGAACACGAGCAAG 544  
Db 566 TGGAGAACCCAGCTCGACAGATCCCTAGGAGATTCTATCTGTCTGGGAACCAAGAGCAAG 625  
Qy 545 AGTTCTTAAGGTACCAGCAACAAGCAGACAAAGCAGACGAAGAAGCTTACCATATAGCC 604  
Db 626 AGTTCTTAATAATACGAAGAG----- 648  
Qy 605 CATACAGCCCGCAAAGTTCAGCTTAGACAAAGAAGAGCGTGAATTTAGCCCTCGAGGACAGC 664  
Db 649 -----CAAGGAGGTCAATC 661  
Qy 665 ACAGCCGACAGAAACGAGCAGGACAAAGAAGAAACGAGAGTGGAAACATCTTCAGCG 724  
Db 662 AAAGCCAGAAAGGAAGCATFCAGCAAGAAAGAAACGAAAGGAGCGCATATTGAGTG 721  
Qy 725 GCTTCAGCCGCGAGTTCTCGAAACAAGCCTTCCAGGTTGACGACACAGACATAGTGCAAA 784  
Db 722 GCTTCACCTCGAATCTTGGAAACATGCTTACAGCT---GGACAAGCAGATAGCGAAA 778  
Qy 785 ACTTAAGAGCGAGACGAGAGTGAAGAAGAGGAGGCCATTGTGAAGTGAAGGGAGGCC 844  
Db 779 ACCTAAGAGAGAAACGAAGGGAGAGACAAGGGAGCCATTGTGACAGTGAAGAGGAGT 838  
Qy 845 TCAGATCTTGAGCCCA-----GATAGAAGAGAGCGTGGCGACGAGAGAGGAAT 895  
Db 839 TGAGCGTGATAAAACCAACCACCGAGCAGCAGCAACAAGACCCCGAGGAAGAGAAAG 898  
Qy 896 ACCATGAAGATGAATA-----TGAATACGATGAAGAGGTAGAAGCGCGTG 940  
Db 899 AAGAAGAGATGAAGACCCACAGTGCNAGGTTAAGACAAACACTGCCAACGCCCGGAG 958  
Qy 941 GCAGGGGAAGCAGAGGAGGGGGAATGGTATTGAAGAGAGCATCTGACCGCAAGTGCTA 1000  
Db 959 GAAGCCAAAGAAAGCAGAAAGAAATGGCATTCAGCAGACCATATGCACCATGAGACTTC 1018  
Qy 1001 AAAGAACATTTGTAGAAACAGATCCCTCAGATCTACACCCCTCAAGCTGTTCACTCA 1060  
Db 1019 GCCACAACATTTGCCAGACTTCATCACCCTGACATCTACAAACCCTCAAGCCGGTAGCGTCA 1078  
Qy 1061 AAAGTCCCAACGATCTCAACCTTCTAATACCTTAGTGGCTTGACCTAGTGTCTGAATATG 1120  
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Qy 1121 GAAATCTCTACAGGAATGCAATTTGTTGCTCACTACAAACCAACAGCAACAGCATCA 1180  
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Qy 1241 ACCACGAGGAGCTTCAAGAGGGTCACTGTCTTGTGTGGCCACAGAACTTCGCCGTGCGTG 1300  
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Qy 1301 GAAAGTCCACAGGAGGAATTCGAATACGTGGGATTCAGACAGACTCAAGGCCAGCA 1360  
Db 1319 CAAGATCACAGAGTGACAACTTCGAGTATGTGCTTCAAGACCAATGATACACCCATGA 1378  
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Qy 1421 ATTATATGCGCTTCAAGAGGAGCAGCAAGGAGCTTAAAGAAACAACCCCTTCAAGT 1480

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Db 1499 TCTGTGTTCCACCTCAGGAGTCTCAGAAGAGAGCTGTGGCTTA 1541  
RESULT 2  
US-10-953-349-13154  
; Sequence 13154, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13154  
; LENGTH: 1711  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-953-349-13154  
Query Match 33.1%; Score 504; DB 6; Length 1711;  
Best Local Similarity 62.0%; Pred. No. 4,7e-146;  
Matches 943; Conservative 0; Mismatches 450; Indels 129; Gaps 4;  
Qy 5 AGCAACCGGAGAGAACGCGTCCAGTTCAGCGCTCAATGCGAGAGACCTTGACAATC 64  
Db 106 AGCAGCCACAGCAAAATGAGTCCAGATCCAAAAGCTGAATGCCCTCAAAACCGATAACC 165  
Qy 65 GCATTGAATCAGAGGCGGTTCATTGAGACTTTGAAACCCCAACCAACAGGAGTTGCAAT 124  
Db 166 GTATAGAGTCGGAAGGTGGTTCATTGAGACCTGGAACCTTAACAACAGCCATTCAGT 225  
Qy 125 GCGCGGCGTCCGCTCTCTCGTTCAGTTCCTCGCGCAACGCCCTTCGTAGCCCTTTCT 184  
Db 226 GTGCGCGTGTGCTCTCTCGCTGACCTTTAAACGCAATGCCCTTCGTAGACCTTCCT 285  
Qy 185 ACTTCAATCTCCAGAGGATCTTCATCCAGAGGAAGGGGATACCTTTGGTTGATAT 244  
Db 286 ACACCAACCGTCCCGAGGAATCTACATACACNAGGTAATGTAATTTTGGCATGATAT 345  
Qy 245 TCCCTGGTTGCTTAGACACTATGAAGAGCTTCACACAAGGTCTCGATCTCAGTCCC 304  
Db 346 TCCCGGTTGTCTTAGCACTTATCAAGAGCCGA----- 379  
Qy 305 AAAGACCACCAAGACGTCTCCAGGAGAGAACCAAGCCCAACAGCAACGAGATAGTCACC 364  
Db 380 -----AGAACTCTCAGAACAGGAGAGAACCCAGAGGCCCAAGACCCGTACC 426  
Qy 365 AGAAGGTGACCGTTTCGATGAGGGTGATCTCATTTGCACTTCCACCGGTGTGCTTTCT 424  
Db 427 AAAAGGTACATCGTTTCAGAGAGGGTGATTTGATCGCAGTGCCTACTGTTGTCATGT 486  
Qy 425 GGCTCTAACAGCAGCAGACATGATGTTGTTGCTGTTTCTCTTACTGACCAACAACA 484  
Db 487 GGATGTACAAACAATGAAGACACTCTCTGTTGTTGTCGCTTTCTATTATTGACCAACAGCT 546  
Qy 485 ACACAAACAGCTTGATCAGTTCCTCCAGGAGATTCATTTGGCTGGGAACACGAGCAAG 544  
Db 547 TGGAGAACAGCTCGACAGATGCTTAGAGATTTCTATCTTCTGCTGGAAACCAAGAGCAAG 606  
Qy 545 AGTTCTTAAGGTACCAGCAACAAGCAGACAAAGCAGACGAAGAAGCTTACCATATAGCC 604  
Db 607 AGTTCTTAATAATCAGCAGCAG----- 629  
Qy 605 CATACAGCCCGCAAGTTCAGCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGACAGC 664  
Db 630 -----CAGCAAGGAGGTT 642



Db 900 AGAAGAGGATGAGAGCCACAGTGCAGGGTAAAGCAACACTGCCAAGCCCCCG 959  
QY 939 TGGCAGGGAAGCAGAGCGAGGGGAATGGTATTTGAAGAGAGCATCTGCACGCGCAAGTGC 998  
Db 960 AGGAAGCCAAAGCAAGCAGAAGAAATGGCAITTGACGAGACCATATGACCATGAGACT 1019  
QY 999 TAAAAAGAACATTGGTAGAAACAGATCCCTGTGACATCTACAAACCCCTCAAGCTGGTTCACT 1058  
Db 1020 TCGCCACAACATTGGCCAGACTTTCATCCTGTGACATCTCAACCCCTCAAGCCGTAGCGT 1079  
QY 1059 CAAAACTGCCAAGATCTCAACCTCTTAATACCTTAGTGTGGACCTAGTGTCTGAATA 1118  
Db 1080 CACAACCGCACACGAGCTTGAATCCAGCCCTCTCGTGGCTCAGACTCAGTGTGAGTT 1139  
QY 1119 TGGAAATCTCTACAGGAATGATTTGTTGTGCTCACTACAAACCAACGACACAGCAT 1178  
Db 1140 TGGATCTCTCCGCAAGATGCAATGTTCTGTGCCACACTCAACCTGAACGCGAAGCAT 1199  
QY 1179 CATATATCGATTGAGGGAGCGGCTCACGTGCAAGTCTGGACAGCAA 1226  
Db 1200 AATATATGCAATTGAATGGAGCGGCATTGATACAAGTGGTGAATTGCAA 1247

## RESULT 4

US-10-449-902-7351  
; Sequence 7351, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7351  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK064478  
; DATABASE ENTRY DATE: 2001-12-06  
US-10-449-902-7351

Query Match 11.2%; Score 170.4; DB 6; Length 1768;  
Best Local Similarity 48.6%; Pred. No. 1.1e-42;  
Matches 661; Conservative 0; Mismatches 671; Indels 28; Gaps 6;

QY 113 AGAGTTTGAATGGCGCGGCTCGCCCTCTCTCGTTAGTTCCTCGCGCGCAAGCCCTTC 172  
Db 244 ATGAGTTCCGTTGTGCGGAGTGAGCGTGAGGGCTTAGTCTGTCGAGAGCAAGGGCTTAG 303  
QY 173 GTAGGCTTTCTACTCAATGCTCCCGAGGATCTTCATCCAGCAAGGAAGGGGATACT 232  
Db 304 TTTTACCAATGTATGTAAATGCTCACAAAGTTGTCTACATCGTCCAAAGGTGCGGGAGTGT 363  
QY 233 TTGGGTTGATATTCCTCGTTGTCCTAGACACTATGAAGAGCCCTCACACAAGAGTCTGTC 292  
Db 364 TTGGATGGCACTCCCTGGTTGTCC-----AGAGCGTTCCAGTCAGTTAGGT 411  
QY 293 GATCTCAGTCCAAAGACACCAAGAGCTCTCCAGAGAGGAAGCAAGCAACAGCAAC 352  
Db 412 CTCCTTTTGACGAAGAGGTGGCAACAGCTGGTGGGCTCAATCATCAATCCAAAAATGA 471  
QY 353 GAGATAGTCAACAGAGGTGCACCGTTTCGATGAGGGTGATCTCATTTGCAAGTTCACACCG 412

Db 472 GAGACGAGCACAGCAACTTCCACAGTTCACCAAGGTGATGTAATCGCAGTGCACAGTGC 531  
QY 413 GTGTTGCTTTTGGGCTTCTACAAAGCAGCAGCACTGATGTTGTGCTGTTTCTCTTACTGC 472  
Db 532 GAGTAGCCCACTGGCTTACATAAATAATGGTGATTCCTCTGTGGTTGCTTTCACTGTCTATCG 591  
QY 473 ACACCAACAAACAGCAACAGCTTGTATCAGTTCCTCCAGGAGATTC--AATTTGGCTGG 530  
Db 592 ACACGAGCAACAATGCCAACCCAGCTCGATCTCTAAAGAAAGGGTATGCGTACATATGCTCC 651  
QY 531 GAAACGCGAGCAAGAGTTCCTTAAGGTACCCAGCAACAAAGCAGACAAAGCAGACGAGAAG 590  
Db 652 ACACAAGCATATGATATTCATATCACTATTTTGAATTCATGATAACAATACTCTAA 711  
QY 591 CTTTACATATAGCCCATACAGCCCGCAAGTCAAGCTTAGACAAGAGACGCGTGAATTTAG 650  
Db 712 TGTGTATTTGTATCTATGAAATGATAAATGGGTTAGGAGTTTTTCTTGGCTGGAAGCCT 771  
QY 651 CCTCGAGGACAGCAGCGCGCAGAGAACGACGAGACAAGAGAAAGAAACGAAGGTGG 710  
Db 772 AGAAGTAGCTGGCAGCAGCAATCGTACTCATACCAGAC--AGAACAACTGAGCAGAAATCA 830  
QY 711 AAACATCTTTCAGCGGCTTCACGCGGAGTTCCTGGAAACAAGCCTTCCAGGTTGACGACAG 770  
Db 831 GAACATCTTTGCTGGTTCAGCCAGATTTACTTCTGAAGCCCTGAGTGTGAGCAAGCA 890  
QY 771 ACAGATAGTGTCAAAACCTTAAGAGGCGAGACCAGAGTGAAGAGAGGGAGCATTGTGAC 830  
Db 891 AACTGTGTTGAGGCTCCAAG-----CCTGAGTGAACCAAGAGGTGCCATCATTTAG 941  
QY 831 AGTGGGGGAGGCTCAGAACTCTTGAGCCAGATAGAGAAGACGCTGCCGACGAAGAACA 890  
Db 942 AGTTGAAATGGGCTCCAGGCACTGAGCCCTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1001  
QY 891 GGAATACGATGAAGATGAATATGAATACGATGAAGAGGATAGAAG---CGTGGCGAGGG 947  
Db 1002 ACACACCCCAAGCTTACTTGCACCAAGCAGCTACAGCCCACTGCTGTTCCGAAGTGGTG 1061  
QY 948 AAGCAGAGCAGGGGAATGGTATTTGAAGAGAGCATCTCAGCCGCAAGTGTCTAAAAAGAA 1007  
Db 1062 AGCTTGGCGGCAGCAAAATGCTCTAGATGAAATTTATGTGTGATTTAAGTTGAGGAAGAA 1121  
QY 1008 CATTTGTGAAACAGATCCCTGACATCTACAACCCCTCAAGCTGGTTCACTCAAAAATCTC 1067  
Db 1122 CATAGACAACCACAAATCCAGTGACATATTAACCCCACTGTTGGAAGGATCACAGGGC 1181  
QY 1068 CAACGATCTCAACCTTTCTAATCTTAGTGGCTTGGACCTTAGTGTGAATATGGAATCT 1127  
Db 1182 CAATAGCCAGAATTTCCCAATATCTCAATATCATCCAGATGAGTGCACCCAGAAATCTCT 1241  
QY 1128 CTACAGGAATGATTTGTTGTGCTCCTACATAACACCAAGCAGCAGCATCATATATCG 1187  
Db 1242 CCAAAAATAATGCTTGTCTTACTCTCTATTTGGACGGTAAACGACACACCGGTGATGACGT 1301  
QY 1188 ATTTGAGGACGGGCTCAGTGCAGTCTGTGACACAAACGCGCAACAGAGTGTACGACGA 1247  
Db 1302 GACCGTGGCCAAAGGCGACATCCAGTGTGATACCGTGTGAGTGTCTTTGATGG 1361  
QY 1248 GGAGCTTCAAGAGGGTCACTGCTTGTGTGCCACAGAACTTCGCGCTCGCTGGAAGTC 1307  
Db 1362 TGAGCTTCCCAACAGCAGATCTTGTGTGATCCACAGAACTTTGCACT--GGTGTGAAGGC 1420  
QY 1308 CAGACGAGAGACTTCGAATACGTGCATTCAGACAGACTCAAGGCCAGCATAGCCAA 1367  
Db 1421 TCAGCTGAAGGATTTGCAATGGGTATCTCTCAAGACCAATCAATGCTGTCTGACAGTCA 1480  
QY 1368 CTTGCGCGGTGAAACCTCGCTCATAGATAACCTGCGCGAGGAGGTGGTTGCAAAATTCATA 1427  
Db 1481 GATCGCAGGAGGCGCTCCATTTCTGCTCTACCGTTGACGTGTGCGCAATGCTTA 1540  
QY 1428 TGGCTTCCAAAGGAGCAGGCAAGGCGCTTAAGAAACAAC 1467



Db 1327 CAAACCCTAACTCTATGGTAAGCCACATTGCAGGAAAGAGTTCATCTTCCGTGCTCTCC 1386

QY 1403 CCGAGGAGTGGTTCGCAATTCATATGGCTCCATAGGGAGCAGGCAGCTTAAGA 1408

Db	1387	CAACTGATGTTCTAGCAAAATGCATATCGCATCTCAAGAGAAGAGGCTCAGAGGCTCAAGC	1446
Qy	1463	ACAACA	1468
Db	1447	ATAACA	1452

RESULT 6  
US-10-449-902-9937

; Sequence 9937, Application US/10449902  
; Publication No. US20060123505A1

; GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

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; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
;

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; CURRENT FILING DATE: 2003-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-20

; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11

; PRIOR FILING DATE: 2002-12-11  
 ;  
 ; NUMBER OF SEQ ID NOS: 56791  
 ;  
 ; SOFTWARE: PatentIn Ver. 2.1

COLL: JMW. PULLEN: VET. 2.1  
; SEQ ID NO 9937  
; LENGTH: 1586

/ **Accession:** 1300  
 / **TYPE:** DNA  
 / **ORGANISM:** *Oryza sativa*

:  
 : PUBLICATION INFORMATION:  
 : DATABASE ACCESSION NUMBER: AK107285

US-10-449-902-9937  
DATABASE ENTRY DATE: 2002-08-28

Query Match 10.5%; Score 160.6; DB 6; Length 1586;

Best Local Similarity 56.8%; Pred. No. 1.2e-39;  
Matches 295; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 950 GCAGAGGCAGGGGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGCTAAAAAGAACA 1009

D**b** 878 GAAGTGGCTGCTAAACGGTTTGGATGAGACCTTTTGACCCCTGAGGGTAAGGCAAAACA 937

Qy 1010 TTGGTAGAAACAGATCCCCTGACATCTACAACCTCAAGCTGGTTCACCTCAAAACTGCCA 1069

Db 938 TCGATAATCCTAACCGTGCTGATACATACAATCCAAGAGCTGAAGGGTTACAAATCTCA 997

1070 ACGATCTCAACCTTCTAATACTTAGTGGCTTAGTGGAATATGGAATCTCT 1129

Db 998 ACACCCAGAATTTCCCCATTCTTAGTCTTGACAGATGAGTGCGAGTCAAGTAAATCTAT 1057

Qy 1130 ACAGGAATGCATTTGTTGCTCACTAACACCAAGCACAGCATCATATATCGAT 1189

Db 1058 ACCAGAATGCACCTCCTCTTTACCAATTTGGAACATCAACGGCTCACAGCGTCGTGTATATTA 1117

1190 TGAGGGGACGGGCTCACGTGTCAAGTTCGTGGACAGCAACGGCAACAGAGTGTACGACGAGG 1249

Db 1118 CTCAAGGCGTGCCCGGTTCAAGTTGTCAACAACAATGGAAGACAGTGTTCACGGCG 1177

1250 AGCTTCAAGAGGTCACGTCCTTGTGGTGCCACAGAACTTCGCCGTCGCTGGAAAGTCCC 1309

D6 1178 AGCTTCGCCCGCGGACAGCTGCTATTATATACCAACAACATATGCAGTGTGTAAAGAGAGGCAC 1233

QY  
1310 A GAGCGAGAACTTCGAAATACGTGGCATTCAGACAGACTCAAGSCCCACATAGCCAAC  
1309 | | | | | | | | | | | | | | | | | | | | |  
1308 | | | | | | | | | | | | | | | | | | | | |

1238 AAAAGAGAGAGGAAGTGGCTTACATTCGATTCAGAGACCAATCCCTAACCTCTATGGTAAAGCCACAA 1239

QY 1370 TCGCCGGTGTAATACCTCGCATAGTAACTTCGCCGAGGAGGTGCCTTCAGGATTCATTATG

Db 1298 TTGCAGGAAGAGTTCCATCTTCCTGCTCTCCCAATGATGTTCTAGCAATGCATATC 1357

QY 1430 GCTTCAAAGGGAGCAGGCAAGCGACTTAAGACAACA 1468

Db 1358 GCATCTCAAGAGAAGAGGCTCAGAGGCTCAAGCATAATA 1396

RESULT 7

US-10-449-902-9923  
; Sequence 9923, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9923  
; LENGTH: 1655  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK107271  
; DATABASE ENTRY DATE: 2002-08-28  
US-10-449-902-9923

Query Match 9.5%; Score 145; DB 6; Length 1655;  
Best Local Similarity 55.4%; Pred. No. 8,2e-35;  
Matches 280; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 964 AATGTTATTGAAGAGACGATCTCCACCGCAAGTGCTTAAAGAACATTTGGTAGAAACAGA 1023

Db 942 AATGTTTGGATGAGACCTTTTGTACCATGAGGGTAAGGCAAAATATCGAACCCCAAAAC 1001

QY 1024 TCCCTTGACATCTACAAACCTTCAAGCTGTTCACTCAAACCTGCCAACGATCTCAACCTT 1083

Db 1002 CTGCGAGATACATACAAACCCAGACGAGGAAGGATCACATATCTAAATGGCCAAAGTTC 1061

QY 1084 CTAATACTTAGTGGCTTGGACCTAGTGTGAATATGGAATCTCTACAGGAATGCATTG 1143

Db 1062 CCAATCTTTAATCTTGACAGATGAGTGCCGTTAAAGTAAATTTATATCAGAACGCACTC 1121

QY 1144 TTTGTCGCTCACTACAAACCAACGACACAGCATCATATATCGATTTGAGGGACGGGCT 1203

Db 1122 CTTTCACCTTTTGGAACTCAACGCTCATAGTGTGCTGTATATTACTCAAGGTCGTGCC 1181

QY 1204 CAGTGAAGTCTGTGACACACGCAACGCAACAGATGTACGACAGGCTTCAAGAGGT 1263

Db 1182 CGAGTTCAAGTCGTCAACAAACAAATGGAAGACAGTGTTCATGAGAGCTCCGTCTGTGG 1241

QY 1264 CACGTGCTTGTGTGCCACAGAACTTCGCGCTCGCTGGAAAGTCCACAGACGAGAACTTC 1323

Db 1242 CAGCTTCTAATTAATACCAACACCATGTAGTCAATTAAGAGCAACAAGGGAAGGATGC 1301

QY 1324 GAATACGTGGCATTCAGACAGACTCAAGGCCACGACATAGCCAACTTCGCGGTGAAAC 1383

Db 1302 TCATATATTGCAATGAAACCAACCCCTGACTCCATGGTTAGCCACATGCGCAGGAAAGAAAT 1361

QY 1384 TCCGTATAGATAACCTCGCGAGGAGGTGTTGCAAAATTCATATGCGCTCCAAAGGAG 1443

Db 1362 TCCATCTTCGCGCAGCTTCCTGACGATGTTGTAGCAAAATGCATATCGTATCTCAAGAGAA 1421

QY 1444 CAGCGAAGGCAGCTTAAAGACAACA 1468

Db 1422 GAAGCTAGGAGGCTCAAGCACAACA 1446

RESULT 8

US-10-449-902-9995  
; Sequence 9995, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9995  
; LENGTH: 1650  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK107343  
; DATABASE ENTRY DATE: 2002-08-28  
US-10-449-902-9995

Query Match 9.0%; Score 137; DB 6; Length 1650;  
Best Local Similarity 52.1%; Pred. No. 2,5e-32;  
Matches 305; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

QY 884 AAGAAGAGGAATACGATGAAGATGAATATGAATACGATGAAGAGGATAGAAGCGTGGCA 943

Db 866 AACAGCAAGAACAAGCACAAGCACAAGATCAATATCAACAAGTTCAATACAGTGAACGAC 925

QY 944 GGGGAAGCAGAGCGAGGGGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGCTAAAA 1003

Db 926 AGCAAAACATCTTCTCGATGAAACGGATTGGAGGAGAACTTTTGCAGATCAAGGTGAGAG 985

QY 1004 AGAACATTTGGTAGAAACAGATCCCTTGACATCTACAAACCTCAAGCTGGTTCACTCAAAA 1063

Db 986 TAAACATTTGAAATCTCTAGTGTGATTCATACAAACCACTGCGGGAAGGATAACAA 1045

QY 1064 CTGCCAACGATCTCAACCTTCTAATACTTAGGTGGCTTGGACCTAGTGTGTAATATGGAA 1123

Db 1046 GTGTCAATAGTCAGAAAGTTCCCCATCCTTAAACCTCATCCAAATGAGCGCTACCAGAGTAA 1105

QY 1124 ATCTCTACAGGAATGCATTGTTGTGCTCACTACAAACCAACGACACACAGCATCATAT 1183

Db 1106 ACCATATACCAGAATGCTATTCTCTCGCCGTTCTGGAAACGCTCAATGCTCATAGTTTGGTCT 1165

QY 1184 ATCGATTGAGGGACGGGCTCAGCTGCAAGTCTGTGACACGCAACGCAACAGAGTGTACG 1243

Db 1166 ATATGATTCAAGGGCGATCTCGAGTTCAAGTCTGTTAGTAACTTTGATAGACTGTGTTG 1225

QY 1244 ACGAGAGCTTCAAGAGGTCACGTCCTTGTGGTGGCCACAGAACTTCGCGGTGCTGGAA 1303

Db 1226 ATGGTGTCTTCGCCCAGGACAATTTATGATCATTTCCGCAACATTATGCTGTCTTGAAGA 1285

QY 1304 AGTCCACAGCGAGAACTTCGATACGTCGATTCGAAGTTCAGAGCTCAAGSCCCAGCATAG 1363

Db 1286 AAGCAGAGCGTGAAGGATGCCAATATATCGCAATCAAGAACAAACGTTAACCCCTTGTCA 1345

QY 1364 CCAACCTTCGCGGTGAAAACTCCGTCATAGATAAACCTGCGGAGGAGGTGTTGCAAAAT 1423

Db 1346 GCCACCTTCGAGGGAAGAACTCAGTATTCGTCGCTTGCAGTTGATGTAGTCGCTAATG 1405

QY 1424 CATATGCTCTCCAAAGGAGCGAGGCAAGCGAGCTTAAAGACAACA 1468

Db 1406 CGTATCGCATCTCAAGGAGCAAGCCGGAAGCCTCAAGAAACA 1450

RESULT 9  
US-10-449-902-9890  
; Sequence 9890, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9890  
; LENGTH: 1667  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK107238  
; DATABASE ENTRY DATE: 2002-08-28  
US-10-449-902-9890

Query Match 9.0%; Score 137; DB 6; Length 1667;  
Best Local Similarity 51.3%; Pred. No. 2.5e-32;  
Matches 343; Conservative 0; Mismatches 322; Indels 3; Gaps 1;

QY 801 CGAGAGTGAAGAGAGGAGGCCATTTGTGACAGTGAGGGGAGGCTCAGAAATCTTGAGCCC 860  
Db 785 CCAAAACGACCAAGAGGAGAGATCATACGGGTAAAGAAATGGCCTTAAACTGTTGAGACC 844

QY 861 AGATGAAGAGAGAGCGTCCGACGAAGAGAGGATGATGAAGATGAATATCAATACGA 920  
Db 845 TGCTTTTGCACAACAACAGGAACAAGCAACAGAGGAAACAAGCAAGCTCAATACCA 904

QY 921 TGAAGAGGATAGAAGCGTGGCAGGGAAGCAGAGGCGAGGGGAATGGTATTGAAGAGAC 980  
Db 905 AGTTTCAGTA---CAGTGAAGAAACAACCAACCATCTACCGGTTGCAACGGTTTAGATGAGAA 961

QY 981 GATCTGCACCGCAAGTGCTAAAAGAACATTTGTTAGAAAACAGATCCCTTGACATCTACAA 1040  
Db 962 CTTCTGCACAATCAAGGCAAGGTTGAACATCGAAATCCCTAGCCATGCTGATACTTACAA 1021

QY 1041 CCCTCAAGCTGTTCACTCAAACTGCCAAGATCTCAACCTTCTAATACTTAGTGGCT 1100  
Db 1022 CCCAGTGTGGAAGGATCACAGTCTCAACAGTCAGAGTCTCCCATCTTAACTTGT 1081

QY 1101 TGGACCTAGTGTGAATATGGAATCTCTACAGGAATGCAATTTGTCGCTCACTACAA 1160  
Db 1082 ACAATTGAGTGCTACTAGAGTAATCTATACAGAAATGCTATTCTCTCCGTTTGGAA 1141

QY 1161 CACCAACGCAACAGCATCATATATCGATTGAGGGGACGGGCTCACGTCGAAGTCGTGGA 1220  
Db 1142 CGTTAATGCCCATAGCTGCTGTATATCGTTCAAGGGCATGCTCGAGTTCAGGTCGTAG 1201

QY 1221 CAGCAACGGCAACAGAGTGTTACACGAGGAGCTTCAAGAGGTCACGTCGTTGCTGTC 1280  
Db 1202 TAACTTTGGAAGACGGTATTCAATGCGGTTCTACGTCAGGTCATTTGCTGATCATTC 1261

QY 1281 ACAGAACTTCGCGCTCGCTGGAAGTCCCAAGAGCGAACTTCGAATACGTGGCATTCAA 1340  
Db 1262 GCACACTAGCTGTCTTTGAGAAAGCAGAGCATGAAGATGCCATACATTTCAATTC 1321

QY 1341 GACAGACTCAAGGCCAGCATAGCCAACTCTCGCGGTGAAAACTCCGCTCATAGATACCT 1400

Db 1322 GACCAATGCAAACTCCATGTTGAGCCACCTTGAGCGAAGAACTCAATATTCCTGTCAT 1381

QY 1401 GCGGAGGAGTGTGTTGCAAAATTCATATGCGCTCCAAAGGAGCAGCAGGAGCAGCTTAA 1460  
Db 1382 GCCAGTGGATGTGATCGCTAATGCTTACCGCATATCAGGGAGCAAGCAGGAGCCTTAA 1441

QY 1461 GAACAACA 1468  
Db 1442 GAATAATA 1449

RESULT 10  
US-11-284-201-4  
; Sequence 4, Application US/11284201  
; Publication No. US20060130184A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott, Shane E.  
; APPLICANT: Jung, Rudolf  
; TITLE OF INVENTION: Seed-Preferred Regulatory Elements  
; FILE REFERENCE: 1650  
; CURRENT APPLICATION NUMBER: US/11/284,201  
; CURRENT FILING DATE: 2005-11-21  
; PRIOR APPLICATION NUMBER: 60/634,914  
; PRIOR FILING DATE: 2004-12-10  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1654  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (34)...(1482)  
; OTHER INFORMATION: Legi coding sequence  
US-11-284-201-4

Query Match 8.7%; Score 133; DB 7; Length 1654;  
Best Local Similarity 56.5%; Pred. No. 4.3e-31;  
Matches 247; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 1028 CTGACATCTACACCCCTCAAGCTGGTTCACTCAAACTGCCACGATCTCAACCTTCTAA 1087  
Db 965 CGACGCTCTACAGCCCTGGGCTGGGAGGATCACGCTCACAGCCCAAGTTCCCG 1024

QY 1088 TACTTAGTGGCTTGGACCTAGTGTGTAATATGGAATCTCTACAGGAATGCAATTTGT 1147  
Db 1025 TCCTCAACCTGTACAGATGAGCGGCTGGGGTAGACCTGTACAGGAGCCATCATGT 1084

QY 1148 TCGCTCACTACAAACCAACGACACAGCATCATATATCGATTGAGGGGACGGGCTCAG 1207  
Db 1085 CGCGGTTCTGGAACCTTCAACGCCCAACAGCGCATGTACGCGCATCAGGGGCAAGG 1144

QY 1208 TGCAGTCTGACAGCAGCAACGCGCAACAGAGTGTACAGGAGGCTTCAAGAGGTCAG 1267  
Db 1145 TCAGGTCCCGACGCAACCGGACCCAGCGTGTTCAGACGCTGCTCCGCGGGGAGC 1204

QY 1268 TGCTTGTGTGCCACAACTTCGCGCTCGCTGGAAGTCCCAAGAGCGAGAACTTCGAAT 1327  
Db 1205 TGCTCATCTACCCAGGCTACCTCTGCGCACCAAGGCGCAGGAGAGGCTTCCAGT 1264

QY 1328 AGTGGCATTCAGACAGACTCAAGGCCAGCATAGCCAACTTCGCGGTGAAATTCG 1387  
Db 1265 ACATCGCTTCGAGACGAACCTTGACCATGCTGAGCCACGTCGCGCGGAGAACTCCG 1324

QY 1388 TCATAGATAACCTCGCGAGGAGGTGTTGCAATTCATATGCGCTCCAAAGGAGCAG 1447  
Db 1325 TCTGAGCACTTGGCGCGCGCTCATCGCAGCTCGTATGCCATCTCCATGAGGAAG 1384

QY 1448 CAGGCGCTTAAAGAAC 1464  
Db 1385 CTGCAGAGCTCAAGAAC 1401

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RESULT 11
US-10-449-902-7968
; Sequence 7968, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7968
; LENGTH: 1796
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK105316
; DATABASE ENTRY DATE: 2002-08-28
; US-10-449-902-7968

Query Match          7.0%; Score 107.2; DB 6; Length 1796;
Best Local Similarity 49.8%; Pred. No. 4.5e-23;
Matches 271; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 918 CGATGAAGAGATAGAAAGCGTGGCAGGGGAGCAGAGGAGGGGGAATGTATTGAAGA 977
Db 981 CGACGAGGAGATGATGAGGGGGCCCAACGCCCGCGCGCGCGGGAACGGGATCGACGA 1040

QY 978 GAGCATCTGCACCGCAAGTCTAAAAGAAACATTTGGTAGAAACAGATCCCTCGACATCTA 1037
Db 1041 GGCCTGTCTGTTGATGAAGCTCGCGGAGAACGTCGCGGACCCCGATGAAGGCGCACCTCTA 1100

QY 1038 CAACCTCTAAGCTGGTTTCACTCAAAACTGCGCAACGATCTCAACTTCTAATCTTAGGTG 1097
Db 1101 CACCCCAATGGCGCGCGGATCACCGTCTCAACAGCCAGAGCTCCCGCTCTCAAGCT 1160

QY 1098 GCTTGGACCTAGTGTGAATATGAAATCTTACAGGAATGCAATTTGTTGCTGCTCACTA 1157
Db 1161 CATCAAGATGAGCGTCAACCGCGGCTCATGCGCGGAACGCGATCCTGCGCGCGCACTG 1220

QY 1158 CAACCAACGACACACAGCATCATATATCGATTGAGGGGACGGCTCACGTGCAAGTGT 1217
Db 1221 GAACATCAACGCGCACGCGCGGTGTACGCGACGAGCGGGAGCGGAGCTGCAGGTGGT 1280

QY 1218 GGACAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTCACTGCTTGTGGT 1277
Db 1281 GACGAGGAGGGGGGGGGTGTTCAGCGCGAGCTCCGCGCGGGCAGATGTTGTTGGT 1340

QY 1278 GCCACAGAACTTCGCCGTGCTGGAAGTCCCAGAGCGAGAACTTCGAATACGTGGCAAT 1337
Db 1341 GCCGACAGAGCTTCGCGTGGCGGGCGCGCGCGGACGAGGGTTCGCGTGGTGTGCTT 1400

QY 1338 CAAGACAGACTCAAGGCCAGCATAGCCAACTTCGCGGTGAAATCCGTCATAGATAA 1397
Db 1401 CCAGACGAGGAGCGGCGCCATGAACGCGCGGTGGTTGGCAAGTCGTGCGCGCTGCGCGG 1460

QY 1398 CTTGCGGAGGAGTGGTTTCAATATCATATGCTTCAAGGAGGAGCAGGCAAGGAGCT 1457
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QY 1458 TAAG 1461
Db 1521 CAAG 1524
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RESULT 12
US-10-449-902-3323
; Sequence 3323, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3323
; LENGTH: 1478
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK061022
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-3323

Query Match          2.9%; Score 44.8; DB 6; Length 1478;
Best Local Similarity 51.5%; Pred. No. 0.00086;
Matches 103; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1190 TGAGGGGACGGGCTCACGTGCAAGTGTGTGGACAGCAACGGCAACAGAGTGTACGACGAG 1249
Db 871 TCGGGGGCAGCGGGCGGTGCAGGTGGTGGGATCGACGGGACGCGCTGTGGAGACCC 930

QY 1250 AGTTTCAAGAGGGTCACTGCTTGTGGTGTCCACAGAACTTCCCGCTCGTGGAAAGTCCC 1309
Db 931 GCGCGGAGGGTGGCTTCTTCATCGTCCCGAGGTTCTTCGTGCTCTCCAAGATCGCGG 990

QY 1310 AGAGCGAGAACTTCGAATACGTGGCATTCAGACAGACTCAAGGGCCAGCATAGCCAAAC 1369
Db 991 ACACACCGGATGAGTGTCTCCATCATCACCACTCCCAACCCCATCTTCTCCACC 1050

QY 1370 TCGCGCGTGAAAACTCCCGTC 1389
Db 1051 TCGCGGGAGGACCTCCGTC 1070
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RESULT 13
US-11-260-842-1/c
; Sequence 1, Application US/11260842
; Publication No. US20060115845A1
; GENERAL INFORMATION:
; APPLICANT: Vance, Jeffrey M.
; APPLICANT: Kraus, William E.
; APPLICANT: Goldschmidt, Pascal J.
; APPLICANT: Gregory, Simon G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
; FILE REFERENCE: CARDIOVASCULAR DISEASE
; CURRENT APPLICATION NUMBER: US/11/260,842
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US 60/662,447
; PRIOR FILING DATE: 2004-10-27
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 261789
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-260-842-1
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